Match length	125
% identity	15
NCBI Description	(AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No.	173437
Seq. ID	jC-atXLIB327414P4b02b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	53
E value	3.0e-21
Match length	81
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	173438
Seq. ID	jC-atXLIB327414P4b04a1
Method	BLASTN
NCBI GI	g2358139
BLAST score	39
E value	2.0e-12
Match length	72
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	173439
Seq. ID	jC-atXLIB327414P4b04a2
Method	BLASTX
NCBI GI	g2388562
BLAST score	331
E value	9.0e-31
Match length	72
% identity	85
NCBI Description	(AC000098) EST gb_ATTS0295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	173440
Seq. ID	jC-atXLIB327414P4b05a2
Method	BLASTN
NCBI GI	g4713943
BLAST score	75
E value	6.0e-34
Match length	252
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	173441
Seq. ID	jC-atXLIB327414P4b08a2
Method	BLASTX
NCBI GI	g127045
BLAST score	604
E value	8.0e-63
Match length	144
% identity	82
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	173442
Seq. ID	jC-atXLIB327414P4b09a1
Method	BLASTN
NCBI GI	g4757390
BLAST score	43
E value	2.0e-15
Match length	122
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	173443
Seq. ID	jC-atXLIB327414P4b09a2
Method	BLASTX
NCBI GI	g3269288
BLAST score	420
E value	3.0e-41
Match length	105
% identity	75
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	173444
Seq. ID	jC-atXLIB327414P4c03a2
Method	BLASTX
NCBI GI	g3980254
BLAST score	259
E value	2.0e-22
Match length	144
% identity	37
NCBI Description	(AJ006053) peroxisomal membrane protein [Arabidopsis thaliana] >gi_4773886_gb_AAD29759.1_AF076243_6 (AF076243) pmp22 peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	173445
Seq. ID	jC-atXLIB327414P4c03b2
Method	BLASTN
NCBI GI	g3980253
BLAST score	200
E value	1.0e-108
Match length	200
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for peroxisomal membrane protein

Seq. No.	173446
Seq. ID	jC-atXLIB327414P4c04a2
Method	BLASTX
NCBI GI	g115767
BLAST score	527
E value	9.0e-54
Match length	127

% identity	80
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	173447
Seq. ID	jC-atXLIB327414P4c05a2
Method	BLASTX
NCBI GI	g4263525
BLAST score	179
E value	6.0e-13
Match length	141
% identity	19
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	173448
Seq. ID	jC-atXLIB327414P4c11a2
Method	BLASTX
NCBI GI	g2443755
BLAST score	150
E value	1.0e-09
Match length	143
% identity	29
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	173449
Seq. ID	jC-atXLIB327414P4c12a2
Method	BLASTX
NCBI GI	g4538963
BLAST score	243
E value	1.0e-26
Match length	101
% identity	64
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	173450
Seq. ID	jC-atXLIB327414P4d01a2
Method	BLASTX
NCBI GI	g166702
BLAST score	192
E value	2.0e-14
Match length	85
% identity	55
NCBI Description	(M64114) glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]

Seq. No.	173451
Seq. ID	jC-atXLIB327414P4d03b2
Method	BLASTN
NCBI GI	g4220510

BLAST score 50
E value 5.0e-19
Match length 70
% identity 93
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No. 173452
Seq. ID jC-atXLIB327414P4d05b1
Method BLASTN
NCBI GI g681901
BLAST score 48
E value 9.0e-18
Match length 223
% identity 86
NCBI Description Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No. 173453
Seq. ID jC-atXLIB327414P4d09b1
Method BLASTN
NCBI GI g531828
BLAST score 41
E value 1.0e-13
Match length 75
% identity 89
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 173454
Seq. ID jC-atXLIB327414P4d12a2
Method BLASTX
NCBI GI g2244782
BLAST score 132
E value 6.0e-09
Match length 96
% identity 47
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 173455
Seq. ID jC-atXLIB327414P4e07a2
Method BLASTN
NCBI GI g2827538
BLAST score 100
E value 8.0e-49
Match length 278
% identity 87
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No. 173456
Seq. ID jC-atXLIB327414P4f03b2
Method BLASTX
NCBI GI g2707336
BLAST score 587
E value 1.0e-65
Match length 145
% identity 89

NCBI Description	(AF037442) histone acetyltransferase [Arabidopsis thaliana]

Seq. No.	173457
Seq. ID	jC-atXLIB327414P4f06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173458
Seq. ID	jC-atXLIB327414P4g02a2
Method	BLASTN
NCBI GI	g3241927
BLAST score	200
E value	1.0e-108
Match length	340
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	173459
Seq. ID	jC-atXLIB327414P4g10b1
Method	BLASTN
NCBI GI	g3776000
BLAST score	46
E value	1.0e-16
Match length	50
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12

Seq. No.	173460
Seq. ID	jC-atXLIB327414P4g11a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173461
Seq. ID	jC-atXLIB327414P4g11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	2.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173462
Seq. ID	jC-atXLIB327414P4g12a2
Method	BLASTN

NCBI GI	g434686
BLAST score	66
E value	2.0e-28
Match length	206
% identity	83
NCBI Description	Arabidopsis thaliana ER retention receptor mRNA

Seq. No.	173463
Seq. ID	jC-atXLIB327414P4h02a2
Method	BLASTN
NCBI GI	g2564050
BLAST score	86
E value	2.0e-40
Match length	178
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	173464
Seq. ID	jC-atXLIB327414P4h02b2
Method	BLASTN
NCBI GI	g2564050
BLAST score	79
E value	2.0e-36
Match length	182
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	173465
Seq. ID	jC-atXLIB327414P4h03a2
Method	BLASTN
NCBI GI	g4512656
BLAST score	65
E value	6.0e-28
Match length	214
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	173466
Seq. ID	jC-atXLIB327414P4h04a2
Method	BLASTN
NCBI GI	g4512656
BLAST score	37
E value	3.0e-11
Match length	190
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	173467
Seq. ID	jC-atXLIB327414P4h07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	9.0e-24

Match length	69
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173468
Seq. ID	jC-atXLIB327414P4h08a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173469
Seq. ID	jC-atXLIB327415P1a08a1
Method	BLASTN
NCBI GI	g2145357
BLAST score	48
E value	4.0e-18
Match length	76
% identity	92
NCBI Description	A.thaliana ATHB-9 gene

Seq. No.	173470
Seq. ID	jC-atXLIB327415P1a11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173471
Seq. ID	jC-atXLIB327415P1b02b1
Method	BLASTX
NCBI GI	g2282584
BLAST score	281
E value	5.0e-25
Match length	119
% identity	40
NCBI Description	(U76259) elongation factor 1-alpha [Zea mays]

Seq. No.	173472
Seq. ID	jC-atXLIB327415P1b07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	1.0e-09
Match length	34
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173473

Seq. ID	jC-atXLIB327415P1b08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	7.0e-15
Match length	47
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173474
Seq. ID	jC-atXLIB327415P1c05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	1.0e-12
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173475
Seq. ID	jC-atXLIB327415P1c06b1
Method	BLASTN
NCBI GI	g4713943
BLAST score	103
E value	1.0e-50
Match length	349
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	173476
Seq. ID	jC-atXLIB327415P1c10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173477
Seq. ID	jC-atXLIB327415P1c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	2.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173478
Seq. ID	jC-atXLIB327415P1c11b1
Method	BLASTN
NCBI GI	g2564051
BLAST score	111
E value	2.0e-55
Match length	146

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	173479
Seq. ID	jC-atXLIB327415P1d06a1
Method	BLASTN
NCBI GI	g3702737
BLAST score	108
E value	1.0e-53
Match length	264
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	173480
Seq. ID	jC-atXLIB327415P1e02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	2.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173481
Seq. ID	jC-atXLIB327415P1e02b1
Method	BLASTX
NCBI GI	g4033365
BLAST score	557
E value	2.0e-57
Match length	117
% identity	91
NCBI Description	(AJ223499) ATP sulfurylase [Brassica juncea]

Seq. No.	173482
Seq. ID	jC-atXLIB327415P1e04a1
Method	BLASTN
NCBI GI	g3687221
BLAST score	113
E value	6.0e-57
Match length	192
% identity	70
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173483
Seq. ID	jC-atXLIB327415P1e04b1
Method	BLASTN
NCBI GI	g3687221
BLAST score	97
E value	4.0e-47
Match length	183
% identity	69
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173484
Seq. ID	jC-atXLIB327415P1e05b1
Method	BLASTN
NCBI GI	g1592673
BLAST score	330
E value	0.0e+00
Match length	363
% identity	98
NCBI Description	A.thaliana mRNA for HMG-I/Y protein

Seq. No.	173485
Seq. ID	jC-atXLIB327415P1e06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	4.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173486
Seq. ID	jC-atXLIB327415P1e07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	1.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173487
Seq. ID	jC-atXLIB327415P1e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	2.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173488
Seq. ID	jC-atXLIB327415P1e10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173489
Seq. ID	jC-atXLIB327415P1e11b1
Method	BLASTX
NCBI GI	g1527221
BLAST score	513
E value	1.0e-61

Match length	118
% identity	97
NCBI Description	(U68219) catalase [Brassica napus]

Seq. No.	173490
Seq. ID	jC-atXLIB327415P2a01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173491
Seq. ID	jC-atXLIB327415P2a02a1
Method	BLASTN
NCBI GI	g2853071
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	173492
Seq. ID	jC-atXLIB327415P2a03b2
Method	BLASTN
NCBI GI	g2853071
BLAST score	98
E value	1.0e-47
Match length	226
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	173493
Seq. ID	jC-atXLIB327415P2a05a2
Method	BLASTN
NCBI GI	g2264311
BLAST score	73
E value	8.0e-33
Match length	207
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	173494
Seq. ID	jC-atXLIB327415P2a06a2
Method	BLASTN
NCBI GI	g2264311
BLAST score	364
E value	0.0e+00
Match length	376
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	173495
Seq. ID	jC-atXLIB327415P2a07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173496
Seq. ID	jC-atXLIB327415P2a09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	5.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173497
Seq. ID	jC-atXLIB327415P2a11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	57
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173498
Seq. ID	jC-atXLIB327415P2a11a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173499
Seq. ID	jC-atXLIB327415P2b02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	9.0e-21
Match length	73
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173500
Seq. ID	jC-atXLIB327415P2b07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	58

E value	9.0e-24
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173501
Seq. ID	jC-atXLIB327415P2b07b1
Method	BLASTN
NCBI GI	g3264774
BLAST score	43
E value	2.0e-15
Match length	47
% identity	98
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	173502
Seq. ID	jC-atXLIB327415P2b08a2
Method	BLASTN
NCBI GI	g3763944
BLAST score	109
E value	3.0e-54
Match length	295
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	173503
Seq. ID	jC-atXLIB327415P2c03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	8.0e-17
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173504
Seq. ID	jC-atXLIB327415P2c05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	1.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173505
Seq. ID	jC-atXLIB327415P2c06a2
Method	BLASTX
NCBI GI	g4056433
BLAST score	182
E value	2.0e-13
Match length	64
% identity	48
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	173506
Seq. ID	jC-atXLIB327415P2c09a2
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	2.0e-11
Match length	45
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173507
Seq. ID	jC-atXLIB327415P2c10a2
Method	BLASTN
NCBI GI	g540252
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173508
Seq. ID	jC-atXLIB327415P2c11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	3.0e-12
Match length	66
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173509
Seq. ID	jC-atXLIB327415P2c12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	7.0e-21
Match length	69
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173510
Seq. ID	jC-atXLIB327415P2c12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	1.0e-18
Match length	53
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173511
Seq. ID	jC-atXLIB327415P2d01b2
Method	BLASTN
NCBI GI	g166701

BLAST score	41
E value	1.0e-13
Match length	41
% identity	100
NCBI Description	Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase A subunit (GapA) mRNA, complete cds

Seq. No.	173512
Seq. ID	jC-atXLIB327415P2d06a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	1.0e-22
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173513
Seq. ID	jC-atXLIB327415P2d08a1
Method	BLASTN
NCBI GI	g2213606
BLAST score	55
E value	3.0e-22
Match length	171
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	173514
Seq. ID	jC-atXLIB327415P2d08a2
Method	BLASTX
NCBI GI	g2213629
BLAST score	296
E value	1.0e-26
Match length	71
% identity	82
NCBI Description	(AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No.	173515
Seq. ID	jC-atXLIB327415P2d08b1
Method	BLASTN
NCBI GI	g2213606
BLAST score	49
E value	2.0e-18
Match length	80
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	173516
Seq. ID	jC-atXLIB327415P2d09b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	114
E value	3.0e-57
Match length	218

% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	173517
Seq. ID	jC-atXLIB327415P2d11a1
Method	BLASTX
NCBI GI	g2661422
BLAST score	432
E value	9.0e-43
Match length	91
% identity	96
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	173518
Seq. ID	jC-atXLIB327415P2e01a2
Method	BLASTN
NCBI GI	g540252
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173519
Seq. ID	jC-atXLIB327415P2e05b2
Method	BLASTN
NCBI GI	g2459406
BLAST score	70
E value	7.0e-31
Match length	189
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173520
Seq. ID	jC-atXLIB327415P2e09a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	58
E value	6.0e-24
Match length	62
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173521
Seq. ID	jC-atXLIB327415P2e09b2
Method	BLASTX
NCBI GI	g1931637
BLAST score	273
E value	2.0e-24
Match length	81
% identity	69

NCBI Description	(U95973) receptor-associated kinase isolog [Arabidopsis thaliana]

Seq. No.	173522
Seq. ID	jC-atXLIB327415P2f05a2
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19
Match length	70
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173523
Seq. ID	jC-atXLIB327415P2f06a2
Method	BLASTN
NCBI GI	g3128476
BLAST score	62
E value	4.0e-26
Match length	82
% identity	94
NCBI Description	Arabidopsis thaliana metalloproteinase mRNA, complete cds

Seq. No.	173524
Seq. ID	jC-atXLIB327415P2f07b2
Method	BLASTX
NCBI GI	g112741
BLAST score	126
E value	2.0e-29
Match length	137
% identity	34
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	173525
Seq. ID	jC-atXLIB327415P2f09a1
Method	BLASTN
NCBI GI	g2285791
BLAST score	173
E value	1.0e-92
Match length	196
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for cyanase, complete cds

Seq. No.	173526
Seq. ID	jC-atXLIB327415P2f11a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	203
E value	1.0e-110
Match length	275
% identity	94

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	173527
Seq. ID	jC-atXLIB327415P2g01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173528
Seq. ID	jC-atXLIB327415P2g05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	1.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173529
Seq. ID	jC-atXLIB327415P2h02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	4.0e-17
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173530
Seq. ID	jC-atXLIB327415P2h03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	71
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173531
Seq. ID	jC-atXLIB327415P2h04a2
Method	BLASTN
NCBI GI	g2924734
BLAST score	232
E value	1.0e-127
Match length	367
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	173532
Seq. ID	jC-atXLIB327415P2h07b2
Method	BLASTX
NCBI GI	g1402904
BLAST score	305
E value	5.0e-40
Match length	117
% identity	71
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	173533
Seq. ID	jC-atXLIB327415P3a11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	2.0e-11
Match length	45
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173534
Seq. ID	jC-atXLIB327415P3b04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173535
Seq. ID	jC-atXLIB327415P3b06b1
Method	BLASTN
NCBI GI	g4678371
BLAST score	185
E value	2.0e-99
Match length	257
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	173536
Seq. ID	jC-atXLIB327415P3b07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	1.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173537
Seq. ID	jC-atXLIB327415P3b07b1
Method	BLASTN

NCBI GI	g2582640
BLAST score	47
E value	4.0e-17
Match length	71
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173538
Seq. ID	jC-atXLIB327415P3b09b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	43
E value	8.0e-15
Match length	51
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	173539
Seq. ID	jC-atXLIB327415P3b12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	1.0e-25
Match length	77
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173540
Seq. ID	jC-atXLIB327415P3c07b1
Method	BLASTN
NCBI GI	g3426033
BLAST score	111
E value	2.0e-55
Match length	148
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173541
Seq. ID	jC-atXLIB327415P3c09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173542
Seq. ID	jC-atXLIB327415P3c10b1
Method	BLASTN
NCBI GI	g3548797
BLAST score	262

E value	1.0e-145
Match length	293
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173543
Seq. ID	jC-atXLIB327415P3d01b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	230
E value	6.0e-19
Match length	47
% identity	100
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	173544
Seq. ID	jC-atXLIB327415P3d02b1
Method	BLASTN
NCBI GI	g2924653
BLAST score	103
E value	1.0e-50
Match length	198
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	173545
Seq. ID	jC-atXLIB327415P3d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	3.0e-20
Match length	60
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173546
Seq. ID	jC-atXLIB327415P3d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173547
Seq. ID	jC-atXLIB327415P3d07b1
Method	BLASTN
NCBI GI	g2341023
BLAST score	71
E value	1.0e-31
Match length	123
% identity	92

NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	173548
Seq. ID	jC-atXLIB327415P3e04b1
Method	BLASTN
NCBI GI	g4678258
BLAST score	134
E value	4.0e-69
Match length	134
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)
Seq. No.	173549
Seq. ID	jC-atXLIB327415P3e06b1
Method	BLASTN
NCBI GI	g3341671
BLAST score	46
E value	1.0e-16
Match length	46
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	173550
Seq. ID	jC-atXLIB327415P3e07b1
Method	BLASTX
NCBI GI	g129232
BLAST score	155
E value	4.0e-10
Match length	48
% identity	62
NCBI Description	ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain (EC 3.4.22.-) beta precursor - rice >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor [Oryza sativa]
Seq. No.	173551
Seq. ID	jC-atXLIB327415P3e08a1
Method	BLASTX
NCBI GI	g4309722
BLAST score	434
E value	8.0e-43
Match length	85
% identity	100
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]
Seq. No.	173552
Seq. ID	jC-atXLIB327415P3e11b1
Method	BLASTN
NCBI GI	g3063438
BLAST score	129
E value	4.0e-66
Match length	333
% identity	96
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence

[Arabidopsis thaliana]

Seq. No.	173553
Seq. ID	jC-atXLIB327415P3f05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173554
Seq. ID	jC-atXLIB327415P3f07b1
Method	BLASTN
NCBI GI	g3395421
BLAST score	100
E value	8.0e-49
Match length	104
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173555
Seq. ID	jC-atXLIB327415P3f08b1
Method	BLASTN
NCBI GI	g4056476
BLAST score	247
E value	1.0e-136
Match length	267
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173556
Seq. ID	jC-atXLIB327415P3f10b1
Method	BLASTN
NCBI GI	g2477521
BLAST score	298
E value	1.0e-167
Match length	313
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173557
Seq. ID	jC-atXLIB327415P3h02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	5.0e-15
Match length	43
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173558
Seq. ID	jC-atXLIB327415P3h03b1

Method	BLASTN
NCBI GI	g11486
BLAST score	49
E value	2.0e-18
Match length	81
% identity	94
NCBI Description	Euglena gracilis chloroplast 23S ribosomal RNA gene

Seq. No.	173559
Seq. ID	jC-atXLIB327415P3h12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173560
Seq. ID	jC-atXLIB327415P4a01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	73
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173561
Seq. ID	jC-atXLIB327415P4a09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173562
Seq. ID	jC-atXLIB327415P4a09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173563
Seq. ID	jC-atXLIB327415P4c12a1
Method	BLASTN
NCBI GI	g4734011
BLAST score	380
E value	0.0e+00
Match length	392

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	173564
Seq. ID	jC-atXLIB327415P4d10a1
Method	BLASTN
NCBI GI	g681901
BLAST score	292
E value	1.0e-163
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No.	173565
Seq. ID	jC-atXLIB327415P4f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	3.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173566
Seq. ID	jC-atXLIB327415P4f12a1
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	7.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173567
Seq. ID	jC-atXLIB327415P4g01a1
Method	BLASTN
NCBI GI	g3869068
BLAST score	376
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	173568
Seq. ID	jC-atXLIB327415P4g02b1
Method	BLASTX
NCBI GI	g730456
BLAST score	436
E value	4.0e-43
Match length	118
% identity	65
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	173569
Seq. ID	jC-atXLIB327415P4h01a1
Method	BLASTN
NCBI GI	g3869068
BLAST score	211
E value	1.0e-115
Match length	373
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	173570
Seq. ID	jC-atXLIB327415P4h01b1
Method	BLASTN
NCBI GI	g3869068
BLAST score	68
E value	1.0e-29
Match length	264
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	173571
Seq. ID	jC-atXLIB327415P4h04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173572
Seq. ID	jC-atXLIB327415P4h04b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	33
E value	7.0e-09
Match length	49
% identity	94
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	173573
Seq. ID	jC-atXLIB327415P4h06a1
Method	BLASTN
NCBI GI	g540252
BLAST score	51
E value	1.0e-19
Match length	59
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173574
Seq. ID	jC-atXLIB327416P1a09a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173575
Seq. ID	jC-atXLIB327416P1a09b1
Method	BLASTX
NCBI GI	g550486
BLAST score	160
E value	1.0e-10
Match length	80
% identity	47
NCBI Description	(L36530) pyruvate carboxylase [Aedes aegypti]

Seq. No.	173576
Seq. ID	jC-atXLIB327416P1c05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	4.0e-17
Match length	66
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173577
Seq. ID	jC-atXLIB327416P1d04a1
Method	BLASTX
NCBI GI	g3928103
BLAST score	336
E value	2.0e-31
Match length	63
% identity	98
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	173578
Seq. ID	jC-atXLIB327416P1d10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	49
E value	2.0e-18
Match length	64
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173579
Seq. ID	jC-atXLIB327416P1e03b1
Method	BLASTX
NCBI GI	g1905876
BLAST score	698
E value	9.0e-74
Match length	144
% identity	94
NCBI Description	(U90879) biotin carboxylase subunit [Arabidopsis thaliana]

	>gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]
Seq. No.	173580
Seq. ID	jC-atXLIB327416P1e04b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	5.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds
Seq. No.	173581
Seq. ID	jC-atXLIB327416P1e06a1
Method	BLASTX
NCBI GI	g2244750
BLAST score	240
E value	5.0e-20
Match length	45
% identity	100
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]
Seq. No.	173582
Seq. ID	jC-atXLIB327416P1f03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	173583
Seq. ID	jC-atXLIB327416P1f07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	1.0e-19
Match length	66
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	173584
Seq. ID	jC-atXLIB327416P1f11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	49
E value	2.0e-18
Match length	64
% identity	94

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173585
Seq. ID	jC-atXLIB327416P1g03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173586
Seq. ID	jC-atXLIB327416P1g04b1
Method	BLASTN
NCBI GI	g4159700
BLAST score	232
E value	1.0e-127
Match length	339
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	173587
Seq. ID	jC-atXLIB327416P1g05a1
Method	BLASTN
NCBI GI	g16553
BLAST score	175
E value	1.0e-93
Match length	292
% identity	90
NCBI Description	A.thaliana mRNA for eukaryotic translation initiation factor 4A-1

Seq. No.	173588
Seq. ID	jC-atXLIB327416P1g05b1
Method	BLASTX
NCBI GI	g1170503
BLAST score	491
E value	2.0e-49
Match length	125
% identity	80
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	173589
Seq. ID	jC-atXLIB327416P1g08b1
Method	BLASTX
NCBI GI	g3511223
BLAST score	658
E value	4.0e-69
Match length	144
% identity	90

NCBI Description	(AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]

Seq. No.	173590
Seq. ID	jC-atXLIB327416P1h01a1
Method	BLASTN
NCBI GI	g3241926
BLAST score	63
E value	8.0e-27
Match length	83
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	173591
Seq. ID	jC-atXLIB327416P1h05b1
Method	BLASTX
NCBI GI	g3075394
BLAST score	742
E value	6.0e-79
Match length	148
% identity	98
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	173592
Seq. ID	jC-atXLIB327416P1h08a1
Method	BLASTN
NCBI GI	g4757678
BLAST score	41
E value	1.0e-13
Match length	109
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	173593
Seq. ID	jC-atXLIB327416P1h10b1
Method	BLASTX
NCBI GI	g1703108
BLAST score	176
E value	2.0e-14
Match length	104
% identity	55
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	173594
Seq. ID	jC-atXLIB327416P2a03b1
Method	BLASTX
NCBI GI	g2191153
BLAST score	137
E value	5.0e-08
Match length	115

% identity	24
NCBI Description	(AF007269) contains similarity to blue copper proteins [Arabidopsis thaliana]

Seq. No.	173595
Seq. ID	jC-atXLIB327416P2a07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	5.0e-09
Match length	37
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173596
Seq. ID	jC-atXLIB327416P2b04a1
Method	BLASTN
NCBI GI	g16491
BLAST score	92
E value	4.0e-44
Match length	124
% identity	94
NCBI Description	A. thaliana mRNA for root-specific gene

Seq. No.	173597
Seq. ID	jC-atXLIB327416P2b07b1
Method	BLASTX
NCBI GI	g115783
BLAST score	735
E value	4.0e-78
Match length	143
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	173598
Seq. ID	jC-atXLIB327416P2b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173599
Seq. ID	jC-atXLIB327416P2b10b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	308
E value	3.0e-38
Match length	117
% identity	75
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	173600
Seq. ID	jC-atXLIB327416P2c01b1
Method	BLASTN
NCBI GI	g16251
BLAST score	59
E value	2.0e-24
Match length	170
% identity	87
NCBI Description	A.thaliana mRNA DRT

Seq. No.	173601
Seq. ID	jC-atXLIB327416P2c04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173602
Seq. ID	jC-atXLIB327416P2c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173603
Seq. ID	jC-atXLIB327416P2d10b1
Method	BLASTX
NCBI GI	g2191135
BLAST score	282
E value	4.0e-25
Match length	138
% identity	45
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	173604
Seq. ID	jC-atXLIB327416P2f11a1
Method	BLASTN
NCBI GI	g16491
BLAST score	105
E value	8.0e-52
Match length	248
% identity	87
NCBI Description	A. thaliana mRNA for root-specific gene

Seq. No.	173605
Seq. ID	jC-atXLIB327416P2h06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33

E value	7.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173606
Seq. ID	jC-atXLIB327416P2h06b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	173607
Seq. ID	jC-atXLIB327416P2h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	76
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173608
Seq. ID	jC-atXLIB327416P3a09b1
Method	BLASTX
NCBI GI	g550486
BLAST score	226
E value	2.0e-18
Match length	97
% identity	51
NCBI Description	(L36530) pyruvate carboxylase [Aedes aegypti]

Seq. No.	173609
Seq. ID	jC-atXLIB327416P3a10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	6.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173610
Seq. ID	jC-atXLIB327416P3a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173611
Seq. ID	jC-atXLIB327416P3a11b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	173612
Seq. ID	jC-atXLIB327416P3b01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173613
Seq. ID	jC-atXLIB327416P3b01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	8.0e-12
Match length	46
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173614
Seq. ID	jC-atXLIB327416P3b02b1
Method	BLASTX
NCBI GI	g1552344
BLAST score	399
E value	9.0e-39
Match length	136
% identity	57
NCBI Description	(Y08020) heat shock protein 70 [Leishmania infantum]

Seq. No.	173615
Seq. ID	jC-atXLIB327416P3b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173616
Seq. ID	jC-atXLIB327416P3b04b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173617
Seq. ID	jC-atXLIB327416P3c01b1
Method	BLASTX
NCBI GI	g2244750
BLAST score	581
E value	4.0e-60
Match length	124
% identity	89
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	173618
Seq. ID	jC-atXLIB327416P3c03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	64
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173619
Seq. ID	jC-atXLIB327416P3c04b1
Method	BLASTX
NCBI GI	g4337027
BLAST score	697
E value	1.0e-73
Match length	140
% identity	99
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	173620
Seq. ID	jC-atXLIB327416P3c05b1
Method	BLASTX
NCBI GI	g2245118
BLAST score	281
E value	6.0e-25
Match length	103
% identity	62
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	173621
Seq. ID	jC-atXLIB327416P3c08a1
Method	BLASTX
NCBI GI	g1778093
BLAST score	338
E value	1.0e-31
Match length	121

% identity	56
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	173622
Seq. ID	jC-atXLIB327416P3c09b1
Method	BLASTN
NCBI GI	g4589436
BLAST score	93
E value	1.0e-44
Match length	371
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	173623
Seq. ID	jC-atXLIB327416P3c11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173624
Seq. ID	jC-atXLIB327416P3c12a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	269
E value	1.0e-149
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	173625
Seq. ID	jC-atXLIB327416P3d01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173626
Seq. ID	jC-atXLIB327416P3d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173627
Seq. ID	jC-atXLIB327416P3d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173628
Seq. ID	jC-atXLIB327416P3d07a1
Method	BLASTN
NCBI GI	g1946354
BLAST score	330
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	173629
Seq. ID	jC-atXLIB327416P3e06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173630
Seq. ID	jC-atXLIB327416P3e06b1
Method	BLASTX
NCBI GI	g2160189
BLAST score	89
E value	2.0e-10
Match length	149
% identity	4
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	173631
Seq. ID	jC-atXLIB327416P3e09a1
Method	BLASTN
NCBI GI	g3046855
BLAST score	340
E value	0.0e+00
Match length	409
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	173632
Seq. ID	jC-atXLIB327416P3f01a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173633
Seq. ID	jC-atXLIB327416P3f01b1
Method	BLASTN
NCBI GI	g3510343
BLAST score	421
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	173634
Seq. ID	jC-atXLIB327416P3f04b1
Method	BLASTX
NCBI GI	g1076442
BLAST score	612
E value	1.0e-63
Match length	137
% identity	78
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	173635
Seq. ID	jC-atXLIB327416P3f06a1
Method	BLASTX
NCBI GI	g1076362
BLAST score	167
E value	1.0e-11
Match length	57
% identity	65
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_804948_emb_CAA85388_ (Z36911) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	173636
Seq. ID	jC-atXLIB327416P3f06b1
Method	BLASTX
NCBI GI	g1076360
BLAST score	226
E value	4.0e-67
Match length	132
% identity	93
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis thaliana >gi_634003_emb_CAA85387_ (Z36910) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	173637
Seq. ID	jC-atXLIB327416P3g01b1
Method	BLASTX
NCBI GI	g2642443
BLAST score	374
E value	8.0e-36
Match length	119
% identity	64
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	173638
Seq. ID	jC-atXLIB327416P3g02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173639
Seq. ID	jC-atXLIB327416P3g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173640
Seq. ID	jC-atXLIB327416P3h01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173641
Seq. ID	jC-atXLIB327416P3h03a1
Method	BLASTN
NCBI GI	g3510343
BLAST score	406
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	173642
Seq. ID	jC-atXLIB327416P3h05a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	45
E value	5.0e-16
Match length	57
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173643
Seq. ID	jC-atXLIB327416P3h05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173644
Seq. ID	jC-atXLIB327416P3h12a1
Method	BLASTN
NCBI GI	g2760173
BLAST score	374
E value	0.0e+00
Match length	394
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	173645
Seq. ID	jC-atXLIB327416P4c06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173646
Seq. ID	jC-atXLIB327416P4d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173647
Seq. ID	jC-atXLIB327417P1a02a1
Method	BLASTX
NCBI GI	g3047078
BLAST score	44
E value	4.0e-74
Match length	153
% identity	95

NCBI Description	(AF058914) similar to 11-S seed storage proteins (Pfam: Seedstore_11s.hmm, score: 19.95) [Arabidopsis thaliana]

Seq. No.	173648
Seq. ID	jC-atXLIB327417P1a05b1
Method	BLASTX
NCBI GI	g2459417
BLAST score	217
E value	2.0e-17
Match length	72
% identity	67
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	173649
Seq. ID	jC-atXLIB327417P1a07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173650
Seq. ID	jC-atXLIB327417P1b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	3.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173651
Seq. ID	jC-atXLIB327417P1b05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	6.0e-21
Match length	72
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173652
Seq. ID	jC-atXLIB327417P1b08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	4.0e-21
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173653
Seq. ID	jC-atXLIB327417P1b11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	2.0e-09
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173654
Seq. ID	jC-atXLIB327417P1c02a1
Method	BLASTN
NCBI GI	g3176694
BLAST score	71
E value	3.0e-31
Match length	307
% identity	81
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173655
Seq. ID	jC-atXLIB327417P1c10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	7.0e-12
Match length	58
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173656
Seq. ID	jC-atXLIB327417P1d04b1
Method	BLASTN
NCBI GI	g1293564
BLAST score	109
E value	2.0e-54
Match length	205
% identity	89
NCBI Description	Arabidopsis thaliana isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP2) mRNA, complete cds

Seq. No.	173657
Seq. ID	jC-atXLIB327417P1d05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173658
Seq. ID	jC-atXLIB327417P1d07a1
Method	BLASTN

NCBI GI	g3641835
BLAST score	158
E value	2.0e-83
Match length	311
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	173659
Seq. ID	jC-atXLIB327417P1d12b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	173660
Seq. ID	jC-atXLIB327417P1f07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	2.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173661
Seq. ID	jC-atXLIB327417P1g09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	3.0e-15
Match length	66
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173662
Seq. ID	jC-atXLIB327417P1h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	4.0e-11
Match length	45
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173663
Seq. ID	jC-atXLIB327417P1h05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	2.0e-11

Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173664
Seq. ID	jC-atXLIB327417P1h12a1
Method	BLASTX
NCBI GI	g1418335
BLAST score	337
E value	3.0e-31
Match length	86
% identity	78
NCBI Description	(X98672) zinc finger protein [Arabidopsis thaliana]

Seq. No.	173665
Seq. ID	jC-atXLIB327417P2a05b1
Method	BLASTN
NCBI GI	g4589451
BLAST score	90
E value	8.0e-43
Match length	197
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T32G24, complete sequence

Seq. No.	173666
Seq. ID	jC-atXLIB327417P2a06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173667
Seq. ID	jC-atXLIB327417P2a06b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	62
E value	5.0e-26
Match length	178
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	173668
Seq. ID	jC-atXLIB327417P2b06a1
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173669
Seq. ID	jC-atXLIB327417P2c01a1
Method	BLASTN
NCBI GI	g4220640
BLAST score	53
E value	9.0e-21
Match length	187
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	173670
Seq. ID	jC-atXLIB327417P2c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173671
Seq. ID	jC-atXLIB327417P2d05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	7.0e-11
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173672
Seq. ID	jC-atXLIB327417P2d06b1
Method	BLASTN
NCBI GI	g3108025
BLAST score	79
E value	2.0e-36
Match length	119
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	173673
Seq. ID	jC-atXLIB327417P2e12a1
Method	BLASTX
NCBI GI	g4678368
BLAST score	275
E value	3.0e-24
Match length	50
% identity	100
NCBI Description	(AJ132436) GA 2-oxidase [Arabidopsis thaliana]

Seq. No.	173674
Seq. ID	jC-atXLIB327417P2f07a1
Method	BLASTN
NCBI GI	g3449332

BLAST score	384
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSF19, complete sequence [Arabidopsis thaliana]

Seq. No.	173675
Seq. ID	jC-atXLIB327417P2f07b1
Method	BLASTN
NCBI GI	g3449332
BLAST score	118
E value	2.0e-59
Match length	437
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSF19, complete sequence [Arabidopsis thaliana]

Seq. No.	173676
Seq. ID	jC-atXLIB327417P2g01a1
Method	BLASTN
NCBI GI	g166899
BLAST score	59
E value	2.0e-24
Match length	107
% identity	93
NCBI Description	Arabidopsis thaliana bete-3 tubulin (TUB3) gene, complete cds

Seq. No.	173677
Seq. ID	jC-atXLIB327417P2g01b1
Method	BLASTX
NCBI GI	g4165490
BLAST score	219
E value	9.0e-18
Match length	93
% identity	54
NCBI Description	(AJ132400) beta-tubulin 2 [Hordeum vulgare]

Seq. No.	173678
Seq. ID	jC-atXLIB327417P2g05a1
Method	BLASTN
NCBI GI	g4309683
BLAST score	128
E value	2.0e-65
Match length	230
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173679
Seq. ID	jC-atXLIB327417P2g08b1
Method	BLASTN
NCBI GI	g2264305
BLAST score	326
E value	0.0e+00
Match length	467

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	173680
Seq. ID	jC-atXLIB327417P2h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173681
Seq. ID	jC-atXLIB327417P2h05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	3.0e-17
Match length	73
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173682
Seq. ID	jC-atXLIB327417P2h06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173683
Seq. ID	jC-atXLIB327417P2h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173684
Seq. ID	jC-atXLIB327417P2h09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	6.0e-14
Match length	78
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173685

Seq. ID	jC-atXLIB327417P2h10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173686
Seq. ID	jC-atXLIB327417P2h12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173687
Seq. ID	jC-atXLIB327417P3a02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	6.0e-15
Match length	51
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173688
Seq. ID	jC-atXLIB327417P3a03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	9.0e-27
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173689
Seq. ID	jC-atXLIB327417P3a05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	1.0e-15
Match length	60
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173690
Seq. ID	jC-atXLIB327417P3a08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54

% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173691
Seq. ID	jC-atXLIB327417P3a10a1
Method	BLASTN
NCBI GI	g2749918
BLAST score	36
E value	9.0e-11
Match length	60
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173692
Seq. ID	jC-atXLIB327417P3a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173693
Seq. ID	jC-atXLIB327417P3b03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	1.0e-20
Match length	64
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173694
Seq. ID	jC-atXLIB327417P3b04a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	290
E value	1.0e-162
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	173695
Seq. ID	jC-atXLIB327417P3b07a1
Method	BLASTN
NCBI GI	g499163
BLAST score	93
E value	8.0e-45
Match length	181
% identity	88
NCBI Description	A.thaliana mRNA Athb-7

Seq. No. 173696

Seq. ID	jC-atXLIB327417P3c02a1
Method	BLASTX
NCBI GI	g2935342
BLAST score	365
E value	5.0e-35
Match length	84
% identity	81
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No.	173697
Seq. ID	jC-atXLIB327417P3c04a1
Method	BLASTN
NCBI GI	g4589435
BLAST score	103
E value	9.0e-51
Match length	211
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	173698
Seq. ID	jC-atXLIB327417P3c06b1
Method	BLASTX
NCBI GI	g4584546
BLAST score	481
E value	3.0e-48
Match length	202
% identity	51
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	173699
Seq. ID	jC-atXLIB327417P3c08b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	324
E value	0.0e+00
Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	173700
Seq. ID	jC-atXLIB327417P3d02a1
Method	BLASTN
NCBI GI	g166633
BLAST score	120
E value	7.0e-61
Match length	251
% identity	98
NCBI Description	Arabidopsis thaliana vacuolar H+ - pyrophosphatase (AVP-3) mRNA, complete cds

Seq. No.	173701
Seq. ID	jC-atXLIB327417P3d04a1
Method	BLASTX
NCBI GI	g2146741

BLAST score	93
E value	4.0e-15
Match length	45
% identity	98
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	173702
Seq. ID	jC-atXLIB327417P3d07a1
Method	BLASTN
NCBI GI	g2275194
BLAST score	60
E value	4.0e-25
Match length	242
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173703
Seq. ID	jC-atXLIB327417P3d10a1
Method	BLASTN
NCBI GI	g3046851
BLAST score	219
E value	1.0e-120
Match length	261
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	173704
Seq. ID	jC-atXLIB327417P3d11a1
Method	BLASTN
NCBI GI	g3687221
BLAST score	117
E value	4.0e-59
Match length	231
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173705
Seq. ID	jC-atXLIB327417P3f01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	1.0e-12
Match length	51
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173706
Seq. ID	jC-atXLIB327417P3f02a1
Method	BLASTN
NCBI GI	g166899
BLAST score	59

E value	2.0e-24
Match length	95
% identity	91
NCBI Description	Arabidopsis thaliana bete-3 tubulin (TUB3) gene, complete cds

Seq. No.	173707
Seq. ID	jC-atXLIB327417P3f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	4.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173708
Seq. ID	jC-atXLIB327417P3h03a1
Method	BLASTX
NCBI GI	g543751
BLAST score	206
E value	3.0e-16
Match length	42
% identity	98
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir__JT0755 ethylene-forming enzyme - Arabidopsis thaliana >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme [Arabidopsis thaliana]

Seq. No.	173709
Seq. ID	jC-atXLIB327417P3h05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	4.0e-16
Match length	49
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173710
Seq. ID	jC-atXLIB327417P3h07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	7.0e-17
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173711
Seq. ID	jC-atXLIB327417P3h09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	5.0e-12

Match length	54
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173712
Seq. ID	jC-atXLIB327417P4a01a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	258
E value	1.0e-143
Match length	437
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	173713
Seq. ID	jC-atXLIB327417P4a06a1
Method	BLASTX
NCBI GI	g544018
BLAST score	244
E value	1.0e-20
Match length	84
% identity	67
NCBI Description	NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from this gene. [Arabidopsis thaliana]

Seq. No.	173714
Seq. ID	jC-atXLIB327417P4a09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173715
Seq. ID	jC-atXLIB327417P4a12a1
Method	BLASTX
NCBI GI	g2829910
BLAST score	205
E value	6.0e-16
Match length	61
% identity	56
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	173716
Seq. ID	jC-atXLIB327417P4b01a1
Method	BLASTN

NCBI GI	g2894557
BLAST score	98
E value	1.0e-47
Match length	331
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	173717
Seq. ID	jC-atXLIB327417P4b07a1
Method	BLASTX
NCBI GI	g3169569
BLAST score	209
E value	1.0e-16
Match length	56
% identity	77
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	173718
Seq. ID	jC-atXLIB327417P4b07b1
Method	BLASTX
NCBI GI	g3169569
BLAST score	214
E value	2.0e-17
Match length	74
% identity	66
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	173719
Seq. ID	jC-atXLIB327417P4c01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173720
Seq. ID	jC-atXLIB327417P4c01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	8.0e-24
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173721
Seq. ID	jC-atXLIB327417P4c06a1
Method	BLASTN
NCBI GI	g4757678

BLAST score	51
E value	2.0e-19
Match length	171
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	173722
Seq. ID	jC-atXLIB327417P4c06b1
Method	BLASTX
NCBI GI	g1806146
BLAST score	128
E value	2.0e-19
Match length	112
% identity	56
NCBI Description	(X97317) cdc2MsF [Medicago sativa]

Seq. No.	173723
Seq. ID	jC-atXLIB327417P4c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173724
Seq. ID	jC-atXLIB327417P4d01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	8.0e-15
Match length	47
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173725
Seq. ID	jC-atXLIB327417P4d01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	9.0e-25
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173726
Seq. ID	jC-atXLIB327417P4d05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173727
Seq. ID	jC-atXLIB327417P4d07b1
Method	BLASTN
NCBI GI	g2288979
BLAST score	29
E value	2.0e-06
Match length	306
% identity	66
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173728
Seq. ID	jC-atXLIB327417P4d10b1
Method	BLASTX
NCBI GI	g2970034
BLAST score	394
E value	1.0e-49
Match length	113
% identity	84
NCBI Description	(D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	173729
Seq. ID	jC-atXLIB327417P4d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173730
Seq. ID	jC-atXLIB327417P4e03a1
Method	BLASTN
NCBI GI	g2529657
BLAST score	83
E value	8.0e-39
Match length	271
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173731
Seq. ID	jC-atXLIB327417P4e03b1
Method	BLASTX
NCBI GI	g2529680
BLAST score	226
E value	2.0e-18
Match length	135
% identity	22
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No.	173732
Seq. ID	jC-atXLIB327417P4f03a1
Method	BLASTN

NCBI GI	g2290120
BLAST score	55
E value	5.0e-22
Match length	62
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173733
Seq. ID	jC-atXLIB327417P4f09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173734
Seq. ID	jC-atXLIB327417P4f12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173735
Seq. ID	jC-atXLIB327417P4g03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173736
Seq. ID	jC-atXLIB327417P4g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173737
Seq. ID	jC-atXLIB327417P4g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	9.0e-24
Match length	70

% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173738
Seq. ID	jC-atXLIB327417P4h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173739
Seq. ID	jC-atXLIB327417P4h05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	9.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173740
Seq. ID	jC-atXLIB327417P4h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	3.0e-26
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173741
Seq. ID	jC-atXLIB327417P4h08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173742
Seq. ID	jC-atXLIB327417P4h08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173743

Seq. ID	jC-atXLIB327417P4h09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	3.0e-14
Match length	64
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173744
Seq. ID	jC-atXLIB327417P4h11a1
Method	BLASTN
NCBI GI	g3108024
BLAST score	53
E value	9.0e-21
Match length	77
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173745
Seq. ID	jC-atXLIB327417P4h11b1
Method	BLASTN
NCBI GI	g4678371
BLAST score	150
E value	1.0e-78
Match length	459
% identity	42
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	173746
Seq. ID	jC-atXLIB327418P1a01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	3.0e-26
Match length	66
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173747
Seq. ID	jC-atXLIB327418P1a04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	2.0e-22
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173748
Seq. ID	jC-atXLIB327418P1b02b1
Method	BLASTX

NCBI GI	g3158469
BLAST score	98
E value	3.0e-03
Match length	215
% identity	9
NCBI Description	(AF067216) No definition line found [Caenorhabditis elegans]

Seq. No.	173749
Seq. ID	jC-atXLIB327418P1b07a1
Method	BLASTN
NCBI GI	g3985949
BLAST score	79
E value	3.0e-36
Match length	111
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	173750
Seq. ID	jC-atXLIB327418P1b08a1
Method	BLASTN
NCBI GI	g4455321
BLAST score	53
E value	9.0e-21
Match length	113
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	173751
Seq. ID	jC-atXLIB327418P1b11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173752
Seq. ID	jC-atXLIB327418P1d03b1
Method	BLASTN
NCBI GI	g4220633
BLAST score	127
E value	5.0e-65
Match length	311
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	173753
Seq. ID	jC-atXLIB327418P1d11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09

Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173754
Seq. ID	jC-atXLIB327418P1d11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173755
Seq. ID	jC-atXLIB327418P1d12b1
Method	BLASTN
NCBI GI	g3426033
BLAST score	65
E value	1.0e-27
Match length	85
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173756
Seq. ID	jC-atXLIB327418P1e05b1
Method	BLASTX
NCBI GI	g3941412
BLAST score	124
E value	2.0e-06
Match length	117
% identity	20
NCBI Description	(AF062860) putative transcription factor [Arabidopsis thaliana]

Seq. No.	173757
Seq. ID	jC-atXLIB327418P1e06b1
Method	BLASTN
NCBI GI	g1532162
BLAST score	82
E value	8.0e-38
Match length	156
% identity	93
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	173758
Seq. ID	jC-atXLIB327418P1f02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	7.0e-12
Match length	42

% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173759
Seq. ID	jC-atXLIB327418P1f02b1
Method	BLASTX
NCBI GI	g2244807
BLAST score	267
E value	4.0e-23
Match length	176
% identity	40
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	173760
Seq. ID	jC-atXLIB327418P1f10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173761
Seq. ID	jC-atXLIB327418P1g03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	6.0e-29
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173762
Seq. ID	jC-atXLIB327418P1g07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	4.0e-21
Match length	62
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173763
Seq. ID	jC-atXLIB327418P1h08b1
Method	BLASTN
NCBI GI	g3702734
BLAST score	50
E value	1.0e-18
Match length	94
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	173764
Seq. ID	jC-atXLIB327418P2a04b2
Method	BLASTN
NCBI GI	g3150006
BLAST score	39
E value	2.0e-12
Match length	82
% identity	88
NCBI Description	CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No.	173765
Seq. ID	jC-atXLIB327418P2a06a1
Method	BLASTN
NCBI GI	g4490717
BLAST score	59
E value	2.0e-24
Match length	115
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	173766
Seq. ID	jC-atXLIB327418P2a08a1
Method	BLASTN
NCBI GI	g3785968
BLAST score	86
E value	2.0e-40
Match length	126
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173767
Seq. ID	jC-atXLIB327418P2a09a1
Method	BLASTN
NCBI GI	g3335356
BLAST score	82
E value	4.0e-38
Match length	102
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173768
Seq. ID	jC-atXLIB327418P2a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173769
Seq. ID	jC-atXLIB327418P2a12b2
Method	BLASTN

NCBI GI	g1049306
BLAST score	36
E value	9.0e-11
Match length	110
% identity	88
NCBI Description	Arabidopsis thaliana actin-2 mRNA, complete cds

Seq. No.	173770
Seq. ID	jC-atXLIB327418P2b06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173771
Seq. ID	jC-atXLIB327418P2b07a1
Method	BLASTN
NCBI GI	g4038029
BLAST score	99
E value	3.0e-48
Match length	182
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173772
Seq. ID	jC-atXLIB327418P2b08a1
Method	BLASTN
NCBI GI	g2264310
BLAST score	77
E value	4.0e-35
Match length	170
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	173773
Seq. ID	jC-atXLIB327418P2b12a1
Method	BLASTN
NCBI GI	g2477521
BLAST score	53
E value	9.0e-21
Match length	81
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173774
Seq. ID	jC-atXLIB327418P2c02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21

Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173775
Seq. ID	jC-atXLIB327418P2c04a1
Method	BLASTN
NCBI GI	g2980757
BLAST score	281
E value	1.0e-157
Match length	351
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	173776
Seq. ID	jC-atXLIB327418P2c08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173777
Seq. ID	jC-atXLIB327418P2c10a1
Method	BLASTX
NCBI GI	g4835233
BLAST score	182
E value	2.0e-13
Match length	109
% identity	44
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	173778
Seq. ID	jC-atXLIB327418P2d02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173779
Seq. ID	jC-atXLIB327418P2d04a1
Method	BLASTX
NCBI GI	g2190187
BLAST score	253
E value	1.0e-33
Match length	132
% identity	61
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	173780
Seq. ID	jC-atXLIB327418P2d12b2
Method	BLASTX
NCBI GI	g3426048
BLAST score	406
E value	1.0e-39
Match length	129
% identity	64
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	173781
Seq. ID	jC-atXLIB327418P2e02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173782
Seq. ID	jC-atXLIB327418P2e02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	9.0e-27
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173783
Seq. ID	jC-atXLIB327418P2e03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	7.0e-12
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173784
Seq. ID	jC-atXLIB327418P2e04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173785
Seq. ID	jC-atXLIB327418P2e04b2
Method	BLASTX
NCBI GI	g294845

BLAST score	162
E value	6.0e-11
Match length	54
% identity	59
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	173786
Seq. ID	jC-atXLIB327418P2e07a1
Method	BLASTN
NCBI GI	g2618600
BLAST score	97
E value	3.0e-47
Match length	183
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	173787
Seq. ID	jC-atXLIB327418P2e08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173788
Seq. ID	jC-atXLIB327418P2e12a1
Method	BLASTX
NCBI GI	g3342904
BLAST score	720
E value	2.0e-76
Match length	141
% identity	99
NCBI Description	(AF077855) flower-specific pectin methylesterase precursor [Arabidopsis thaliana]

Seq. No.	173789
Seq. ID	jC-atXLIB327418P2f01b2
Method	BLASTX
NCBI GI	g2288887
BLAST score	418
E value	5.0e-41
Match length	110
% identity	74
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thali >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	173790
Seq. ID	jC-atXLIB327418P2f04a1
Method	BLASTN
NCBI GI	g3510343

BLAST score	166
E value	3.0e-88
Match length	349
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	173791
Seq. ID	jC-atXLIB327418P2f07a1
Method	BLASTN
NCBI GI	g2264304
BLAST score	211
E value	1.0e-115
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	173792
Seq. ID	jC-atXLIB327418P2f09b2
Method	BLASTX
NCBI GI	g2501011
BLAST score	178
E value	7.0e-13
Match length	79
% identity	49
NCBI Description	ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS) >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA synthetase [Synechocystis sp.]

Seq. No.	173793
Seq. ID	jC-atXLIB327418P2f11b2
Method	BLASTX
NCBI GI	g1168750
BLAST score	217
E value	2.0e-17
Match length	121
% identity	39
NCBI Description	CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No.	173794
Seq. ID	jC-atXLIB327418P2g02b2
Method	BLASTN
NCBI GI	g2944179
BLAST score	48
E value	6.0e-18
Match length	163
% identity	83
NCBI Description	Arabidopsis thaliana trehalose-6-phosphate phosphatase (AtTPPB) mRNA, complete cds

Seq. No.	173795
Seq. ID	jC-atXLIB327418P2g04a1
Method	BLASTN
NCBI GI	g3985954

BLAST score	197
E value	1.0e-106
Match length	330
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	173796
Seq. ID	jC-atXLIB327418P2g07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	8.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173797
Seq. ID	jC-atXLIB327418P2g07b2
Method	BLASTX
NCBI GI	g2146740
BLAST score	279
E value	1.0e-24
Match length	128
% identity	48
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	173798
Seq. ID	jC-atXLIB327418P2g08a1
Method	BLASTN
NCBI GI	g4519191
BLAST score	122
E value	6.0e-62
Match length	248
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	173799
Seq. ID	jC-atXLIB327418P2g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173800
Seq. ID	jC-atXLIB327418P2h02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	4.0e-25
Match length	71

% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173801
Seq. ID	jC-atXLIB327418P2h07b2
Method	BLASTX
NCBI GI	g16225
BLAST score	362
E value	2.0e-34
Match length	93
% identity	47
NCBI Description	(Z12023) calmodulin [Arabidopsis thaliana]

Seq. No.	173802
Seq. ID	jC-atXLIB327418P2h08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173803
Seq. ID	jC-atXLIB327418P2h11b2
Method	BLASTN
NCBI GI	g3510347
BLAST score	74
E value	1.0e-33
Match length	98
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	173804
Seq. ID	jC-atXLIB327418P3a06b1
Method	BLASTN
NCBI GI	g4220641
BLAST score	35
E value	9.0e-10
Match length	95
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	173805
Seq. ID	jC-atXLIB327418P3a07a2
Method	BLASTN
NCBI GI	g3059018
BLAST score	98
E value	1.0e-47
Match length	274
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	173806
Seq. ID	jC-atXLIB327418P3a08b1
Method	BLASTN
NCBI GI	g3643588
BLAST score	152
E value	1.0e-79
Match length	217
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173807
Seq. ID	jC-atXLIB327418P3b07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173808
Seq. ID	jC-atXLIB327418P3b08a2
Method	BLASTN
NCBI GI	g2760167
BLAST score	63
E value	9.0e-27
Match length	212
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	173809
Seq. ID	jC-atXLIB327418P3b09a2
Method	BLASTN
NCBI GI	g2351061
BLAST score	146
E value	3.0e-76
Match length	266
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	173810
Seq. ID	jC-atXLIB327418P3b10b1
Method	BLASTN
NCBI GI	g2244991
BLAST score	360
E value	0.0e+00
Match length	414
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	173811
Seq. ID	jC-atXLIB327418P3b12b1
Method	BLASTX

NCBI GI	g4263525
BLAST score	243
E value	3.0e-20
Match length	164
% identity	26
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	173812
Seq. ID	jC-atXLIB327418P3c01a2
Method	BLASTN
NCBI GI	g2924733
BLAST score	114
E value	3.0e-57
Match length	271
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	173813
Seq. ID	jC-atXLIB327418P3c03b1
Method	BLASTX
NCBI GI	g1237102
BLAST score	217
E value	3.0e-31
Match length	133
% identity	69
NCBI Description	(L40358) calmodulin-binding protein [Arabidopsis thaliana] >gi_1589171_prf__2210340A calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	173814
Seq. ID	jC-atXLIB327418P3c05b1
Method	BLASTN
NCBI GI	g17674
BLAST score	64
E value	5.0e-27
Match length	90
% identity	93
NCBI Description	A.thaliana U4.2 snRNA gene

Seq. No.	173815
Seq. ID	jC-atXLIB327418P3c06a2
Method	BLASTX
NCBI GI	g4210451
BLAST score	156
E value	3.0e-10
Match length	52
% identity	65
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No.	173816
Seq. ID	jC-atXLIB327418P3c06b1
Method	BLASTN
NCBI GI	g4210448
BLAST score	194
E value	1.0e-105

Match length	392
% identity	91
NCBI Description	Arabidopsis thaliana gene for ARR1 protein, complete cds

Seq. No.	173817
Seq. ID	jC-atXLIB327418P3c10a2
Method	BLASTN
NCBI GI	g2351073
BLAST score	144
E value	4.0e-75
Match length	345
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	173818
Seq. ID	jC-atXLIB327418P3c11a2
Method	BLASTN
NCBI GI	g3776004
BLAST score	186
E value	1.0e-100
Match length	246
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH15

Seq. No.	173819
Seq. ID	jC-atXLIB327418P3c11b1
Method	BLASTN
NCBI GI	g3776004
BLAST score	254
E value	1.0e-140
Match length	305
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH15

Seq. No.	173820
Seq. ID	jC-atXLIB327418P3c12a2
Method	BLASTN
NCBI GI	g531832
BLAST score	41
E value	1.0e-13
Match length	57
% identity	93
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	173821
Seq. ID	jC-atXLIB327418P3d01b1
Method	BLASTX
NCBI GI	g1145699
BLAST score	66
E value	5.0e-16
Match length	138
% identity	53
NCBI Description	(U39486) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	173822

Seq. ID	jC-atXLIB327418P3d02a2
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	68
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173823
Seq. ID	jC-atXLIB327418P3d02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	7.0e-26
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173824
Seq. ID	jC-atXLIB327418P3d08b1
Method	BLASTX
NCBI GI	g2190968
BLAST score	194
E value	1.0e-14
Match length	132
% identity	36
NCBI Description	(AF002677) DEAD-box RNA helicase [Dictyostelium discoideum]

Seq. No.	173825
Seq. ID	jC-atXLIB327418P3d10a2
Method	BLASTX
NCBI GI	g2440035
BLAST score	412
E value	3.0e-40
Match length	88
% identity	88
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	173826
Seq. ID	jC-atXLIB327418P3d10b1
Method	BLASTX
NCBI GI	g2440035
BLAST score	593
E value	3.0e-61
Match length	183
% identity	70
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	173827
Seq. ID	jC-atXLIB327418P3d11b1
Method	BLASTX
NCBI GI	g729880
BLAST score	739
E value	2.0e-78
Match length	175

% identity	81
NCBI Description	CASEIN KINASE II BETA CHAIN (CK II) >gi_1076299_pir__S47967 casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis thaliana >gi_468264 (L22563) casein kinase II beta subunit CKB1 [Arabidopsis thaliana]

Seq. No.	173828
Seq. ID	jC-atXLIB327418P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	44
E value	4.0e-15
Match length	60
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173829
Seq. ID	jC-atXLIB327418P3e07a2
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	3.0e-14
Match length	68
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173830
Seq. ID	jC-atXLIB327418P3e08b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	42
E value	4.0e-14
Match length	54
% identity	59
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	173831
Seq. ID	jC-atXLIB327418P3e12b1
Method	BLASTX
NCBI GI	g3892712
BLAST score	243
E value	4.0e-20
Match length	95
% identity	59
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	173832
Seq. ID	jC-atXLIB327418P3f02b1
Method	BLASTX
NCBI GI	g3776029
BLAST score	206
E value	3.0e-16
Match length	97
% identity	44
NCBI Description	(AJ010476) RNA helicase [Arabidopsis thaliana]

Seq. No.	173833
Seq. ID	jC-atXLIB327418P3f04a2
Method	BLASTN
NCBI GI	g4455321
BLAST score	81
E value	2.0e-37
Match length	188
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	173834
Seq. ID	jC-atXLIB327418P3f05b1
Method	BLASTX
NCBI GI	g1703108
BLAST score	184
E value	3.0e-13
Match length	148
% identity	37
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	173835
Seq. ID	jC-atXLIB327418P3f06a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	46
E value	1.0e-16
Match length	69
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173836
Seq. ID	jC-atXLIB327418P3f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	2.0e-13
Match length	57
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173837
Seq. ID	jC-atXLIB327418P3f07b1
Method	BLASTN
NCBI GI	g1143391
BLAST score	62
E value	7.0e-26
Match length	62
% identity	100
NCBI Description	A.thaliana mRNA for uridine diphosphate glucose epimerase

Seq. No.	173838
Seq. ID	jC-atXLIB327418P3f08a2
Method	BLASTX
NCBI GI	g2119846
BLAST score	264
E value	7.0e-23
Match length	72
% identity	71
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	173839
Seq. ID	jC-atXLIB327418P3f08b1
Method	BLASTX
NCBI GI	g115767
BLAST score	315
E value	1.0e-28
Match length	228
% identity	39
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	173840
Seq. ID	jC-atXLIB327418P3f10a2
Method	BLASTN
NCBI GI	g3869069
BLAST score	164
E value	5.0e-87
Match length	288
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	173841
Seq. ID	jC-atXLIB327418P3g01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173842
Seq. ID	jC-atXLIB327418P3g02a2
Method	BLASTN

NCBI GI	g531828
BLAST score	47
E value	3.0e-17
Match length	69
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173843
Seq. ID	jC-atXLIB327418P3g05a2
Method	BLASTN
NCBI GI	g4757404
BLAST score	55
E value	5.0e-22
Match length	189
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	173844
Seq. ID	jC-atXLIB327418P3g07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	1.0e-08
Match length	37
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173845
Seq. ID	jC-atXLIB327418P3g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	2.0e-20
Match length	64
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173846
Seq. ID	jC-atXLIB327418P3g12a2
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	68
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173847
Seq. ID	jC-atXLIB327418P3h08a2
Method	BLASTN
NCBI GI	g2980757
BLAST score	285
E value	1.0e-159
Match length	394

% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	173848
Seq. ID	jC-atXLIB327418P4a04a1
Method	BLASTN
NCBI GI	g4220510
BLAST score	133
E value	9.0e-69
Match length	185
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	173849
Seq. ID	jC-atXLIB327418P4a08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	3.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173850
Seq. ID	jC-atXLIB327418P4b01a1
Method	BLASTN
NCBI GI	g2924651
BLAST score	87
E value	3.0e-41
Match length	150
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	173851
Seq. ID	jC-atXLIB327418P4b05a1
Method	BLASTX
NCBI GI	g4650842
BLAST score	80
E value	2.0e-12
Match length	59
% identity	73
NCBI Description	(AB026185) elongation factor 2 [Lithospermum erythrorhizon]

Seq. No.	173852
Seq. ID	jC-atXLIB327418P4b05b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	590
E value	5.0e-61
Match length	178
% identity	71
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	173853

Seq. ID	jC-atXLIB327418P4b06a1
Method	BLASTN
NCBI GI	g2264303
BLAST score	399
E value	0.0e+00
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	173854
Seq. ID	jC-atXLIB327418P4b06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	5.0e-12
Match length	53
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173855
Seq. ID	jC-atXLIB327418P4b08a1
Method	BLASTN
NCBI GI	g540252
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173856
Seq. ID	jC-atXLIB327418P4b09a1
Method	BLASTN
NCBI GI	g1495250
BLAST score	243
E value	1.0e-134
Match length	338
% identity	93
NCBI Description	A.thaliana mRNA for heat-shock protein

Seq. No.	173857
Seq. ID	jC-atXLIB327418P4b12a1
Method	BLASTN
NCBI GI	g4510323
BLAST score	241
E value	1.0e-133
Match length	383
% identity	92
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	173858
Seq. ID	jC-atXLIB327418P4c01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52

E value	6.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173859
Seq. ID	jC-atXLIB327418P4c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	4.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173860
Seq. ID	jC-atXLIB327418P4c06a1
Method	BLASTN
NCBI GI	g540252
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173861
Seq. ID	jC-atXLIB327418P4c07a1
Method	BLASTN
NCBI GI	g2914688
BLAST score	111
E value	4.0e-55
Match length	279
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173862
Seq. ID	jC-atXLIB327418P4c08a1
Method	BLASTN
NCBI GI	g540252
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	173863
Seq. ID	jC-atXLIB327418P4c11a1
Method	BLASTN
NCBI GI	g4753195
BLAST score	227
E value	1.0e-124
Match length	383
% identity	91
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	173864
Seq. ID	jC-atXLIB327418P4d01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173865
Seq. ID	jC-atXLIB327418P4d02a1
Method	BLASTN
NCBI GI	g3128134
BLAST score	72
E value	6.0e-32
Match length	120
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	173866
Seq. ID	jC-atXLIB327418P4d06a1
Method	BLASTN
NCBI GI	g2058281
BLAST score	191
E value	1.0e-103
Match length	256
% identity	95
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	173867
Seq. ID	jC-atXLIB327418P4d06b1
Method	BLASTX
NCBI GI	g2058282
BLAST score	254
E value	2.0e-21
Match length	222
% identity	30
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	173868
Seq. ID	jC-atXLIB327418P4e03b1
Method	BLASTX
NCBI GI	g4567286
BLAST score	236
E value	9.0e-20
Match length	118
% identity	40
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	173869
Seq. ID	jC-atXLIB327418P4e05a1
Method	BLASTN
NCBI GI	g3869069

BLAST score 191
E value 1.0e-103
Match length 287
% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 173870
Seq. ID jC-atXLIB327418P4e09a1
Method BLASTN
NCBI GI g2264304
BLAST score 188
E value 1.0e-101
Match length 415
% identity 95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 173871
Seq. ID jC-atXLIB327418P4f01a1
Method BLASTN
NCBI GI g3985954
BLAST score 90
E value 4.0e-43
Match length 121
% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No. 173872
Seq. ID jC-atXLIB327418P4f02a1
Method BLASTN
NCBI GI g3212102
BLAST score 97
E value 4.0e-47
Match length 250
% identity 91
NCBI Description Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 173873
Seq. ID jC-atXLIB327418P4f03a1
Method BLASTN
NCBI GI g2462264
BLAST score 44
E value 3.0e-15
Match length 56
% identity 95
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 173874
Seq. ID jC-atXLIB327418P4f04a1
Method BLASTN
NCBI GI g4049332
BLAST score 363
E value 0.0e+00
Match length 478

% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	173875
Seq. ID	jC-atXLIB327418P4f05a1
Method	BLASTN
NCBI GI	g4220510
BLAST score	66
E value	2.0e-28
Match length	133
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	173876
Seq. ID	jC-atXLIB327418P4f06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173877
Seq. ID	jC-atXLIB327418P4f08a1
Method	BLASTN
NCBI GI	g2642214
BLAST score	198
E value	1.0e-107
Match length	415
% identity	88
NCBI Description	Arabidopsis thaliana NOI protein mRNA, complete cds

Seq. No.	173878
Seq. ID	jC-atXLIB327418P4f08b1
Method	BLASTX
NCBI GI	g2642215
BLAST score	183
E value	3.0e-13
Match length	74
% identity	57
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	173879
Seq. ID	jC-atXLIB327418P4f12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	4.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173880

Seq. ID	jC-atXLIB327418P4g01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173881
Seq. ID	jC-atXLIB327418P4g05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173882
Seq. ID	jC-atXLIB327418P4g06a1
Method	BLASTN
NCBI GI	g4589412
BLAST score	184
E value	1.0e-98
Match length	336
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	173883
Seq. ID	jC-atXLIB327418P4g07a1
Method	BLASTN
NCBI GI	g3738313
BLAST score	210
E value	1.0e-114
Match length	277
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173884
Seq. ID	jC-atXLIB327418P4g07b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	112
E value	9.0e-56
Match length	291
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173885
Seq. ID	jC-atXLIB327418P4g08a1
Method	BLASTN
NCBI GI	g2894591

BLAST score	166
E value	4.0e-88
Match length	334
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	173886
Seq. ID	jC-atXLIB327418P4g10a1
Method	BLASTN
NCBI GI	g2226430
BLAST score	43
E value	8.0e-15
Match length	43
% identity	100
NCBI Description	Mus saxicola haptoglobin mRNA, complete cds

Seq. No.	173887
Seq. ID	jC-atXLIB327418P4g11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	4.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173888
Seq. ID	jC-atXLIB327418P4h02a1
Method	BLASTN
NCBI GI	g4567259
BLAST score	132
E value	1.0e-67
Match length	266
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	173889
Seq. ID	jC-atXLIB327418P4h08b1
Method	BLASTN
NCBI GI	g2980757
BLAST score	100
E value	1.0e-48
Match length	119
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	173890
Seq. ID	jC-atXLIB327418P4h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173891
Seq. ID	jC-atXLIB327418P4h11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173892
Seq. ID	jC-atXLIB327419P1a06a2
Method	BLASTN
NCBI GI	g1877523
BLAST score	131
E value	2.0e-67
Match length	417
% identity	93
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	173893
Seq. ID	jC-atXLIB327419P1b02a2
Method	BLASTN
NCBI GI	g3985931
BLAST score	266
E value	1.0e-148
Match length	338
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	173894
Seq. ID	jC-atXLIB327419P1b09a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173895
Seq. ID	jC-atXLIB327419P1c07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	60
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173896
Seq. ID	jC-atXLIB327419P1c12a2

Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173897
Seq. ID	jC-atXLIB327419P1d07a2
Method	BLASTN
NCBI GI	g4757678
BLAST score	139
E value	4.0e-72
Match length	197
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	173898
Seq. ID	jC-atXLIB327419P1e05a2
Method	BLASTN
NCBI GI	g3548797
BLAST score	140
E value	1.0e-72
Match length	361
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173899
Seq. ID	jC-atXLIB327419P1e10a2
Method	BLASTX
NCBI GI	g4314378
BLAST score	389
E value	5.0e-38
Match length	116
% identity	63
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	173900
Seq. ID	jC-atXLIB327419P1e11a2
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173901
Seq. ID	jC-atXLIB327419P1e12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	3.0e-10
Match length	50

% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	173902
Seq. ID	jC-atXLIB327419P1g05a2
Method	BLASTX
NCBI GI	g3785986
BLAST score	442
E value	9.0e-44
Match length	82
% identity	100
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]
Seq. No.	173903
Seq. ID	jC-atXLIB327419P1h03a2
Method	BLASTX
NCBI GI	g3738327
BLAST score	243
E value	2.0e-20
Match length	83
% identity	53
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]
Seq. No.	173904
Seq. ID	jC-atXLIB327419P2a01a1
Method	BLASTN
NCBI GI	g4262221
BLAST score	81
E value	7.0e-38
Match length	149
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	173905
Seq. ID	jC-atXLIB327419P2a02a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	188
E value	1.0e-101
Match length	216
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]
Seq. No.	173906
Seq. ID	jC-atXLIB327419P2a03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	173907

Seq. ID	jC-atXLIB327419P2a05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	7.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173908
Seq. ID	jC-atXLIB327419P2a08a1
Method	BLASTN
NCBI GI	g2564045
BLAST score	91
E value	2.0e-43
Match length	138
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	173909
Seq. ID	jC-atXLIB327419P2a08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	67
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173910
Seq. ID	jC-atXLIB327419P2a09b2
Method	BLASTX
NCBI GI	g3935157
BLAST score	220
E value	5.0e-18
Match length	64
% identity	77
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.	173911
Seq. ID	jC-atXLIB327419P2a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	52
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173912
Seq. ID	jC-atXLIB327419P2a12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13

Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173913
Seq. ID	jC-atXLIB327419P2b03a1
Method	BLASTN
NCBI GI	g549974
BLAST score	62
E value	3.0e-26
Match length	152
% identity	89
NCBI Description	Arabidopsis thaliana Col-0 nucleosome assembly protein I-like protein mRNA, partial cds

Seq. No.	173914
Seq. ID	jC-atXLIB327419P2b05a1
Method	BLASTN
NCBI GI	g4704661
BLAST score	159
E value	5.0e-84
Match length	267
% identity	79
NCBI Description	Arabidopsis thaliana uracil phosphoribosyltransferase 1 (UPT1) mRNA, partial cds

Seq. No.	173915
Seq. ID	jC-atXLIB327419P2b07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173916
Seq. ID	jC-atXLIB327419P2b08b2
Method	BLASTN
NCBI GI	g3366536
BLAST score	56
E value	8.0e-23
Match length	120
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	173917
Seq. ID	jC-atXLIB327419P2b12b2
Method	BLASTN
NCBI GI	g4580744
BLAST score	130
E value	9.0e-67
Match length	309
% identity	91
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	173918
Seq. ID	jC-atXLIB327419P2c02a1
Method	BLASTN
NCBI GI	g1336083
BLAST score	59
E value	2.0e-24
Match length	204
% identity	88
NCBI Description	Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds

Seq. No.	173919
Seq. ID	jC-atXLIB327419P2c03a1
Method	BLASTN
NCBI GI	g2342673
BLAST score	151
E value	3.0e-79
Match length	272
% identity	90
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	173920
Seq. ID	jC-atXLIB327419P2c04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173921
Seq. ID	jC-atXLIB327419P2c04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	64
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173922
Seq. ID	jC-atXLIB327419P2c06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	6.0e-21
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173923
Seq. ID	jC-atXLIB327419P2c08b2

Method	BLASTN
NCBI GI	g3702724
BLAST score	117
E value	5.0e-59
Match length	198
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	173924
Seq. ID	jC-atXLIB327419P2c09a1
Method	BLASTX
NCBI GI	g4006934
BLAST score	278
E value	1.0e-24
Match length	55
% identity	98
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	173925
Seq. ID	jC-atXLIB327419P2c09b2
Method	BLASTX
NCBI GI	g4006934
BLAST score	242
E value	1.0e-20
Match length	60
% identity	82
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	173926
Seq. ID	jC-atXLIB327419P2c10a1
Method	BLASTX
NCBI GI	g1710851
BLAST score	43
E value	2.0e-23
Match length	68
% identity	85
NCBI Description	GTP-BINDING PROTEIN SAR2 >gi_1084403_pir__S42528 GTPase-like protein - Tomato >gi_473684 (L12051) GTPase [Lycopersicon esculentum]

Seq. No.	173927
Seq. ID	jC-atXLIB327419P2c12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	38
E value	5.0e-12
Match length	50
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173928
Seq. ID	jC-atXLIB327419P2c12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13

Match length	68
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173929
Seq. ID	jC-atXLIB327419P2d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	3.0e-13
Match length	48
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173930
Seq. ID	jC-atXLIB327419P2d06a1
Method	BLASTX
NCBI GI	g464707
BLAST score	206
E value	3.0e-16
Match length	61
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	173931
Seq. ID	jC-atXLIB327419P2d07b2
Method	BLASTX
NCBI GI	g1710770
BLAST score	258
E value	2.0e-22
Match length	82
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S5

Seq. No.	173932
Seq. ID	jC-atXLIB327419P2d08a1
Method	BLASTN
NCBI GI	g4159704
BLAST score	113
E value	1.0e-56
Match length	366
% identity	95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	173933
Seq. ID	jC-atXLIB327419P2d11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	6.0e-12
Match length	54
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173934
Seq. ID	jC-atXLIB327419P2d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173935
Seq. ID	jC-atXLIB327419P2e05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173936
Seq. ID	jC-atXLIB327419P2e07a1
Method	BLASTN
NCBI GI	g4314374
BLAST score	279
E value	1.0e-155
Match length	351
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173937
Seq. ID	jC-atXLIB327419P2e08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173938
Seq. ID	jC-atXLIB327419P2e08b2

Method	BLASTX
NCBI GI	g4538906
BLAST score	239
E value	3.0e-20
Match length	85
% identity	55
NCBI Description	(AL049482) choline kinase GmCK2p-like protein [Arabidopsis thaliana]

Seq. No.	173939
Seq. ID	jC-atXLIB327419P2e10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	7.0e-24
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173940
Seq. ID	jC-atXLIB327419P2e11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173941
Seq. ID	jC-atXLIB327419P2e11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	55
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173942
Seq. ID	jC-atXLIB327419P2e12a1
Method	BLASTN
NCBI GI	g3132469
BLAST score	195
E value	1.0e-105
Match length	318
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173943
Seq. ID	jC-atXLIB327419P2f04a1
Method	BLASTN
NCBI GI	g4063730
BLAST score	103

E value	1.0e-50
Match length	228
% identity	92
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	173944
Seq. ID	jC-atXLIB327419P2f05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173945
Seq. ID	jC-atXLIB327419P2f05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	9.0e-23
Match length	60
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173946
Seq. ID	jC-atXLIB327419P2f06a1
Method	BLASTN
NCBI GI	g4415928
BLAST score	83
E value	7.0e-39
Match length	142
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173947
Seq. ID	jC-atXLIB327419P2f07b2
Method	BLASTN
NCBI GI	g3983259
BLAST score	82
E value	3.0e-38
Match length	186
% identity	86
NCBI Description	Arabidopsis thaliana sigma-like factor (SIG4) mRNA, complete cds

Seq. No.	173948
Seq. ID	jC-atXLIB327419P2f08a1
Method	BLASTN
NCBI GI	g3608126
BLAST score	312
E value	1.0e-175
Match length	401

% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173949
Seq. ID	jC-atXLIB327419P2f09a1
Method	BLASTN
NCBI GI	g4263694
BLAST score	117
E value	5.0e-59
Match length	334
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173950
Seq. ID	jC-atXLIB327419P2f09b2
Method	BLASTN
NCBI GI	g3831448
BLAST score	57
E value	4.0e-23
Match length	292
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	173951
Seq. ID	jC-atXLIB327419P2f11b2
Method	BLASTN
NCBI GI	g2924732
BLAST score	106
E value	2.0e-52
Match length	231
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	173952
Seq. ID	jC-atXLIB327419P2g03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	6.0e-09
Match length	53
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173953
Seq. ID	jC-atXLIB327419P2g05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	6.0e-18
Match length	66
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	173954
Seq. ID	jC-atXLIB327419P2g07a1
Method	BLASTN
NCBI GI	g2358139
BLAST score	78
E value	9.0e-36
Match length	227
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	173955
Seq. ID	jC-atXLIB327419P2g07b2
Method	BLASTX
NCBI GI	g2388581
BLAST score	339
E value	9.0e-39
Match length	112
% identity	77
NCBI Description	(AC000098) Similar to Zea DWARF3 (gb_U32579). [Arabidopsis thaliana]

Seq. No.	173956
Seq. ID	jC-atXLIB327419P2g09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	44
E value	1.0e-15
Match length	67
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173957
Seq. ID	jC-atXLIB327419P2g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	46
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173958
Seq. ID	jC-atXLIB327419P2h06b2
Method	BLASTN
NCBI GI	g2494106
BLAST score	153
E value	2.0e-80
Match length	356
% identity	86
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 173959

Seq. ID	jC-atXLIB327419P2h11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	67
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173960
Seq. ID	jC-atXLIB327419P3a01b2
Method	BLASTX
NCBI GI	g2851538
BLAST score	169
E value	1.0e-14
Match length	120
% identity	42
NCBI Description	TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)

Seq. No.	173961
Seq. ID	jC-atXLIB327419P3a02a2
Method	BLASTN
NCBI GI	g3228389
BLAST score	60
E value	2.0e-25
Match length	92
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	173962
Seq. ID	jC-atXLIB327419P3a03b2
Method	BLASTX
NCBI GI	g549975
BLAST score	236
E value	1.0e-19
Match length	104
% identity	54
NCBI Description	(U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana]

Seq. No.	173963
Seq. ID	jC-atXLIB327419P3a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	59
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173964
Seq. ID	jC-atXLIB327419P3a08b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173965
Seq. ID	jC-atXLIB327419P3a11a2
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	5.0e-16
Match length	60
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173966
Seq. ID	jC-atXLIB327419P3b01a2
Method	BLASTN
NCBI GI	g2244788
BLAST score	67
E value	4.0e-29
Match length	235
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	173967
Seq. ID	jC-atXLIB327419P3b04a2
Method	BLASTN
NCBI GI	g3451055
BLAST score	135
E value	1.0e-69
Match length	394
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	173968
Seq. ID	jC-atXLIB327419P3b07a2
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19
Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173969
Seq. ID	jC-atXLIB327419P3b10a2
Method	BLASTX
NCBI GI	g2341028
BLAST score	150
E value	1.0e-09

Match length	50
% identity	58
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	173970
Seq. ID	jC-atXLIB327419P3c02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173971
Seq. ID	jC-atXLIB327419P3c03a2
Method	BLASTX
NCBI GI	g1213442
BLAST score	377
E value	3.0e-36
Match length	90
% identity	84
NCBI Description	(U48961) isopentenyl pyrophosphate isomerase [Arabidopsis thaliana]

Seq. No.	173972
Seq. ID	jC-atXLIB327419P3c05a2
Method	BLASTX
NCBI GI	g4490737
BLAST score	373
E value	1.0e-35
Match length	74
% identity	65
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	173973
Seq. ID	jC-atXLIB327419P3c06b1
Method	BLASTN
NCBI GI	g2789659
BLAST score	73
E value	1.0e-32
Match length	134
% identity	89
NCBI Description	Arabidopsis thaliana p105 mRNA, complete cds

Seq. No.	173974
Seq. ID	jC-atXLIB327419P3c08b1
Method	BLASTN
NCBI GI	g3641835
BLAST score	108
E value	6.0e-54
Match length	142
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	173975
Seq. ID	jC-atXLIB327419P3c11a2
Method	BLASTX
NCBI GI	g4115363
BLAST score	258
E value	3.0e-22
Match length	55
% identity	87
NCBI Description	(AC005957) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	173976
Seq. ID	jC-atXLIB327419P3d01a2
Method	BLASTN
NCBI GI	g4519193
BLAST score	82
E value	4.0e-38
Match length	151
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	173977
Seq. ID	jC-atXLIB327419P3d02a2
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	173978
Seq. ID	jC-atXLIB327419P3d04b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	77
E value	4.0e-35
Match length	89
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	173979
Seq. ID	jC-atXLIB327419P3d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173980
Seq. ID	jC-atXLIB327419P3d08a2

Method	BLASTX
NCBI GI	g1173345
BLAST score	471
E value	3.0e-47
Match length	105
% identity	91
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	173981
Seq. ID	jC-atXLIB327419P3d09a2
Method	BLASTN
NCBI GI	g1699022
BLAST score	250
E value	1.0e-138
Match length	346
% identity	93
NCBI Description	Arabidopsis thaliana putative arginine-aspartate-rich RNA binding protein (gene1500), (gene1000), and (gene400) genes, complete cds

Seq. No.	173982
Seq. ID	jC-atXLIB327419P3d09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173983
Seq. ID	jC-atXLIB327419P3d10a2
Method	BLASTX
NCBI GI	g2317902
BLAST score	283
E value	4.0e-25
Match length	62
% identity	89
NCBI Description	(U89959) hypothetical protein [Arabidopsis thaliana]

Seq. No.	173984
Seq. ID	jC-atXLIB327419P3d11a2
Method	BLASTN
NCBI GI	g4558521
BLAST score	124
E value	4.0e-63
Match length	287
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	173985
Seq. ID	jC-atXLIB327419P3d12b2
Method	BLASTX
NCBI GI	g1513228
BLAST score	221
E value	6.0e-18
Match length	47
% identity	94
NCBI Description	(U66307) myo-inositol 1-phosphate synthase [Brassica napus]

Seq. No.	173986
Seq. ID	jC-atXLIB327419P3e02b2
Method	BLASTN
NCBI GI	g531832
BLAST score	40
E value	4.0e-13
Match length	55
% identity	95
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	173987
Seq. ID	jC-atXLIB327419P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	173988
Seq. ID	jC-atXLIB327419P3f01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173989
Seq. ID	jC-atXLIB327419P3f05a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	3.0e-20
Match length	67
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	173990
Seq. ID	jC-atXLIB327419P3f10a2
Method	BLASTX
NCBI GI	g730526

BLAST score	281
E value	6.0e-25
Match length	58
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	173991
Seq. ID	jC-atXLIB327419P3f11b2
Method	BLASTX
NCBI GI	g4335714
BLAST score	189
E value	4.0e-14
Match length	75
% identity	60
NCBI Description	(AC006248) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	173992
Seq. ID	jC-atXLIB327419P3f12b2
Method	BLASTN
NCBI GI	g3702732
BLAST score	39
E value	2.0e-12
Match length	155
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	173993
Seq. ID	jC-atXLIB327419P3g02a2
Method	BLASTX
NCBI GI	g3738327
BLAST score	156
E value	6.0e-16
Match length	81
% identity	57
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	173994
Seq. ID	jC-atXLIB327419P3g03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173995
Seq. ID	jC-atXLIB327419P3g06a2
Method	BLASTN
NCBI GI	g4199934
BLAST score	62

E value	4.0e-26
Match length	200
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	173996
Seq. ID	jC-atXLIB327419P3g08a2
Method	BLASTN
NCBI GI	g4455339
BLAST score	167
E value	8.0e-89
Match length	255
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	173997
Seq. ID	jC-atXLIB327419P3h03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	173998
Seq. ID	jC-atXLIB327419P3h04a2
Method	BLASTN
NCBI GI	g2264367
BLAST score	167
E value	8.0e-89
Match length	275
% identity	90
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	173999
Seq. ID	jC-atXLIB327419P3h05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174000
Seq. ID	jC-atXLIB327419P3h07a2
Method	BLASTX
NCBI GI	g1906828
BLAST score	148
E value	3.0e-09
Match length	59
% identity	56
NCBI Description	(Y11828) heat shock protein [Arabidopsis thaliana]

Seq. No.	174001
Seq. ID	jC-atXLIB327419P4a01b1
Method	BLASTX
NCBI GI	g1174592
BLAST score	89
E value	2.0e-11
Match length	48
% identity	72
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	174002
Seq. ID	jC-atXLIB327419P4a05a2
Method	BLASTN
NCBI GI	g4220633
BLAST score	75
E value	6.0e-34
Match length	206
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	174003
Seq. ID	jC-atXLIB327419P4a06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	3.0e-19
Match length	72
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174004
Seq. ID	jC-atXLIB327419P4a09a2
Method	BLASTX
NCBI GI	g133872
BLAST score	393
E value	4.0e-38
Match length	87
% identity	92
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	174005
Seq. ID	jC-atXLIB327419P4a12a2
Method	BLASTN
NCBI GI	g4388714
BLAST score	241
E value	1.0e-133

Match length	413
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174006
Seq. ID	jC-atXLIB327419P4b06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	1.0e-27
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174007
Seq. ID	jC-atXLIB327419P4b11a2
Method	BLASTN
NCBI GI	g2582638
BLAST score	28
E value	6.0e-06
Match length	150
% identity	90
NCBI Description	Arabidosis thaliana mRNA for a hnRNP-like protein

Seq. No.	174008
Seq. ID	jC-atXLIB327419P4c05a2
Method	BLASTN
NCBI GI	g3046854
BLAST score	50
E value	5.0e-19
Match length	98
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	174009
Seq. ID	jC-atXLIB327419P4c07a2
Method	BLASTN
NCBI GI	g3292807
BLAST score	33
E value	7.0e-09
Match length	89
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	174010
Seq. ID	jC-atXLIB327419P4c09a2
Method	BLASTN
NCBI GI	g2351064
BLAST score	105
E value	8.0e-52
Match length	340
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	174011
Seq. ID	jC-atXLIB327419P4d08a2
Method	BLASTN
NCBI GI	g3980374
BLAST score	62
E value	4.0e-26
Match length	82
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174012
Seq. ID	jC-atXLIB327419P4d09a2
Method	BLASTN
NCBI GI	g2827513
BLAST score	96
E value	1.0e-46
Match length	183
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	174013
Seq. ID	jC-atXLIB327419P4e02a2
Method	BLASTN
NCBI GI	g2459406
BLAST score	95
E value	7.0e-46
Match length	107
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174014
Seq. ID	jC-atXLIB327419P4e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	2.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174015
Seq. ID	jC-atXLIB327419P4e07a2
Method	BLASTN
NCBI GI	g2245031
BLAST score	76
E value	2.0e-34
Match length	76
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174016
Seq. ID	jC-atXLIB327419P4f10a2
Method	BLASTN
NCBI GI	g728520
BLAST score	46
E value	1.0e-16
Match length	259
% identity	84
NCBI Description	A.thaliana (Columbia) cyc3b mRNA for cyclin 3b protein

Seq. No.	174017
Seq. ID	jC-atXLIB327419P4g06a2
Method	BLASTN
NCBI GI	g4199934
BLAST score	100
E value	8.0e-49
Match length	184
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	174018
Seq. ID	jC-atXLIB327419P4g08a2
Method	BLASTN
NCBI GI	g871991
BLAST score	92
E value	5.0e-44
Match length	108
% identity	96
NCBI Description	A.thaliana TGG2 gene for myrosinase

Seq. No.	174019
Seq. ID	jC-atXLIB327419P4g11a2
Method	BLASTN
NCBI GI	g4589435
BLAST score	171
E value	3.0e-91
Match length	242
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	174020
Seq. ID	jC-atXLIB327419P4g12a2
Method	BLASTN
NCBI GI	g3241916
BLAST score	51
E value	1.0e-19
Match length	217
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	174021
Seq. ID	jC-atXLIB327419P4h04b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	58
E value	4.0e-24
Match length	66
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174022
Seq. ID	jC-atXLIB327419P4h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	60
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174023
Seq. ID	jC-atXLIB327419P4h09a2
Method	BLASTN
NCBI GI	g2337888
BLAST score	94
E value	3.0e-45
Match length	302
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	174024
Seq. ID	jC-atXLIB327420P1a12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174025
Seq. ID	jC-atXLIB327420P1a12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174026
Seq. ID	jC-atXLIB327420P1b09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	1.0e-11
Match length	53

% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174027
Seq. ID	jC-atXLIB327420P1d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	1.0e-11
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174028
Seq. ID	jC-atXLIB327420P1e05a1
Method	BLASTN
NCBI GI	g2828188
BLAST score	66
E value	1.0e-28
Match length	200
% identity	35
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	174029
Seq. ID	jC-atXLIB327420P1e08a1
Method	BLASTN
NCBI GI	g2351066
BLAST score	312
E value	1.0e-175
Match length	463
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	174030
Seq. ID	jC-atXLIB327420P1e12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	9.0e-13
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174031
Seq. ID	jC-atXLIB327420P1e12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174032

Seq. ID	jC-atXLIB327420P1f02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	3.0e-10
Match length	67
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174033
Seq. ID	jC-atXLIB327420P1f09a1
Method	BLASTN
NCBI GI	g3449325
BLAST score	80
E value	1.0e-36
Match length	120
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	174034
Seq. ID	jC-atXLIB327420P1f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	3.0e-12
Match length	69
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174035
Seq. ID	jC-atXLIB327420P1g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174036
Seq. ID	jC-atXLIB327420P1h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	61
E value	1.0e-25
Match length	61
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174037
Seq. ID	jC-atXLIB327420P1h06a1
Method	BLASTX
NCBI GI	g3641252
BLAST score	292
E value	6.0e-26

Match length	156
% identity	45
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	174038
Seq. ID	jC-atXLIB327420P1h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	5.0e-20
Match length	72
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174039
Seq. ID	jC-atXLIB327420P1h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174040
Seq. ID	jC-atXLIB327420P1h12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174041
Seq. ID	jC-atXLIB327420P1h12b1
Method	BLASTX
NCBI GI	g3776005
BLAST score	252
E value	2.0e-21
Match length	150
% identity	43
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	174042
Seq. ID	jC-atXLIB327420P2a07a2
Method	BLASTX
NCBI GI	g1076777
BLAST score	278
E value	1.0e-24
Match length	96
% identity	61
NCBI Description	protein H2A - wheat >gi_536890_dbj_BAA07277_ (D38088) protein H2A [Triticum aestivum]

Seq. No.	174043
Seq. ID	jC-atXLIB327420P2a09a2
Method	BLASTN
NCBI GI	g2351063
BLAST score	70
E value	6.0e-31
Match length	114
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	174044
Seq. ID	jC-atXLIB327420P2a10a2
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	62
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174045
Seq. ID	jC-atXLIB327420P2d02a2
Method	BLASTX
NCBI GI	g1046225
BLAST score	254
E value	1.0e-21
Match length	76
% identity	62
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	174046
Seq. ID	jC-atXLIB327420P2d05a2
Method	BLASTN
NCBI GI	g4741184
BLAST score	198
E value	1.0e-107
Match length	347
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	174047
Seq. ID	jC-atXLIB327420P2d11a2
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	73
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174048
Seq. ID	jC-atXLIB327420P2e02a2

Method	BLASTN
NCBI GI	g3449320
BLAST score	145
E value	1.0e-75
Match length	383
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	174049
Seq. ID	jC-atXLIB327420P2e05a2
Method	BLASTN
NCBI GI	g4220633
BLAST score	66
E value	2.0e-28
Match length	198
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	174050
Seq. ID	jC-atXLIB327420P2e07a2
Method	BLASTX
NCBI GI	g1514639
BLAST score	180
E value	4.0e-13
Match length	78
% identity	46
NCBI Description	(X85181) alpha-glucan phosphorylase [Spinacia oleracea]

Seq. No.	174051
Seq. ID	jC-atXLIB327420P2e10a2
Method	BLASTX
NCBI GI	g3367523
BLAST score	156
E value	3.0e-10
Match length	59
% identity	49
NCBI Description	(AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No.	174052
Seq. ID	jC-atXLIB327420P2e11a2
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	8.0e-15
Match length	71
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174053
Seq. ID	jC-atXLIB327420P2f03a2
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	8.0e-15

Match length	67
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174054
Seq. ID	jC-atXLIB327420P2f04a2
Method	BLASTX
NCBI GI	g2462737
BLAST score	224
E value	3.0e-18
Match length	98
% identity	56
NCBI Description	(AC002292) similar to "Mx" GTP-binding proteins [Arabidopsis thaliana]

Seq. No.	174055
Seq. ID	jC-atXLIB327420P2f06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174056
Seq. ID	jC-atXLIB327420P2f12a2
Method	BLASTN
NCBI GI	g2264307
BLAST score	136
E value	2.0e-70
Match length	263
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	174057
Seq. ID	jC-atXLIB327420P2g02a2
Method	BLASTN
NCBI GI	g3056579
BLAST score	51
E value	1.0e-19
Match length	199
% identity	85
NCBI Description	Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174058
Seq. ID	jC-atXLIB327420P2g03a2
Method	BLASTN
NCBI GI	g4760411
BLAST score	169
E value	5.0e-90
Match length	269
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	174059
Seq. ID	jC-atXLIB327420P2h02a2
Method	BLASTN
NCBI GI	g3341671
BLAST score	65
E value	6.0e-28
Match length	172
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174060
Seq. ID	jC-atXLIB327420P2h03a2
Method	BLASTN
NCBI GI	g4519197
BLAST score	133
E value	2.0e-68
Match length	208
% identity	20
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MTC11, complete sequence

Seq. No.	174061
Seq. ID	jC-atXLIB327420P2h05a2
Method	BLASTX
NCBI GI	g4415994
BLAST score	324
E value	6.0e-30
Match length	62
% identity	100
NCBI Description	(AF059289) beta-tubulin 3 [Eleusine indica]

Seq. No.	174062
Seq. ID	jC-atXLIB327420P2h07a2
Method	BLASTX
NCBI GI	g4455307
BLAST score	179
E value	6.0e-13
Match length	70
% identity	57
NCBI Description	(AL035528) methionyl-tRNA synthetase-like protein [Arabidopsis thaliana]

Seq. No.	174063
Seq. ID	jC-atXLIB327420P3a01b1
Method	BLASTN
NCBI GI	g2264302
BLAST score	64
E value	3.0e-27
Match length	268
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	174064
Seq. ID	jC-atXLIB327420P3a02b1

Method	BLASTX
NCBI GI	g115767
BLAST score	496
E value	2.0e-52
Match length	123
% identity	86
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	174065
Seq. ID	jC-atXLIB327420P3a11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174066
Seq. ID	jC-atXLIB327420P3b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	1.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174067
Seq. ID	jC-atXLIB327420P3c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	79
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174068
Seq. ID	jC-atXLIB327420P3c03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No. 174069

Seq. ID	jC-atXLIB327420P3c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174070
Seq. ID	jC-atXLIB327420P3c10a1
Method	BLASTN
NCBI GI	g2275194
BLAST score	60
E value	9.0e-25
Match length	143
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174071
Seq. ID	jC-atXLIB327420P3c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	1.0e-18
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174072
Seq. ID	jC-atXLIB327420P3d09b1
Method	BLASTX
NCBI GI	g3334404
BLAST score	770
E value	3.0e-82
Match length	149
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	174073
Seq. ID	jC-atXLIB327420P3e05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174074
Seq. ID	jC-atXLIB327420P3e06b1
Method	BLASTX
NCBI GI	g3122753
BLAST score	569
E value	1.0e-58
Match length	105
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	174075
Seq. ID	jC-atXLIB327420P3e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	76
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174076
Seq. ID	jC-atXLIB327420P3e11a1
Method	BLASTX
NCBI GI	g1076290
BLAST score	256
E value	7.0e-22
Match length	69
% identity	74
NCBI Description	amino acid transporter AAP4 - Arabidopsis thaliana >gi_608671_emb_CAA54631_ (X77500) amino acid transporter [Arabidopsis thaliana]

Seq. No.	174077
Seq. ID	jC-atXLIB327420P3e12a1
Method	BLASTN
NCBI GI	g531832
BLAST score	48
E value	1.0e-17
Match length	48
% identity	100
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	174078
Seq. ID	jC-atXLIB327420P3f01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	72
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174079
Seq. ID	jC-atXLIB327420P3f03a1

Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	1.0e-08
Match length	37
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174080
Seq. ID	jC-atXLIB327420P3g03b1
Method	BLASTN
NCBI GI	g3273201
BLAST score	98
E value	1.0e-47
Match length	168
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for responce reactor4, complete cds

Seq. No.	174081
Seq. ID	jC-atXLIB327420P3g06b1
Method	BLASTN
NCBI GI	g3869074
BLAST score	196
E value	1.0e-106
Match length	361
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	174082
Seq. ID	jC-atXLIB327420P3g08a1
Method	BLASTN
NCBI GI	g2895509
BLAST score	69
E value	1.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana putative pectin methylesterase (PME3) gene, complete cds

Seq. No.	174083
Seq. ID	jC-atXLIB327420P3g09b1
Method	BLASTX
NCBI GI	g4106340
BLAST score	403
E value	4.0e-39
Match length	80
% identity	97
NCBI Description	(AF062396) protein phosphatase 2A regulatory subunit isoform B' delta [Arabidopsis thaliana]

Seq. No.	174084
Seq. ID	jC-atXLIB327420P3g10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	34

E value	3.0e-09
Match length	38
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174085
Seq. ID	jC-atXLIB327420P3h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174086
Seq. ID	jC-atXLIB327420P3h04a1
Method	BLASTN
NCBI GI	g4538972
BLAST score	35
E value	3.0e-10
Match length	83
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)

Seq. No.	174087
Seq. ID	jC-atXLIB327420P3h07b1
Method	BLASTX
NCBI GI	g4567313
BLAST score	441
E value	1.0e-43
Match length	97
% identity	82
NCBI Description	(AC005956) putative SUPERMAN transcription factor [Arabidopsis thaliana]

Seq. No.	174088
Seq. ID	jC-atXLIB327420P4a02a1
Method	BLASTN
NCBI GI	g4757413
BLAST score	118
E value	2.0e-59
Match length	299
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	174089
Seq. ID	jC-atXLIB327420P4a08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	96

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174090
Seq. ID	jC-atXLIB327420P4b03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174091
Seq. ID	jC-atXLIB327420P4b05a1
Method	BLASTN
NCBI GI	g3869072
BLAST score	182
E value	7.0e-98
Match length	308
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	174092
Seq. ID	jC-atXLIB327420P4b09a1
Method	BLASTX
NCBI GI	g1709825
BLAST score	247
E value	1.0e-20
Match length	85
% identity	64
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	174093
Seq. ID	jC-atXLIB327420P4b12b1
Method	BLASTX
NCBI GI	g2854070
BLAST score	515
E value	2.0e-52
Match length	125
% identity	82
NCBI Description	(AF044914) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	174094
Seq. ID	jC-atXLIB327420P4c01a1
Method	BLASTN
NCBI GI	g3046851
BLAST score	43
E value	8.0e-15
Match length	200
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	174095
Seq. ID	jC-atXLIB327420P4c04a1
Method	BLASTX
NCBI GI	g2149640
BLAST score	309
E value	4.0e-28
Match length	86
% identity	72
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	174096
Seq. ID	jC-atXLIB327420P4c08a1
Method	BLASTN
NCBI GI	g4220637
BLAST score	60
E value	4.0e-25
Match length	213
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	174097
Seq. ID	jC-atXLIB327420P4c12a1
Method	BLASTN
NCBI GI	g4415905
BLAST score	108
E value	1.0e-53
Match length	479
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174098
Seq. ID	jC-atXLIB327420P4d01a1
Method	BLASTX
NCBI GI	g4204272
BLAST score	260
E value	4.0e-22
Match length	83
% identity	57
NCBI Description	(AC005223) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	174099
Seq. ID	jC-atXLIB327420P4d04a1
Method	BLASTN
NCBI GI	g2245031
BLAST score	61
E value	2.0e-25
Match length	215
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174100
Seq. ID	jC-atXLIB327420P4d06a1
Method	BLASTN
NCBI GI	g540252

BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174101
Seq. ID	jC-atXLIB327420P4d09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174102
Seq. ID	jC-atXLIB327420P4d10a1
Method	BLASTN
NCBI GI	g710625
BLAST score	272
E value	1.0e-151
Match length	484
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	174103
Seq. ID	jC-atXLIB327420P4e01a1
Method	BLASTN
NCBI GI	g2842474
BLAST score	88
E value	2.0e-41
Match length	179
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	174104
Seq. ID	jC-atXLIB327420P4e05a1
Method	BLASTN
NCBI GI	g2760172
BLAST score	90
E value	5.0e-43
Match length	248
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	174105
Seq. ID	jC-atXLIB327420P4e07a1
Method	BLASTN
NCBI GI	g16285
BLAST score	44
E value	4.0e-15
Match length	213
% identity	88
NCBI Description	A.thaliana mRNA GBF1 for G-box binding factor

Seq. No.	174106
Seq. ID	jC-atXLIB327420P4e09a1
Method	BLASTN
NCBI GI	g3702315
BLAST score	104
E value	5.0e-51
Match length	209
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174107
Seq. ID	jC-atXLIB327420P4e10a1
Method	BLASTN
NCBI GI	g2252848
BLAST score	168
E value	2.0e-89
Match length	358
% identity	91
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	174108
Seq. ID	jC-atXLIB327420P4e12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174109
Seq. ID	jC-atXLIB327420P4f01a1
Method	BLASTN
NCBI GI	g4589425
BLAST score	109
E value	4.0e-54
Match length	286
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBA10, complete sequence

Seq. No.	174110
Seq. ID	jC-atXLIB327420P4f02a1
Method	BLASTN
NCBI GI	g2226430
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Mus saxicola haptoglobin mRNA, complete cds

Seq. No.	174111
Seq. ID	jC-atXLIB327420P4f03a1
Method	BLASTN
NCBI GI	g2252823

BLAST score	64
E value	4.0e-27
Match length	245
% identity	85
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	174112
Seq. ID	jC-atXLIB327420P4f06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	1.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174113
Seq. ID	jC-atXLIB327420P4f06b1
Method	BLASTX
NCBI GI	g2119846
BLAST score	71
E value	2.0e-27
Match length	127
% identity	58
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	174114
Seq. ID	jC-atXLIB327420P4f08a1
Method	BLASTX
NCBI GI	g4539330
BLAST score	144
E value	1.0e-08
Match length	159
% identity	30
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	174115
Seq. ID	jC-atXLIB327420P4f10a1
Method	BLASTX
NCBI GI	g729477
BLAST score	271
E value	2.0e-23
Match length	111
% identity	52
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No.	174116
Seq. ID	jC-atXLIB327420P4g03a1
Method	BLASTN
NCBI GI	g540252
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174117
Seq. ID	jC-atXLIB327420P4g04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174118
Seq. ID	jC-atXLIB327420P4g06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	6.0e-14
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174119
Seq. ID	jC-atXLIB327420P4g09a1
Method	BLASTN
NCBI GI	g3790586
BLAST score	339
E value	0.0e+00
Match length	423
% identity	95
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHF2a mRNA, complete cds

Seq. No.	174120
Seq. ID	jC-atXLIB327420P4g11a1
Method	BLASTN
NCBI GI	g3980374
BLAST score	190
E value	1.0e-102
Match length	414
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174121
Seq. ID	jC-atXLIB327420P4h06a1
Method	BLASTN
NCBI GI	g1046224

BLAST score	90
E value	7.0e-43
Match length	337
% identity	85
NCBI Description	Arabidopsis thaliana ethylene response sensor (ERS) gene, complete cds

Seq. No.	174122
Seq. ID	jC-atXLIB327420P4h09a1
Method	BLASTX
NCBI GI	g2118222
BLAST score	100
E value	1.0e-14
Match length	53
% identity	86
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	174123
Seq. ID	jC-atXLIB327420P4h11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174124
Seq. ID	jC-atXLIB327421P1a03a1
Method	BLASTN
NCBI GI	g4092472
BLAST score	146
E value	2.0e-76
Match length	238
% identity	48
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	174125
Seq. ID	jC-atXLIB327421P1a03b1
Method	BLASTN
NCBI GI	g3128134
BLAST score	143
E value	1.0e-74
Match length	146
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	174126
Seq. ID	jC-atXLIB327421P1a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60

E value	4.0e-25
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174127
Seq. ID	jC-atXLIB327421P1a09a1
Method	BLASTX
NCBI GI	g480450
BLAST score	68
E value	6.0e-14
Match length	58
% identity	74
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	174128
Seq. ID	jC-atXLIB327421P1a10b1
Method	BLASTX
NCBI GI	g4512712
BLAST score	270
E value	1.0e-23
Match length	49
% identity	100
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	174129
Seq. ID	jC-atXLIB327421P1b01b1
Method	BLASTN
NCBI GI	g4454447
BLAST score	62
E value	3.0e-26
Match length	136
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174130
Seq. ID	jC-atXLIB327421P1b02a1
Method	BLASTN
NCBI GI	g3150396
BLAST score	109
E value	3.0e-54
Match length	128
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174131
Seq. ID	jC-atXLIB327421P1b02b1
Method	BLASTX
NCBI GI	g3150406
BLAST score	312
E value	2.0e-28
Match length	110

% identity	65
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	174132
Seq. ID	jC-atXLIB327421P1b03a1
Method	BLASTX
NCBI GI	g3643603
BLAST score	274
E value	4.0e-24
Match length	53
% identity	98
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	174133
Seq. ID	jC-atXLIB327421P1b06a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	185
E value	1.0e-99
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174134
Seq. ID	jC-atXLIB327421P1b07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174135
Seq. ID	jC-atXLIB327421P1b07b1
Method	BLASTX
NCBI GI	g4585882
BLAST score	194
E value	9.0e-15
Match length	68
% identity	65
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	174136
Seq. ID	jC-atXLIB327421P1b08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	5.0e-12
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174137

Seq. ID	jC-atXLIB327421P1b09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	2.0e-30
Match length	81
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174138
Seq. ID	jC-atXLIB327421P1b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	53
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174139
Seq. ID	jC-atXLIB327421P1b12a1
Method	BLASTN
NCBI GI	g2924733
BLAST score	262
E value	1.0e-145
Match length	294
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	174140
Seq. ID	jC-atXLIB327421P1b12b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	313
E value	1.0e-176
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	174141
Seq. ID	jC-atXLIB327421P1c01b1
Method	BLASTX
NCBI GI	g3242709
BLAST score	610
E value	2.0e-63
Match length	126
% identity	94
NCBI Description	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No.	174142
Seq. ID	jC-atXLIB327421P1c02a1
Method	BLASTN
NCBI GI	g3927822

BLAST score	130
E value	1.0e-66
Match length	130
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174143
Seq. ID	jC-atXLIB327421P1c05b1
Method	BLASTX
NCBI GI	g1703328
BLAST score	169
E value	3.0e-45
Match length	142
% identity	62
NCBI Description	CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN) >gi_1174262 (U44890) DdApm1 [Dictyostelium discoideum]

Seq. No.	174144
Seq. ID	jC-atXLIB327421P1c07a1
Method	BLASTN
NCBI GI	g4220468
BLAST score	49
E value	2.0e-18
Match length	101
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174145
Seq. ID	jC-atXLIB327421P1c10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	9.0e-21
Match length	64
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174146
Seq. ID	jC-atXLIB327421P1d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174147
Seq. ID	jC-atXLIB327421P1d09a1
Method	BLASTN
NCBI GI	g4584339

BLAST score	115
E value	9.0e-58
Match length	119
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	174148
Seq. ID	jC-atXLIB327421P1d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174149
Seq. ID	jC-atXLIB327421P1e05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174150
Seq. ID	jC-atXLIB327421P1e06b1
Method	BLASTX
NCBI GI	g3128187
BLAST score	169
E value	9.0e-52
Match length	140
% identity	67
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	174151
Seq. ID	jC-atXLIB327421P1e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174152
Seq. ID	jC-atXLIB327421P1e08b1
Method	BLASTX
NCBI GI	g3157944
BLAST score	394
E value	1.0e-38
Match length	120
% identity	75

NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	174153
Seq. ID	jC-atXLIB327421P1e09a1
Method	BLASTX
NCBI GI	g4512615
BLAST score	351
E value	3.0e-33
Match length	74
% identity	97
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	174154
Seq. ID	jC-atXLIB327421P1e12a1
Method	BLASTN
NCBI GI	g3510337
BLAST score	48
E value	9.0e-18
Match length	68
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	174155
Seq. ID	jC-atXLIB327421P1f01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	50
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174156
Seq. ID	jC-atXLIB327421P1f02a1
Method	BLASTX
NCBI GI	g2765242
BLAST score	209
E value	2.0e-16
Match length	110
% identity	41
NCBI Description	(Y12806) invertase inhibitor homolog [Nicotiana tabacum]

Seq. No.	174157
Seq. ID	jC-atXLIB327421P1f02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	2.0e-26
Match length	77

% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174158
Seq. ID	jC-atXLIB327421P1f03a1
Method	BLASTN
NCBI GI	g3941501
BLAST score	112
E value	5.0e-56
Match length	116
% identity	99
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB72) mRNA, partial cds

Seq. No.	174159
Seq. ID	jC-atXLIB327421P1f06a1
Method	BLASTN
NCBI GI	g3461810
BLAST score	208
E value	1.0e-113
Match length	276
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174160
Seq. ID	jC-atXLIB327421P1f06b1
Method	BLASTN
NCBI GI	g3461810
BLAST score	202
E value	1.0e-109
Match length	233
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174161
Seq. ID	jC-atXLIB327421P1f07a1
Method	BLASTN
NCBI GI	g2702261
BLAST score	311
E value	1.0e-174
Match length	331
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174162
Seq. ID	jC-atXLIB327421P1f09b1
Method	BLASTN
NCBI GI	g4584339
BLAST score	72
E value	4.0e-32
Match length	96
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic

sequence, complete sequence

Seq. No.	174163
Seq. ID	jC-atXLIB327421P1f10a1
Method	BLASTN
NCBI GI	g2262155
BLAST score	49
E value	2.0e-18
Match length	123
% identity	93
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	174164
Seq. ID	jC-atXLIB327421P1f12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174165
Seq. ID	jC-atXLIB327421P1g04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174166
Seq. ID	jC-atXLIB327421P1g08a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	81
E value	2.0e-37
Match length	100
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	174167
Seq. ID	jC-atXLIB327421P1g09a1
Method	BLASTN
NCBI GI	g4741959
BLAST score	77
E value	4.0e-35
Match length	142
% identity	94
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	174168
Seq. ID	jC-atXLIB327421P1g11a1

Method	BLASTN
NCBI GI	g3859658
BLAST score	126
E value	2.0e-64
Match length	126
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	174169
Seq. ID	jC-atXLIB327421P1g12a1
Method	BLASTN
NCBI GI	g4678258
BLAST score	210
E value	1.0e-114
Match length	230
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	174170
Seq. ID	jC-atXLIB327421P1h02a1
Method	BLASTN
NCBI GI	g4519183
BLAST score	50
E value	5.0e-19
Match length	106
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	174171
Seq. ID	jC-atXLIB327421P1h04b1
Method	BLASTN
NCBI GI	g4757405
BLAST score	74
E value	3.0e-33
Match length	138
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	174172
Seq. ID	jC-atXLIB327421P1h06a1
Method	BLASTN
NCBI GI	g4159706
BLAST score	77
E value	4.0e-35
Match length	226
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	174173
Seq. ID	jC-atXLIB327421P1h07a1
Method	BLASTN
NCBI GI	g556473

BLAST score	75
E value	7.0e-34
Match length	79
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ERD14 protein, complete cds

Seq. No.	174174
Seq. ID	jC-atXLIB327421P1h07b1
Method	BLASTN
NCBI GI	g556473
BLAST score	99
E value	3.0e-48
Match length	218
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for ERD14 protein, complete cds

Seq. No.	174175
Seq. ID	jC-atXLIB327421P1h08b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	69
E value	2.0e-30
Match length	116
% identity	57
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174176
Seq. ID	jC-atXLIB327421P1h12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174177
Seq. ID	jC-atXLIB327421P2a07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174178
Seq. ID	jC-atXLIB327421P2a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	43
E value	5.0e-15
Match length	58
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174179
Seq. ID	jC-atXLIB327421P2a09b1
Method	BLASTX
NCBI GI	g3123712
BLAST score	551
E value	1.0e-56
Match length	113
% identity	96
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	174180
Seq. ID	jC-atXLIB327421P2c03b1
Method	BLASTX
NCBI GI	g1490554
BLAST score	247
E value	5.0e-21
Match length	47
% identity	96
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	174181
Seq. ID	jC-atXLIB327421P2c04b1
Method	BLASTN
NCBI GI	g499161
BLAST score	74
E value	2.0e-33
Match length	190
% identity	84
NCBI Description	A.thaliana mRNA Athb-6

Seq. No.	174182
Seq. ID	jC-atXLIB327421P2e02b1
Method	BLASTX
NCBI GI	g1550740
BLAST score	614
E value	6.0e-64
Match length	117
% identity	97
NCBI Description	(Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No.	174183
Seq. ID	jC-atXLIB327421P2f05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	61
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174184
Seq. ID	jC-atXLIB327421P2g07b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	58
E value	7.0e-24
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174185
Seq. ID	jC-atXLIB327421P2h02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174186
Seq. ID	jC-atXLIB327421P2h08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174187
Seq. ID	jC-atXLIB327421P3a02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	75
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174188
Seq. ID	jC-atXLIB327421P3a06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174189
Seq. ID	jC-atXLIB327421P3a09b1
Method	BLASTN
NCBI GI	g3985957
BLAST score	138
E value	2.0e-71
Match length	408

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	174190
Seq. ID	jC-atXLIB327421P3b05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174191
Seq. ID	jC-atXLIB327421P3b11a1
Method	BLASTX
NCBI GI	g3935154
BLAST score	287
E value	1.0e-25
Match length	70
% identity	74
NCBI Description	(AC005106) T25N20.18 [Arabidopsis thaliana]

Seq. No.	174192
Seq. ID	jC-atXLIB327421P3c01a1
Method	BLASTN
NCBI GI	g3046855
BLAST score	141
E value	3.0e-73
Match length	277
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	174193
Seq. ID	jC-atXLIB327421P3c02a1
Method	BLASTN
NCBI GI	g3449326
BLAST score	105
E value	9.0e-52
Match length	271
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	174194
Seq. ID	jC-atXLIB327421P3c05a1
Method	BLASTX
NCBI GI	g4406819
BLAST score	392
E value	6.0e-38
Match length	82
% identity	100
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	174195

Seq. ID	jC-atXLIB327421P3c10a1
Method	BLASTX
NCBI GI	g1076315
BLAST score	385
E value	4.0e-37
Match length	73
% identity	99
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	174196
Seq. ID	jC-atXLIB327421P3d10a1
Method	BLASTN
NCBI GI	g4193381
BLAST score	72
E value	4.0e-32
Match length	170
% identity	88
NCBI Description	Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA, complete cds

Seq. No.	174197
Seq. ID	jC-atXLIB327421P3e07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174198
Seq. ID	jC-atXLIB327421P3e08b1
Method	BLASTX
NCBI GI	g113782
BLAST score	235
E value	2.0e-19
Match length	47
% identity	98
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	174199
Seq. ID	jC-atXLIB327421P3e10a1
Method	BLASTX
NCBI GI	g136251
BLAST score	228
E value	1.0e-18
Match length	63
% identity	71
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20)

beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	174200
Seq. ID	jC-atXLIB327421P3f01a1
Method	BLASTN
NCBI GI	g4757392
BLAST score	119
E value	4.0e-60
Match length	167
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	174201
Seq. ID	jC-atXLIB327421P3f04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174202
Seq. ID	jC-atXLIB327421P3g01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174203
Seq. ID	jC-atXLIB327421P3g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	59
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174204
Seq. ID	jC-atXLIB327421P3g04a1
Method	BLASTX
NCBI GI	g2244871
BLAST score	303
E value	2.0e-27
Match length	62
% identity	94
NCBI Description	(Z97338) phosphocholine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	174205
Seq. ID	jC-atXLIB327421P3g07b1
Method	BLASTX
NCBI GI	g930002
BLAST score	688
E value	1.0e-72
Match length	130
% identity	100
NCBI Description	(X13435) nitrate reductase NR2 (396 AA) [Arabidopsis thaliana]

Seq. No.	174206
Seq. ID	jC-atXLIB327421P3h02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174207
Seq. ID	jC-atXLIB327421P3h03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174208
Seq. ID	jC-atXLIB327421P3h08a1
Method	BLASTX
NCBI GI	g4559354
BLAST score	191
E value	2.0e-14
Match length	129
% identity	5
NCBI Description	(AC006585) unknown protein [Arabidopsis thaliana]

Seq. No.	174209
Seq. ID	jC-atXLIB327421P4a07b1
Method	BLASTN
NCBI GI	g4519194
BLAST score	65
E value	6.0e-28
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	174210
Seq. ID	jC-atXLIB327421P4b02b1
Method	BLASTN
NCBI GI	g3150396

BLAST score	84
E value	3.0e-39
Match length	92
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174211
Seq. ID	jC-atXLIB327421P4b04b1
Method	BLASTN
NCBI GI	g4580745
BLAST score	70
E value	7.0e-31
Match length	156
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	174212
Seq. ID	jC-atXLIB327421P4b05b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	37
E value	3.0e-11
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174213
Seq. ID	jC-atXLIB327421P4b07a1
Method	BLASTN
NCBI GI	g3510346
BLAST score	56
E value	1.0e-22
Match length	249
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	174214
Seq. ID	jC-atXLIB327421P4b08a1
Method	BLASTX
NCBI GI	g2149021
BLAST score	116
E value	4.0e-11
Match length	61
% identity	72
NCBI Description	(U72290) ADPG pyrophosphorylase large subunit [Arabidopsis thaliana]

Seq. No.	174215
Seq. ID	jC-atXLIB327421P4b08b1
Method	BLASTN
NCBI GI	g4586349
BLAST score	51
E value	1.0e-19

Match length	55
% identity	98
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	174216
Seq. ID	jC-atXLIB327421P4b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174217
Seq. ID	jC-atXLIB327421P4b10b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	92
E value	4.0e-44
Match length	149
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	174218
Seq. ID	jC-atXLIB327421P4b11b1
Method	BLASTX
NCBI GI	g464621
BLAST score	318
E value	3.0e-29
Match length	102
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	174219
Seq. ID	jC-atXLIB327421P4b12b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	60
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174220
Seq. ID	jC-atXLIB327421P4c03b1
Method	BLASTN
NCBI GI	g4646215
BLAST score	66
E value	1.0e-28
Match length	66

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No.	174221
Seq. ID	jC-atXLIB327421P4c08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174222
Seq. ID	jC-atXLIB327421P4c09a1
Method	BLASTN
NCBI GI	g540252
BLAST score	45
E value	6.0e-16
Match length	45
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174223
Seq. ID	jC-atXLIB327421P4c10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174224
Seq. ID	jC-atXLIB327421P4c12b1
Method	BLASTX
NCBI GI	g2129622
BLAST score	438
E value	3.0e-43
Match length	110
% identity	77
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	174225
Seq. ID	jC-atXLIB327421P4d04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	6.0e-16
Match length	45
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174226
Seq. ID	jC-atXLIB327421P4d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174227
Seq. ID	jC-atXLIB327421P4d06a1
Method	BLASTN
NCBI GI	g4337186
BLAST score	251
E value	1.0e-139
Match length	299
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174228
Seq. ID	jC-atXLIB327421P4d08b1
Method	BLASTX
NCBI GI	g464662
BLAST score	740
E value	1.0e-78
Match length	145
% identity	60
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	174229
Seq. ID	jC-atXLIB327421P4d10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174230
Seq. ID	jC-atXLIB327421P4d11a1
Method	BLASTN
NCBI GI	g2853071
BLAST score	104

E value	3.0e-51
Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	174231
Seq. ID	jC-atXLIB327421P4e02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14
Match length	46
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174232
Seq. ID	jC-atXLIB327421P4e03b1
Method	BLASTX
NCBI GI	g4587552
BLAST score	662
E value	1.0e-69
Match length	130
% identity	100
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	174233
Seq. ID	jC-atXLIB327421P4e04a1
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174234
Seq. ID	jC-atXLIB327421P4e05a1
Method	BLASTN
NCBI GI	g2245073
BLAST score	97
E value	4.0e-47
Match length	113
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174235
Seq. ID	jC-atXLIB327421P4e08b1
Method	BLASTX
NCBI GI	g2648032
BLAST score	391
E value	5.0e-38

Match length	85
% identity	79
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	174236
Seq. ID	jC-atXLIB327421P4e09b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	61
E value	1.0e-25
Match length	85
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	174237
Seq. ID	jC-atXLIB327421P4e12a1
Method	BLASTN
NCBI GI	g642161
BLAST score	48
E value	8.0e-18
Match length	96
% identity	88
NCBI Description	A.thaliana gene for chloroplast ribosomal protein S13

Seq. No.	174238
Seq. ID	jC-atXLIB327421P4e12b1
Method	BLASTX
NCBI GI	g1173194
BLAST score	288
E value	1.0e-25
Match length	70
% identity	83
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_ (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]

Seq. No.	174239
Seq. ID	jC-atXLIB327421P4f01b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	69
E value	2.0e-30
Match length	142
% identity	45
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174240
Seq. ID	jC-atXLIB327421P4f03a1
Method	BLASTN

NCBI GI	g4455168
BLAST score	117
E value	5.0e-59
Match length	185
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	174241
Seq. ID	jC-atXLIB327421P4f04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174242
Seq. ID	jC-atXLIB327421P4f06b1
Method	BLASTN
NCBI GI	g4063730
BLAST score	250
E value	1.0e-138
Match length	322
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	174243
Seq. ID	jC-atXLIB327421P4f08a1
Method	BLASTN
NCBI GI	g1532162
BLAST score	78
E value	1.0e-35
Match length	96
% identity	95
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	174244
Seq. ID	jC-atXLIB327421P4f10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	46
E value	8.0e-17
Match length	46
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174245
Seq. ID	jC-atXLIB327421P4f10b1

Method	BLASTN
NCBI GI	g3449322
BLAST score	90
E value	3.0e-43
Match length	90
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	174246
Seq. ID	jC-atXLIB327421P4f11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18
Match length	48
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174247
Seq. ID	jC-atXLIB327421P4f12b1
Method	BLASTN
NCBI GI	g3869068
BLAST score	67
E value	4.0e-29
Match length	83
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	174248
Seq. ID	jC-atXLIB327421P4g02a1
Method	BLASTN
NCBI GI	g540252
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174249
Seq. ID	jC-atXLIB327421P4g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174250
Seq. ID	jC-atXLIB327421P4g04a1
Method	BLASTN
NCBI GI	g3434972
BLAST score	50
E value	4.0e-19

Match length	85
% identity	91
NCBI Description	Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive element binding factor 4, complete cds

Seq. No.	174251
Seq. ID	jC-atXLIB327421P4g04b1
Method	BLASTN
NCBI GI	g3434972
BLAST score	73
E value	1.0e-32
Match length	73
% identity	100
NCBI Description	Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive element binding factor 4, complete cds

Seq. No.	174252
Seq. ID	jC-atXLIB327421P4g05b1
Method	BLASTX
NCBI GI	g3599968
BLAST score	743
E value	5.0e-79
Match length	140
% identity	100
NCBI Description	(AF032123) clp protease [Arabidopsis thaliana]

Seq. No.	174253
Seq. ID	jC-atXLIB327421P4g06a1
Method	BLASTN
NCBI GI	g3241923
BLAST score	62
E value	3.0e-26
Match length	114
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	174254
Seq. ID	jC-atXLIB327421P4g08a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	111
E value	2.0e-55
Match length	111
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	174255
Seq. ID	jC-atXLIB327421P4g10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	174256
Seq. ID	jC-atXLIB327421P4g11a1
Method	BLASTN
NCBI GI	g3510344
BLAST score	120
E value	9.0e-61
Match length	132
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	174257
Seq. ID	jC-atXLIB327421P4h02b1
Method	BLASTX
NCBI GI	g1545805
BLAST score	369
E value	3.0e-35
Match length	87
% identity	84
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	174258
Seq. ID	jC-atXLIB327421P4h07b1
Method	BLASTX
NCBI GI	g2244912
BLAST score	182
E value	3.0e-13
Match length	47
% identity	79
NCBI Description	(Z97339) similar to transketolase [Arabidopsis thaliana]

Seq. No.	174259
Seq. ID	jC-atXLIB327422P1a05a1
Method	BLASTN
NCBI GI	g4757417
BLAST score	143
E value	2.0e-74
Match length	396
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	174260
Seq. ID	jC-atXLIB327422P1a06a1
Method	BLASTX
NCBI GI	g3660469
BLAST score	387
E value	2.0e-37
Match length	90
% identity	92
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No. 174261

Seq. ID	jC-atXLIB327422P1b02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174262
Seq. ID	jC-atXLIB327422P1b02b1
Method	BLASTN
NCBI GI	g1946354
BLAST score	78
E value	1.0e-35
Match length	231
% identity	56
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	174263
Seq. ID	jC-atXLIB327422P1c01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	48
E value	9.0e-18
Match length	63
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174264
Seq. ID	jC-atXLIB327422P1c01b1
Method	BLASTX
NCBI GI	g2119848
BLAST score	94
E value	2.0e-17
Match length	107
% identity	51
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	174265
Seq. ID	jC-atXLIB327422P1c07a1
Method	BLASTN
NCBI GI	g531832
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100

NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	174266
Seq. ID	jC-atXLIB327422P1d02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174267
Seq. ID	jC-atXLIB327422P1d03b1
Method	BLASTX
NCBI GI	g4584343
BLAST score	467
E value	1.0e-46
Match length	147
% identity	46
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	174268
Seq. ID	jC-atXLIB327422P1d06a1
Method	BLASTX
NCBI GI	g2642429
BLAST score	259
E value	2.0e-22
Match length	75
% identity	73
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	174269
Seq. ID	jC-atXLIB327422P1d08a1
Method	BLASTN
NCBI GI	g3789706
BLAST score	117
E value	6.0e-59
Match length	221
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174270
Seq. ID	jC-atXLIB327422P1e05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	46
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174271
Seq. ID	jC-atXLIB327422P1e05b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	1.0e-25
Match length	65
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174272
Seq. ID	jC-atXLIB327422P1e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	9.0e-14
Match length	72
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174273
Seq. ID	jC-atXLIB327422P1e10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	3.0e-11
Match length	59
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174274
Seq. ID	jC-atXLIB327422P1e11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174275
Seq. ID	jC-atXLIB327422P1e12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	2.0e-15
Match length	64
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174276
Seq. ID	jC-atXLIB327422P1e12b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	36

E value	1.0e-10
Match length	47
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174277
Seq. ID	jC-atXLIB327422P1f10b1
Method	BLASTN
NCBI GI	g3608126
BLAST score	37
E value	2.0e-11
Match length	53
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174278
Seq. ID	jC-atXLIB327422P1f11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	62
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174279
Seq. ID	jC-atXLIB327422P1f12b1
Method	BLASTX
NCBI GI	g913141
BLAST score	144
E value	5.0e-13
Match length	117
% identity	38
NCBI Description	ARK3 product/receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana, Columbia, Peptide, 851 aa]

Seq. No.	174280
Seq. ID	jC-atXLIB327422P1g03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19
Match length	66
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174281
Seq. ID	jC-atXLIB327422P1g05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	33
E value	5.0e-09
Match length	33
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No.	174282
Seq. ID	jC-atXLIB327422P1g05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	57
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174283
Seq. ID	jC-atXLIB327422P1g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	81
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174284
Seq. ID	jC-atXLIB327422P1h02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174285
Seq. ID	jC-atXLIB327422P1h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	8.0e-18
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174286
Seq. ID	jC-atXLIB327422P1h08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 174287

Seq. ID	jC-atXLIB327422P2a08a2
Method	BLASTN
NCBI GI	g3746057
BLAST score	54
E value	9.0e-22
Match length	126
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174288
Seq. ID	jC-atXLIB327422P2a09b2
Method	BLASTX
NCBI GI	g131398
BLAST score	171
E value	5.0e-12
Match length	74
% identity	42
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174289
Seq. ID	jC-atXLIB327422P2a10a2
Method	BLASTX
NCBI GI	g131398
BLAST score	218
E value	1.0e-17
Match length	53
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174290
Seq. ID	jC-atXLIB327422P2b01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	2.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 174291

Seq. ID	jC-atXLIB327422P2b05a2
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	7.0e-17
Match length	50
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174292
Seq. ID	jC-atXLIB327422P2b07a2
Method	BLASTN
NCBI GI	g2702261
BLAST score	70
E value	2.0e-31
Match length	112
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174293
Seq. ID	jC-atXLIB327422P2b07b2
Method	BLASTN
NCBI GI	g2702261
BLAST score	82
E value	5.0e-38
Match length	226
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174294
Seq. ID	jC-atXLIB327422P2b12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	2.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174295
Seq. ID	jC-atXLIB327422P2c02b2
Method	BLASTX
NCBI GI	g3309086
BLAST score	71
E value	3.0e+00
Match length	131
% identity	29
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	174296
Seq. ID	jC-atXLIB327422P2c04a2
Method	BLASTN
NCBI GI	g2462264

BLAST score	48
E value	8.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174297
Seq. ID	jC-atXLIB327422P2c05b1
Method	BLASTN
NCBI GI	g4467094
BLAST score	109
E value	2.0e-54
Match length	200
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	174298
Seq. ID	jC-atXLIB327422P2c10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174299
Seq. ID	jC-atXLIB327422P2d05a2
Method	BLASTX
NCBI GI	g4467121
BLAST score	220
E value	1.0e-17
Match length	65
% identity	71
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	174300
Seq. ID	jC-atXLIB327422P2d09a2
Method	BLASTN
NCBI GI	g3075383
BLAST score	267
E value	1.0e-148
Match length	347
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174301
Seq. ID	jC-atXLIB327422P2d11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	1.0e-18
Match length	61
% identity	95

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174302
Seq. ID	jC-atXLIB327422P2e03b1
Method	BLASTN
NCBI GI	g1695718
BLAST score	43
E value	8.0e-15
Match length	80
% identity	86
NCBI Description	Arabidopsis thaliana DNA for luminal binding protein, complete cds

Seq. No.	174303
Seq. ID	jC-atXLIB327422P2e04a2
Method	BLASTN
NCBI GI	g540252
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174304
Seq. ID	jC-atXLIB327422P2e04b2
Method	BLASTX
NCBI GI	g1203832
BLAST score	133
E value	5.0e-34
Match length	123
% identity	60
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	174305
Seq. ID	jC-atXLIB327422P2e05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	68
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174306
Seq. ID	jC-atXLIB327422P2e07a2
Method	BLASTN
NCBI GI	g4559344
BLAST score	94
E value	4.0e-45
Match length	206
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	174307
Seq. ID	jC-atXLIB327422P2e09a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	58
E value	1.0e-23
Match length	58
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174308
Seq. ID	jC-atXLIB327422P2f03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	59
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174309
Seq. ID	jC-atXLIB327422P2f06a2
Method	BLASTN
NCBI GI	g2245073
BLAST score	103
E value	4.0e-51
Match length	132
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174310
Seq. ID	jC-atXLIB327422P2f10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	9.0e-19
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174311
Seq. ID	jC-atXLIB327422P2g03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	71
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174312
Seq. ID	jC-atXLIB327422P2g05b1

Method	BLASTN
NCBI GI	g4220631
BLAST score	51
E value	2.0e-19
Match length	66
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	174313
Seq. ID	jC-atXLIB327422P2g10a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	36
E value	1.0e-10
Match length	52
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174314
Seq. ID	jC-atXLIB327422P2g11a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174315
Seq. ID	jC-atXLIB327422P2g11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174316
Seq. ID	jC-atXLIB327422P2h03a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	36
E value	8.0e-11
Match length	40
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174317
Seq. ID	jC-atXLIB327422P3a04a2
Method	BLASTN
NCBI GI	g4490717
BLAST score	144

E value	4.0e-75
Match length	323
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	174318
Seq. ID	jC-atXLIB327422P3a07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174319
Seq. ID	jC-atXLIB327422P3a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	6.0e-24
Match length	62
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174320
Seq. ID	jC-atXLIB327422P3a10b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174321
Seq. ID	jC-atXLIB327422P3b03b2
Method	BLASTX
NCBI GI	g3150414
BLAST score	279
E value	3.0e-32
Match length	123
% identity	64
NCBI Description	(AC004165) AtRanBP1b protein [Arabidopsis thaliana]

Seq. No.	174322
Seq. ID	jC-atXLIB327422P3b06b2
Method	BLASTX
NCBI GI	g4249662
BLAST score	253
E value	1.0e-21
Match length	66
% identity	80
NCBI Description	(AF089810) Altered Response to Gravity [Arabidopsis

thaliana]

Seq. No.	174323
Seq. ID	jC-atXLIB327422P3b10b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	5.0e-13
Match length	52
% identity	94
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174324
Seq. ID	jC-atXLIB327422P3b11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	2.0e-14
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174325
Seq. ID	jC-atXLIB327422P3c03b2
Method	BLASTN
NCBI GI	g4589439
BLAST score	95
E value	8.0e-46
Match length	189
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	174326
Seq. ID	jC-atXLIB327422P3c04a2
Method	BLASTX
NCBI GI	g1402877
BLAST score	343
E value	3.0e-32
Match length	72
% identity	92
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis thaliana]

Seq. No.	174327
Seq. ID	jC-atXLIB327422P3c04b2
Method	BLASTX
NCBI GI	g1402877
BLAST score	258
E value	3.0e-22
Match length	91
% identity	59
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis

thaliana]

Seq. No.	174328
Seq. ID	jC-atXLIB327422P3c05b2
Method	BLASTN
NCBI GI	g3510343
BLAST score	186
E value	1.0e-100
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	174329
Seq. ID	jC-atXLIB327422P3c08a2
Method	BLASTN
NCBI GI	g3641835
BLAST score	60
E value	2.0e-25
Match length	88
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	174330
Seq. ID	jC-atXLIB327422P3c08b2
Method	BLASTN
NCBI GI	g3641835
BLAST score	77
E value	4.0e-35
Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	174331
Seq. ID	jC-atXLIB327422P3c11b2
Method	BLASTN
NCBI GI	g4115352
BLAST score	53
E value	9.0e-21
Match length	133
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174332
Seq. ID	jC-atXLIB327422P3c12b2
Method	BLASTX
NCBI GI	g435805
BLAST score	174
E value	2.0e-12
Match length	71
% identity	41
NCBI Description	(S66176) UNC-18=vesicle transport protein [Caenorhabditis elegans, Peptide, 591 aa] [Caenorhabditis elegans]

Seq. No.	174333
Seq. ID	jC-atXLIB327422P3d01b2
Method	BLASTN
NCBI GI	g4567300
BLAST score	246
E value	1.0e-136
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	174334
Seq. ID	jC-atXLIB327422P3d02b2
Method	BLASTX
NCBI GI	g1710401
BLAST score	152
E value	8.0e-10
Match length	108
% identity	36
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	174335
Seq. ID	jC-atXLIB327422P3d03b1
Method	BLASTN
NCBI GI	g3805839
BLAST score	65
E value	6.0e-28
Match length	154
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	174336
Seq. ID	jC-atXLIB327422P3d07a2
Method	BLASTN
NCBI GI	g3449315
BLAST score	227
E value	1.0e-124
Match length	356
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	174337
Seq. ID	jC-atXLIB327422P3e01b2
Method	BLASTX
NCBI GI	g120667
BLAST score	499
E value	2.0e-50
Match length	116
% identity	90
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	174338
Seq. ID	jC-atXLIB327422P3e04b2
Method	BLASTN
NCBI GI	g2696018
BLAST score	59
E value	2.0e-24
Match length	259
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	174339
Seq. ID	jC-atXLIB327422P3e05a2
Method	BLASTX
NCBI GI	g548490
BLAST score	170
E value	5.0e-12
Match length	49
% identity	59
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_629596_pir__S42549 polygalacturonase - rape >gi_304223 (L19879) polygalacturonase [Brassica napus]

Seq. No.	174340
Seq. ID	jC-atXLIB327422P3e06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	9.0e-22
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174341
Seq. ID	jC-atXLIB327422P3e07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	3.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174342
Seq. ID	jC-atXLIB327422P3e09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	7.0e-15
Match length	43
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174343
Seq. ID	jC-atXLIB327422P3e09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	57
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174344
Seq. ID	jC-atXLIB327422P3e11b1
Method	BLASTN
NCBI GI	g3281847
BLAST score	62
E value	4.0e-26
Match length	109
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	174345
Seq. ID	jC-atXLIB327422P3e12a2
Method	BLASTN
NCBI GI	g2760170
BLAST score	169
E value	4.0e-90
Match length	302
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	174346
Seq. ID	jC-atXLIB327422P3f01b2
Method	BLASTN
NCBI GI	g3449313
BLAST score	105
E value	8.0e-52
Match length	357
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	174347
Seq. ID	jC-atXLIB327422P3f09b1
Method	BLASTN
NCBI GI	g16172
BLAST score	63
E value	1.0e-26
Match length	79
% identity	95
NCBI Description	A.thaliana mRNA for ascorbate peroxidase

Seq. No.	174348
Seq. ID	jC-atXLIB327422P3f11a2

Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	3.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174349
Seq. ID	jC-atXLIB327422P3f11b2
Method	BLASTX
NCBI GI	g2586125
BLAST score	575
E value	2.0e-59
Match length	124
% identity	91
NCBI Description	(U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No.	174350
Seq. ID	jC-atXLIB327422P3g03a2
Method	BLASTX
NCBI GI	g1168529
BLAST score	206
E value	4.0e-16
Match length	81
% identity	58
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	174351
Seq. ID	jC-atXLIB327422P3g03b2
Method	BLASTN
NCBI GI	g1931636
BLAST score	74
E value	3.0e-33
Match length	210
% identity	88
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	174352
Seq. ID	jC-atXLIB327422P3g06a2
Method	BLASTX
NCBI GI	g4704730
BLAST score	252
E value	1.0e-21
Match length	58
% identity	93
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	174353
Seq. ID	jC-atXLIB327422P3g07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40

E value	4.0e-13
Match length	40
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174354
Seq. ID	jC-atXLIB327422P3g08a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	4.0e-22
Match length	55
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174355
Seq. ID	jC-atXLIB327422P3g09b2
Method	BLASTX
NCBI GI	g1944518
BLAST score	220
E value	1.0e-17
Match length	43
% identity	100
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	174356
Seq. ID	jC-atXLIB327422P3g11a2
Method	BLASTN
NCBI GI	g2924730
BLAST score	219
E value	1.0e-120
Match length	326
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	174357
Seq. ID	jC-atXLIB327422P3g11b1
Method	BLASTN
NCBI GI	g2924730
BLAST score	49
E value	2.0e-18
Match length	158
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	174358
Seq. ID	jC-atXLIB327422P3g11b2
Method	BLASTN
NCBI GI	g2924730
BLAST score	333
E value	0.0e+00
Match length	372

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	174359
Seq. ID	jC-atXLIB327422P3h02a2
Method	BLASTN
NCBI GI	g166657
BLAST score	323
E value	0.0e+00
Match length	373
% identity	97
NCBI Description	Arabidopsis thaliana Ccr1 mRNA, complete cds

Seq. No.	174360
Seq. ID	jC-atXLIB327422P3h03a2
Method	BLASTN
NCBI GI	g3065834
BLAST score	159
E value	4.0e-84
Match length	330
% identity	88
NCBI Description	Arabidopsis thaliana putative methyltransferase gene, complete cds

Seq. No.	174361
Seq. ID	jC-atXLIB327422P3h03b2
Method	BLASTN
NCBI GI	g3065834
BLAST score	131
E value	2.0e-67
Match length	351
% identity	96
NCBI Description	Arabidopsis thaliana putative methyltransferase gene, complete cds

Seq. No.	174362
Seq. ID	jC-atXLIB327422P3h06a2
Method	BLASTN
NCBI GI	g3036791
BLAST score	100
E value	6.0e-49
Match length	278
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No.	174363
Seq. ID	jC-atXLIB327422P3h09a2
Method	BLASTN
NCBI GI	g2618605
BLAST score	59
E value	2.0e-24
Match length	236
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	174364
Seq. ID	jC-atXLIB327422P3h11b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174365
Seq. ID	jC-atXLIB327422P3h12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	42
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174366
Seq. ID	jC-atXLIB327422P4a05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	3.0e-18
Match length	61
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174367
Seq. ID	jC-atXLIB327422P4a06a1
Method	BLASTN
NCBI GI	g2351064
BLAST score	112
E value	1.0e-55
Match length	240
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	174368
Seq. ID	jC-atXLIB327422P4a09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174369
Seq. ID	jC-atXLIB327422P4a10a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	49
E value	3.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174370
Seq. ID	jC-atXLIB327422P4a10b1
Method	BLASTX
NCBI GI	g3461821
BLAST score	340
E value	7.0e-32
Match length	93
% identity	69
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	174371
Seq. ID	jC-atXLIB327422P4b03a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	202
E value	1.0e-109
Match length	262
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174372
Seq. ID	jC-atXLIB327422P4b05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	2.0e-23
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174373
Seq. ID	jC-atXLIB327422P4b05b1
Method	BLASTN
NCBI GI	g3241922
BLAST score	108
E value	8.0e-54
Match length	116
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	174374
Seq. ID	jC-atXLIB327422P4b11a1
Method	BLASTX
NCBI GI	g2833380
BLAST score	603
E value	2.0e-62
Match length	119
% identity	100

NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) >gi_1064885_emb_CAA63552_ (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]

Seq. No.	174375
Seq. ID	jC-atXLIB327422P4b12a1
Method	BLASTN
NCBI GI	g4662628
BLAST score	300
E value	1.0e-168
Match length	538
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	174376
Seq. ID	jC-atXLIB327422P4c04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	2.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174377
Seq. ID	jC-atXLIB327422P4c04b1
Method	BLASTN
NCBI GI	g4581138
BLAST score	209
E value	1.0e-114
Match length	247
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	174378
Seq. ID	jC-atXLIB327422P4c09a1
Method	BLASTN
NCBI GI	g540252
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174379
Seq. ID	jC-atXLIB327422P4c10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	174380
Seq. ID	jC-atXLIB327422P4d03a1
Method	BLASTN
NCBI GI	g3298610
BLAST score	134
E value	3.0e-69
Match length	222
% identity	91
NCBI Description	Arabidopsis thaliana BAC T2H3
Seq. No.	174381
Seq. ID	jC-atXLIB327422P4d04a1
Method	BLASTN
NCBI GI	g4678315
BLAST score	63
E value	4.0e-27
Match length	95
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)
Seq. No.	174382
Seq. ID	jC-atXLIB327422P4d05a1
Method	BLASTN
NCBI GI	g2656028
BLAST score	252
E value	1.0e-139
Match length	469
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13
Seq. No.	174383
Seq. ID	jC-atXLIB327422P4d10a1
Method	BLASTX
NCBI GI	g3850044
BLAST score	148
E value	4.0e-09
Match length	76
% identity	36
NCBI Description	(AJ006417) beta-tubulin cofactor D [Homo sapiens]
Seq. No.	174384
Seq. ID	jC-atXLIB327422P4d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	9.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	174385
Seq. ID	jC-atXLIB327422P4d12b1
Method	BLASTN

NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174386
Seq. ID	jC-atXLIB327422P4e01b1
Method	BLASTN
NCBI GI	g1495250
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	A.thaliana mRNA for heat-shock protein

Seq. No.	174387
Seq. ID	jC-atXLIB327422P4e02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174388
Seq. ID	jC-atXLIB327422P4e12a1
Method	BLASTX
NCBI GI	g2270994
BLAST score	177
E value	1.0e-12
Match length	99
% identity	38
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	174389
Seq. ID	jC-atXLIB327422P4f02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174390
Seq. ID	jC-atXLIB327422P4f03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174391
Seq. ID	jC-atXLIB327422P4f10a1
Method	BLASTN
NCBI GI	g3093293
BLAST score	96
E value	3.0e-46
Match length	159
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for putative villin

Seq. No.	174392
Seq. ID	jC-atXLIB327422P4g05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	63
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174393
Seq. ID	jC-atXLIB327422P4g07a1
Method	BLASTN
NCBI GI	g469109
BLAST score	436
E value	0.0e+00
Match length	475
% identity	98
NCBI Description	A.thaliana (Columbia) Di19 mRNA

Seq. No.	174394
Seq. ID	jC-atXLIB327422P4h01a1
Method	BLASTN
NCBI GI	g2584827
BLAST score	263
E value	1.0e-146
Match length	479
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174395
Seq. ID	jC-atXLIB327422P4h04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174396
Seq. ID	jC-atXLIB327422P4h10a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174397
Seq. ID	jC-atXLIB327423P1a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	8.0e-21
Match length	61
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174398
Seq. ID	jC-atXLIB327423P1a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	47
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174399
Seq. ID	jC-atXLIB327423P1a11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174400
Seq. ID	jC-atXLIB327423P1b06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174401
Seq. ID	jC-atXLIB327423P1b06b1
Method	BLASTX
NCBI GI	g3608155
BLAST score	182
E value	5.0e-13
Match length	216
% identity	35
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	174402
Seq. ID	jC-atXLIB327423P1c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174403
Seq. ID	jC-atXLIB327423P1c03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	43
E value	5.0e-15
Match length	55
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174404
Seq. ID	jC-atXLIB327423P1c06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174405
Seq. ID	jC-atXLIB327423P1c08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174406
Seq. ID	jC-atXLIB327423P1d05b1
Method	BLASTN
NCBI GI	g4539331
BLAST score	61
E value	3.0e-25
Match length	133
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	174407
Seq. ID	jC-atXLIB327423P1e05a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174408
Seq. ID	jC-atXLIB327423P1e05b1
Method	BLASTN
NCBI GI	g2331045
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds

Seq. No.	174409
Seq. ID	jC-atXLIB327423P1e12a1
Method	BLASTN
NCBI GI	g2058275
BLAST score	83
E value	1.0e-38
Match length	239
% identity	85
NCBI Description	A.thaliana atran2 gene

Seq. No.	174410
Seq. ID	jC-atXLIB327423P1e12b1
Method	BLASTN
NCBI GI	g398603
BLAST score	151
E value	5.0e-79
Match length	311
% identity	88
NCBI Description	A.thaliana ATAF1 mRNA

Seq. No.	174411
Seq. ID	jC-atXLIB327423P1f04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	3.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174412
Seq. ID	jC-atXLIB327423P1f04b1
Method	BLASTN
NCBI GI	g3063690
BLAST score	61
E value	2.0e-25
Match length	217
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	174413
Seq. ID	jC-atXLIB327423P1f05b1
Method	BLASTX
NCBI GI	g3080424
BLAST score	461
E value	5.0e-84
Match length	168
% identity	98
NCBI Description	(AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	174414
Seq. ID	jC-atXLIB327423P1f06b1
Method	BLASTN
NCBI GI	g531832
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	174415
Seq. ID	jC-atXLIB327423P1f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	2.0e-13
Match length	66
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174416
Seq. ID	jC-atXLIB327423P1g05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174417
Seq. ID	jC-atXLIB327423P1g06a1
Method	BLASTN
NCBI GI	g2226430
BLAST score	47
E value	5.0e-17
Match length	47
% identity	100
NCBI Description	Mus saxicola haptoglobin mRNA, complete cds

Seq. No.	174418
Seq. ID	jC-atXLIB327423P1g10a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	45
E value	1.0e-15
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174419
Seq. ID	jC-atXLIB327423P1h05a1
Method	BLASTX
NCBI GI	g1729444
BLAST score	275
E value	4.0e-24
Match length	107
% identity	61
NCBI Description	(X99279) AKin11 [Arabidopsis thaliana]

Seq. No.	174420
Seq. ID	jC-atXLIB327423P1h06a1
Method	BLASTX
NCBI GI	g267083
BLAST score	502
E value	1.0e-50
Match length	126
% identity	81
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	174421
Seq. ID	jC-atXLIB327423P1h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	47
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174422
Seq. ID	jC-atXLIB327423P2a03a1
Method	BLASTX
NCBI GI	g3334223
BLAST score	218
E value	2.0e-17
Match length	117
% identity	47
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD) >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_2392518 (U89267) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_3098559_gb_AAC15697.1_ (AF047834) 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	174423
Seq. ID	jC-atXLIB327423P2a03b1
Method	BLASTN
NCBI GI	g2392517

BLAST score	40
E value	3.0e-13
Match length	124
% identity	85
NCBI Description	Arabidopsis thaliana p-hydroxyphenylpyruvate dioxygenase (HPD) mRNA, complete cds

Seq. No.	174424
Seq. ID	jC-atXLIB327423P2a07a1
Method	BLASTN
NCBI GI	g4063735
BLAST score	218
E value	1.0e-119
Match length	306
% identity	94
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	174425
Seq. ID	jC-atXLIB327423P2a08a1
Method	BLASTN
NCBI GI	g4191771
BLAST score	73
E value	3.0e-33
Match length	119
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174426
Seq. ID	jC-atXLIB327423P2a08b1
Method	BLASTN
NCBI GI	g4191771
BLAST score	52
E value	3.0e-20
Match length	189
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174427
Seq. ID	jC-atXLIB327423P2a10a1
Method	BLASTN
NCBI GI	g4432829
BLAST score	49
E value	2.0e-18
Match length	97
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174428
Seq. ID	jC-atXLIB327423P2b08a1
Method	BLASTX
NCBI GI	g120667
BLAST score	206
E value	4.0e-16

Match length	108
% identity	44
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	174429
Seq. ID	jC-atXLIB327423P2c01b1
Method	BLASTN
NCBI GI	g2828184
BLAST score	46
E value	7.0e-17
Match length	66
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	174430
Seq. ID	jC-atXLIB327423P2c02b1
Method	BLASTX
NCBI GI	g2342689
BLAST score	290
E value	5.0e-26
Match length	87
% identity	76
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). [Arabidopsis thaliana]

Seq. No.	174431
Seq. ID	jC-atXLIB327423P2c06a1
Method	BLASTX
NCBI GI	g2499706
BLAST score	286
E value	2.0e-25
Match length	58
% identity	93
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1297302 (U36381) phospholipase D [Arabidopsis thaliana]

Seq. No.	174432
Seq. ID	jC-atXLIB327423P2d03b1
Method	BLASTX
NCBI GI	g4262250
BLAST score	252
E value	1.0e-21
Match length	113
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	174433
Seq. ID	jC-atXLIB327423P2d06a1
Method	BLASTN

NCBI GI	g4544405
BLAST score	57
E value	1.0e-23
Match length	105
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	174434
Seq. ID	jC-atXLIB327423P2d10b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	57
E value	3.0e-23
Match length	96
% identity	47
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174435
Seq. ID	jC-atXLIB327423P2d11b1
Method	BLASTX
NCBI GI	g131398
BLAST score	136
E value	5.0e-15
Match length	93
% identity	59
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174436
Seq. ID	jC-atXLIB327423P2e04a1
Method	BLASTN
NCBI GI	g4544435
BLAST score	39
E value	7.0e-13
Match length	69
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	174437
Seq. ID	jC-atXLIB327423P2e07a1
Method	BLASTN
NCBI GI	g3941523
BLAST score	32
E value	1.0e-08
Match length	52
% identity	90
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174438
Seq. ID	jC-atXLIB327423P2e10a1
Method	BLASTN
NCBI GI	g3551051
BLAST score	38
E value	4.0e-12
Match length	107
% identity	83
NCBI Description	Arabidopsis thaliana mRNA for GF14 mu, complete cds

Seq. No.	174439
Seq. ID	jC-atXLIB327423P2e10b1
Method	BLASTX
NCBI GI	g3023216
BLAST score	58
E value	1.0e-10
Match length	85
% identity	54
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	174440
Seq. ID	jC-atXLIB327423P2f02a1
Method	BLASTN
NCBI GI	g166583
BLAST score	83
E value	7.0e-39
Match length	142
% identity	93
NCBI Description	A.thaliana alcohol dehydrogenase gene, complete cds

Seq. No.	174441
Seq. ID	jC-atXLIB327423P2f02b1
Method	BLASTN
NCBI GI	g3176694
BLAST score	100
E value	8.0e-49
Match length	177
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174442
Seq. ID	jC-atXLIB327423P2f03a1
Method	BLASTN
NCBI GI	g4678705
BLAST score	239
E value	1.0e-132
Match length	379
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	174443
Seq. ID	jC-atXLIB327423P2f03b1
Method	BLASTX

NCBI GI	g4567246
BLAST score	406
E value	1.0e-39
Match length	90
% identity	86
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	174444
Seq. ID	jC-atXLIB327423P2f04b1
Method	BLASTN
NCBI GI	g2894591
BLAST score	118
E value	1.0e-59
Match length	300
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	174445
Seq. ID	jC-atXLIB327423P2f07a1
Method	BLASTN
NCBI GI	g3687221
BLAST score	56
E value	8.0e-23
Match length	100
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174446
Seq. ID	jC-atXLIB327423P2f10a1
Method	BLASTN
NCBI GI	g2618599
BLAST score	68
E value	9.0e-30
Match length	194
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	174447
Seq. ID	jC-atXLIB327423P2f10b1
Method	BLASTN
NCBI GI	g992961
BLAST score	57
E value	3.0e-23
Match length	339
% identity	79
NCBI Description	A.thaliana (GIF1) mRNA for thioredoxin

Seq. No.	174448
Seq. ID	jC-atXLIB327423P2g05a1
Method	BLASTN
NCBI GI	g4249393
BLAST score	313
E value	1.0e-176
Match length	380

% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174449
Seq. ID	jC-atXLIB327423P2g09a1
Method	BLASTN
NCBI GI	g2341023
BLAST score	37
E value	2.0e-11
Match length	78
% identity	88
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174450
Seq. ID	jC-atXLIB327423P2h01b1
Method	BLASTX
NCBI GI	g1345660
BLAST score	85
E value	6.0e-12
Match length	93
% identity	52
NCBI Description	CALMODULIN >gi_505152_emb_CAA43142_ (X60737) Calmodulin [Malus domestica]

Seq. No.	174451
Seq. ID	jC-atXLIB327423P2h04b1
Method	BLASTN
NCBI GI	g4115370
BLAST score	164
E value	5.0e-87
Match length	286
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174452
Seq. ID	jC-atXLIB327423P2h05a1
Method	BLASTN
NCBI GI	g3859658
BLAST score	44
E value	2.0e-15
Match length	252
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	174453
Seq. ID	jC-atXLIB327423P2h05b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	52
E value	2.0e-20
Match length	73
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1

(ESSAII project)

Seq. No.	174454
Seq. ID	jC-atXLIB327423P3a03a1
Method	BLASTN
NCBI GI	g2104523
BLAST score	216
E value	1.0e-118
Match length	339
% identity	91
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	174455
Seq. ID	jC-atXLIB327423P3a03b1
Method	BLASTN
NCBI GI	g2154716
BLAST score	136
E value	3.0e-70
Match length	288
% identity	96
NCBI Description	A.thaliana mRNA for Kap alpha protein

Seq. No.	174456
Seq. ID	jC-atXLIB327423P3a04a1
Method	BLASTN
NCBI GI	g3242700
BLAST score	333
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174457
Seq. ID	jC-atXLIB327423P3a06a1
Method	BLASTN
NCBI GI	g4159712
BLAST score	63
E value	8.0e-27
Match length	127
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	174458
Seq. ID	jC-atXLIB327423P3a07a1
Method	BLASTN
NCBI GI	g2760168
BLAST score	38
E value	7.0e-12
Match length	70
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No. 174459

Seq. ID	jC-atXLIB327423P3a07b1
Method	BLASTN
NCBI GI	g2760168
BLAST score	45
E value	5.0e-16
Match length	77
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	174460
Seq. ID	jC-atXLIB327423P3a09a1
Method	BLASTX
NCBI GI	g2191130
BLAST score	240
E value	4.0e-20
Match length	64
% identity	70
NCBI Description	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No.	174461
Seq. ID	jC-atXLIB327423P3a12b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	174462
Seq. ID	jC-atXLIB327423P3b01a1
Method	BLASTN
NCBI GI	g2160155
BLAST score	87
E value	4.0e-41
Match length	222
% identity	89
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174463
Seq. ID	jC-atXLIB327423P3b01b1
Method	BLASTX
NCBI GI	g2160191
BLAST score	203
E value	8.0e-23
Match length	138
% identity	54
NCBI Description	(AC000132) Identical to A. thaliana AtK-1 (gb_X79279). [Arabidopsis thaliana]

Seq. No.	174464
Seq. ID	jC-atXLIB327423P3b02a1
Method	BLASTX
NCBI GI	g2739369

BLAST score	391
E value	7.0e-38
Match length	93
% identity	78
NCBI Description	(AC002505) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	174465
Seq. ID	jC-atXLIB327423P3b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174466
Seq. ID	jC-atXLIB327423P3b05b1
Method	BLASTX
NCBI GI	g1732411
BLAST score	293
E value	2.0e-26
Match length	119
% identity	48
NCBI Description	(U47924) isopeptidase T [Homo sapiens]

Seq. No.	174467
Seq. ID	jC-atXLIB327423P3b07b1
Method	BLASTN
NCBI GI	g3128138
BLAST score	95
E value	7.0e-46
Match length	297
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	174468
Seq. ID	jC-atXLIB327423P3b09a1
Method	BLASTX
NCBI GI	g3851636
BLAST score	370
E value	2.0e-35
Match length	89
% identity	80
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	174469
Seq. ID	jC-atXLIB327423P3c02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	47
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174470
Seq. ID	jC-atXLIB327423P3c03a1
Method	BLASTN
NCBI GI	g2564046
BLAST score	88
E value	1.0e-41
Match length	388
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	174471
Seq. ID	jC-atXLIB327423P3c03b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	174472
Seq. ID	jC-atXLIB327423P3c04a1
Method	BLASTN
NCBI GI	g3236479
BLAST score	36
E value	1.0e-10
Match length	64
% identity	89
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	174473
Seq. ID	jC-atXLIB327423P3c04b1
Method	BLASTN
NCBI GI	g3236479
BLAST score	91
E value	2.0e-43
Match length	278
% identity	94
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	174474
Seq. ID	jC-atXLIB327423P3c07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174475
Seq. ID	jC-atXLIB327423P3c09a1

Method	BLASTX
NCBI GI	g3426062
BLAST score	556
E value	4.0e-57
Match length	118
% identity	95
NCBI Description	(AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No.	174476
Seq. ID	jC-atXLIB327423P3c12a1
Method	BLASTX
NCBI GI	g2642157
BLAST score	240
E value	4.0e-20
Match length	62
% identity	69
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	174477
Seq. ID	jC-atXLIB327423P3d01a1
Method	BLASTN
NCBI GI	g1777311
BLAST score	191
E value	1.0e-103
Match length	362
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for novel serine/threonine protein kinase, complete cds

Seq. No.	174478
Seq. ID	jC-atXLIB327423P3d03a1
Method	BLASTN
NCBI GI	g4455321
BLAST score	85
E value	3.0e-40
Match length	117
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	174479
Seq. ID	jC-atXLIB327423P3d03b1
Method	BLASTN
NCBI GI	g4455321
BLAST score	58
E value	9.0e-24
Match length	147
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	174480
Seq. ID	jC-atXLIB327423P3d06b1
Method	BLASTN
NCBI GI	g2331045
BLAST score	41
E value	1.0e-13

Match length	53
% identity	66
NCBI Description	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds

Seq. No.	174481
Seq. ID	jC-atXLIB327423P3e01a1
Method	BLASTN
NCBI GI	g4558521
BLAST score	244
E value	1.0e-135
Match length	415
% identity	67
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	174482
Seq. ID	jC-atXLIB327423P3e03a1
Method	BLASTX
NCBI GI	g3157937
BLAST score	341
E value	6.0e-32
Match length	67
% identity	96
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	174483
Seq. ID	jC-atXLIB327423P3e03b1
Method	BLASTX
NCBI GI	g1354272
BLAST score	199
E value	3.0e-15
Match length	66
% identity	67
NCBI Description	(U51036) aspartic proteinase [Arabidopsis thaliana]

Seq. No.	174484
Seq. ID	jC-atXLIB327423P3e04b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	45
E value	6.0e-16
Match length	49
% identity	98
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	174485
Seq. ID	jC-atXLIB327423P3e05b1
Method	BLASTX
NCBI GI	g430947
BLAST score	255
E value	7.0e-22

Match length	106
% identity	54
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	174486
Seq. ID	jC-atXLIB327423P3e06b1
Method	BLASTN
NCBI GI	g16446
BLAST score	86
E value	2.0e-40
Match length	118
% identity	93
NCBI Description	A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No.	174487
Seq. ID	jC-atXLIB327423P3e07b1
Method	BLASTN
NCBI GI	g2337888
BLAST score	81
E value	2.0e-37
Match length	105
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	174488
Seq. ID	jC-atXLIB327423P3f01a1
Method	BLASTX
NCBI GI	g4587563
BLAST score	431
E value	2.0e-42
Match length	94
% identity	89
NCBI Description	(AC006550) Similar to gb_U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815 come from this gene. [Arabidopsis thaliana]

Seq. No.	174489
Seq. ID	jC-atXLIB327423P3f01b1
Method	BLASTN
NCBI GI	g4580745
BLAST score	85
E value	7.0e-40
Match length	188
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	174490
Seq. ID	jC-atXLIB327423P3f03a1
Method	BLASTX
NCBI GI	g553038
BLAST score	243
E value	1.0e-40
Match length	90
% identity	98

NCBI Description	(M58464) beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	174491
Seq. ID	jC-atXLIB327423P3f04b1
Method	BLASTN
NCBI GI	g2088638
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174492
Seq. ID	jC-atXLIB327423P3f05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	6.0e-09
Match length	44
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174493
Seq. ID	jC-atXLIB327423P3f06a1
Method	BLASTN
NCBI GI	g16472
BLAST score	233
E value	1.0e-128
Match length	308
% identity	94
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	174494
Seq. ID	jC-atXLIB327423P3f06b1
Method	BLASTN
NCBI GI	g2795802
BLAST score	67
E value	5.0e-29
Match length	109
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174495
Seq. ID	jC-atXLIB327423P3f08a1
Method	BLASTN
NCBI GI	g4699904
BLAST score	153
E value	2.0e-80
Match length	381
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	174496

Seq. ID	jC-atXLIB327423P3f10a1
Method	BLASTX
NCBI GI	g131398
BLAST score	417
E value	7.0e-41
Match length	91
% identity	87
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174497
Seq. ID	jC-atXLIB327423P3f11a1
Method	BLASTN
NCBI GI	g16473
BLAST score	191
E value	1.0e-103
Match length	411
% identity	15
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	174498
Seq. ID	jC-atXLIB327423P3g03b1
Method	BLASTX
NCBI GI	g4220450
BLAST score	91
E value	1.2e-02
Match length	78
% identity	13
NCBI Description	(AC006216) Identical to gb_D85194 mRNA which is similar to gb_AF054906 myrosinase-binding protein homolog from Arabidopsis thaliana. ESTs gb_Z34045 and gb_Z34877 come from this gene. [Arabidopsis thaliana]

Seq. No.	174499
Seq. ID	jC-atXLIB327423P3g04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174500
Seq. ID	jC-atXLIB327423P3g06a1
Method	BLASTN
NCBI GI	g2337888
BLAST score	34
E value	2.0e-09

Match length	54
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	174501
Seq. ID	jC-atXLIB327423P3g07a1
Method	BLASTN
NCBI GI	g1931636
BLAST score	242
E value	1.0e-133
Match length	310
% identity	87
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	174502
Seq. ID	jC-atXLIB327423P3g07b1
Method	BLASTN
NCBI GI	g1931636
BLAST score	79
E value	3.0e-36
Match length	111
% identity	93
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	174503
Seq. ID	jC-atXLIB327423P3g08b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	79
E value	3.0e-36
Match length	198
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	174504
Seq. ID	jC-atXLIB327423P3g09a1
Method	BLASTN
NCBI GI	g2351062
BLAST score	187
E value	1.0e-101
Match length	416
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	174505
Seq. ID	jC-atXLIB327423P3h02a1
Method	BLASTX
NCBI GI	g2055273
BLAST score	389
E value	1.0e-37
Match length	86
% identity	88
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	174506
Seq. ID	jC-atXLIB327423P3h03b1
Method	BLASTN
NCBI GI	g4585952
BLAST score	61
E value	1.0e-25
Match length	125
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	174507
Seq. ID	jC-atXLIB327423P3h05b1
Method	BLASTX
NCBI GI	g2062155
BLAST score	435
E value	6.0e-54
Match length	145
% identity	73
NCBI Description	(AC001645) mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana]

Seq. No.	174508
Seq. ID	jC-atXLIB327423P3h06a1
Method	BLASTN
NCBI GI	g4519194
BLAST score	297
E value	1.0e-166
Match length	524
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	174509
Seq. ID	jC-atXLIB327423P3h07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	45
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174510
Seq. ID	jC-atXLIB327423P3h10a1
Method	BLASTN
NCBI GI	g2264304
BLAST score	123
E value	1.0e-62
Match length	337
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	174511
Seq. ID	jC-atXLIB327423P4a03b1
Method	BLASTN

NCBI GI	g3063690
BLAST score	94
E value	3.0e-45
Match length	133
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	174512
Seq. ID	jC-atXLIB327423P4a09a1
Method	BLASTN
NCBI GI	g4512656
BLAST score	128
E value	1.0e-65
Match length	297
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	174513
Seq. ID	jC-atXLIB327423P4b06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13
Match length	47
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174514
Seq. ID	jC-atXLIB327423P4b07a1
Method	BLASTN
NCBI GI	g2341023
BLAST score	104
E value	3.0e-51
Match length	222
% identity	93
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174515
Seq. ID	jC-atXLIB327423P4b07b1
Method	BLASTX
NCBI GI	g730324
BLAST score	129
E value	3.0e-41
Match length	154
% identity	64
NCBI Description	DEOXYRIBODIPYRIMIDINE PHOTOLYASE (DNA PHOTOLYASE) (PHOTOREACTIVATING ENZYME) >gi_1084356_pir__S48120 deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - white mustard >gi_414196_emb_CAA50898_ (X72019) photolyase [Sinapis alba]

Seq. No.	174516
Seq. ID	jC-atXLIB327423P4b09a1

Method	BLASTN
NCBI GI	g4733953
BLAST score	187
E value	1.0e-100
Match length	327
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	174517
Seq. ID	jC-atXLIB327423P4c02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174518
Seq. ID	jC-atXLIB327423P4c03b1
Method	BLASTN
NCBI GI	g541564
BLAST score	75
E value	6.0e-34
Match length	136
% identity	91
NCBI Description	Arabidopsis thaliana PSI type II chlorophyll a/b-binding protein (Lhca2*1) mRNA, complete cds

Seq. No.	174519
Seq. ID	jC-atXLIB327423P4c09a1
Method	BLASTN
NCBI GI	g3420042
BLAST score	51
E value	9.0e-20
Match length	126
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174520
Seq. ID	jC-atXLIB327423P4c10b1
Method	BLASTX
NCBI GI	g3702323
BLAST score	517
E value	6.0e-62
Match length	141
% identity	82
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	174521
Seq. ID	jC-atXLIB327423P4c12b1
Method	BLASTN
NCBI GI	g4757678
BLAST score	149

E value	4.0e-78
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	174522
Seq. ID	jC-atXLIB327423P4d01b1
Method	BLASTN
NCBI GI	g3747110
BLAST score	67
E value	4.0e-29
Match length	115
% identity	90
NCBI Description	Arabidopsis thaliana MTN3 homolog (MTN3) mRNA, complete cds

Seq. No.	174523
Seq. ID	jC-atXLIB327423P4d02a1
Method	BLASTN
NCBI GI	g4519187
BLAST score	91
E value	2.0e-43
Match length	138
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No.	174524
Seq. ID	jC-atXLIB327423P4d03b1
Method	BLASTN
NCBI GI	g166641
BLAST score	85
E value	7.0e-40
Match length	100
% identity	96
NCBI Description	Arabidopsis thaliana cab1 gene, 5' end

Seq. No.	174525
Seq. ID	jC-atXLIB327423P4d04b1
Method	BLASTX
NCBI GI	g1172872
BLAST score	240
E value	2.0e-26
Match length	95
% identity	69
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	174526
Seq. ID	jC-atXLIB327423P4d06b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	54

E value	2.0e-21
Match length	99
% identity	60
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174527
Seq. ID	jC-atXLIB327423P4d10b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	48
E value	7.0e-18
Match length	48
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	174528
Seq. ID	jC-atXLIB327423P4d11a1
Method	BLASTX
NCBI GI	g131398
BLAST score	272
E value	7.0e-24
Match length	83
% identity	64
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174529
Seq. ID	jC-atXLIB327423P4d12b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	41
E value	1.0e-13
Match length	57
% identity	40
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174530
Seq. ID	jC-atXLIB327423P4e02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174531
Seq. ID	jC-atXLIB327423P4e03b1

Method	BLASTN
NCBI GI	g2338711
BLAST score	34
E value	2.0e-09
Match length	69
% identity	90
NCBI Description	Arabidopsis thaliana metallothionein-like protein (MT3) gene, complete cds

Seq. No.	174532
Seq. ID	jC-atXLIB327423P4e05a1
Method	BLASTN
NCBI GI	g289207
BLAST score	64
E value	2.0e-27
Match length	112
% identity	92
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast DNA repair protein (homologue of E.coli recA) gene, complete cds

Seq. No.	174533
Seq. ID	jC-atXLIB327423P4e05b1
Method	BLASTN
NCBI GI	g16446
BLAST score	44
E value	2.0e-15
Match length	120
% identity	84
NCBI Description	A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No.	174534
Seq. ID	jC-atXLIB327423P4e09a1
Method	BLASTN
NCBI GI	g4678258
BLAST score	35
E value	5.0e-10
Match length	47
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	174535
Seq. ID	jC-atXLIB327423P4e09b1
Method	BLASTX
NCBI GI	g4455242
BLAST score	315
E value	2.0e-30
Match length	141
% identity	54
NCBI Description	(AL035523) geranylgeranylated protein ATGP4 [Arabidopsis thaliana]

Seq. No.	174536
Seq. ID	jC-atXLIB327423P4e12a1
Method	BLASTX
NCBI GI	g1175010
BLAST score	154

E value	5.0e-10
Match length	38
% identity	71
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	174537
Seq. ID	jC-atXLIB327423P4f01a1
Method	BLASTN
NCBI GI	g887938
BLAST score	88
E value	1.0e-41
Match length	180
% identity	93
NCBI Description	Arabidopsis thaliana clone YAP317 GAST1 protein homolog mRNA, complete cds

Seq. No.	174538
Seq. ID	jC-atXLIB327423P4f01b1
Method	BLASTX
NCBI GI	g1169839
BLAST score	209
E value	2.0e-16
Match length	48
% identity	77
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 1 PRECURSOR >gi_2129588_pir__S71441 GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana >gi_887939 (U11766) GAST1 protein homolog [Arabidopsis thaliana]

Seq. No.	174539
Seq. ID	jC-atXLIB327423P4f03b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	42
E value	3.0e-14
Match length	81
% identity	55
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174540
Seq. ID	jC-atXLIB327423P4f04b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174541
Seq. ID	jC-atXLIB327423P4f09a1
Method	BLASTN
NCBI GI	g3128137

BLAST score	147
E value	7.0e-77
Match length	297
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	174542
Seq. ID	jC-atXLIB327423P4f10b1
Method	BLASTX
NCBI GI	g4572665
BLAST score	408
E value	8.0e-40
Match length	131
% identity	24
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	174543
Seq. ID	jC-atXLIB327423P4g01a1
Method	BLASTN
NCBI GI	g3600062
BLAST score	101
E value	2.0e-49
Match length	314
% identity	92
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	174544
Seq. ID	jC-atXLIB327423P4g04a1
Method	BLASTN
NCBI GI	g3449320
BLAST score	35
E value	4.0e-10
Match length	63
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	174545
Seq. ID	jC-atXLIB327423P4g04b1
Method	BLASTN
NCBI GI	g3449320
BLAST score	94
E value	3.0e-45
Match length	122
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	174546
Seq. ID	jC-atXLIB327423P4g05a1
Method	BLASTN
NCBI GI	g4757404
BLAST score	61
E value	2.0e-25
Match length	97
% identity	91

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence
Seq. No.	174547
Seq. ID	jC-atXLIB327423P4g05b1
Method	BLASTX
NCBI GI	g2506443
BLAST score	296
E value	1.0e-26
Match length	148
% identity	49
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]
Seq. No.	174548
Seq. ID	jC-atXLIB327423P4g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	174549
Seq. ID	jC-atXLIB327423P4g10a1
Method	BLASTX
NCBI GI	g132166
BLAST score	207
E value	3.0e-16
Match length	82
% identity	55
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]
Seq. No.	174550
Seq. ID	jC-atXLIB327423P4g11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	174551

Seq. ID	jC-atXLIB327423P4h02a1
Method	BLASTN
NCBI GI	g3297806
BLAST score	103
E value	1.0e-50
Match length	269
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	174552
Seq. ID	jC-atXLIB327423P4h03a1
Method	BLASTN
NCBI GI	g1491614
BLAST score	66
E value	2.0e-28
Match length	86
% identity	94
NCBI Description	A.thaliana mRNA for male sterility 2-like protein

Seq. No.	174553
Seq. ID	jC-atXLIB327423P4h03b1
Method	BLASTX
NCBI GI	g1491615
BLAST score	244
E value	9.0e-24
Match length	104
% identity	68
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	174554
Seq. ID	jC-atXLIB327423P4h05a1
Method	BLASTN
NCBI GI	g2935343
BLAST score	131
E value	3.0e-67
Match length	372
% identity	91
NCBI Description	Arabidopsis thaliana anion channel protein (CLC-a) mRNA, complete cds

Seq. No.	174555
Seq. ID	jC-atXLIB327423P4h05b1
Method	BLASTX
NCBI GI	g1619956
BLAST score	223
E value	4.0e-18
Match length	105
% identity	55
NCBI Description	(U72151) voltage-gated chloride channel [Arabidopsis thaliana]

Seq. No.	174556
Seq. ID	jC-atXLIB327423P4h09a1
Method	BLASTN
NCBI GI	g2708736

BLAST score	33
E value	8.0e-09
Match length	159
% identity	88
NCBI Description	Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	174557
Seq. ID	jC-atXLIB327423P4h11a1
Method	BLASTN
NCBI GI	g3702731
BLAST score	46
E value	1.0e-16
Match length	98
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	174558
Seq. ID	jC-atXLIB327423P4h12a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	78
E value	1.0e-35
Match length	258
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	174559
Seq. ID	jC-atXLIB327424P1a02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174560
Seq. ID	jC-atXLIB327424P1a04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174561
Seq. ID	jC-atXLIB327424P1a06a1
Method	BLASTN
NCBI GI	g2979540
BLAST score	75
E value	6.0e-34
Match length	196
% identity	90

NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174562
Seq. ID	jC-atXLIB327424P1a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174563
Seq. ID	jC-atXLIB327424P1a08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	72
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174564
Seq. ID	jC-atXLIB327424P1a09a1
Method	BLASTX
NCBI GI	g2181186
BLAST score	217
E value	2.0e-17
Match length	61
% identity	79
NCBI Description	(X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi_2230761_emb_CAA69158_ (Y07825) kco1 [Arabidopsis thaliana]

Seq. No.	174565
Seq. ID	jC-atXLIB327424P1a10a1
Method	BLASTX
NCBI GI	g100293
BLAST score	146
E value	4.0e-09
Match length	89
% identity	20
NCBI Description	ribonucleoprotein A, 29K - wood tobacco >gi_19754_emb_CAA43427_ (X61113) 29kD A ribonucleoprotein [Nicotiana sylvestris]

Seq. No.	174566
Seq. ID	jC-atXLIB327424P1b01a1
Method	BLASTX
NCBI GI	g4038042
BLAST score	459
E value	8.0e-46
Match length	96
% identity	95

NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	174567
Seq. ID	jC-atXLIB327424P1b02a1
Method	BLASTN
NCBI GI	g2232145
BLAST score	278
E value	1.0e-155
Match length	389
% identity	93
NCBI Description	Arabidopsis thaliana 14-3-3-like protein GF14 phi (GRF4) gene, complete cds

Seq. No.	174568
Seq. ID	jC-atXLIB327424P1b03a1
Method	BLASTN
NCBI GI	g4558521
BLAST score	331
E value	0.0e+00
Match length	422
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	174569
Seq. ID	jC-atXLIB327424P1b04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174570
Seq. ID	jC-atXLIB327424P1b07a1
Method	BLASTX
NCBI GI	g2529679
BLAST score	153
E value	6.0e-10
Match length	56
% identity	48
NCBI Description	(AC002535) hypothetical protein [Arabidopsis thaliana]

Seq. No.	174571
Seq. ID	jC-atXLIB327424P1b08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174572

Seq. ID	jC-atXLIB327424P1b09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	1.0e-21
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174573
Seq. ID	jC-atXLIB327424P1b12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	42
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174574
Seq. ID	jC-atXLIB327424P1c02a1
Method	BLASTN
NCBI GI	g3298532
BLAST score	40
E value	5.0e-13
Match length	181
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174575
Seq. ID	jC-atXLIB327424P1c04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174576
Seq. ID	jC-atXLIB327424P1c06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	9.0e-18
Match length	52
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174577
Seq. ID	jC-atXLIB327424P1c07b2
Method	BLASTX
NCBI GI	g1710840
BLAST score	236

E value	9.0e-20
Match length	101
% identity	50
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum] >gi_2588781_dbj_BAA23164_ (D49804) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No.	174578
Seq. ID	jC-atXLIB327424P1c08a1
Method	BLASTX
NCBI GI	g629602
BLAST score	334
E value	3.0e-34
Match length	110
% identity	71
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	174579
Seq. ID	jC-atXLIB327424P1c08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174580
Seq. ID	jC-atXLIB327424P1c09b2
Method	BLASTX
NCBI GI	g1351107
BLAST score	274
E value	4.0e-24
Match length	80
% identity	68
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE) >gi_1361971_pir__S55253 sucrose-phosphate synthase - sugar beet >gi_1488568_emb_CAA57500_ (X81975) sucrose-phosphate synthase [Beta vulgaris]

Seq. No.	174581
Seq. ID	jC-atXLIB327424P1c10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174582
Seq. ID	jC-atXLIB327424P1c11b2
Method	BLASTN
NCBI GI	g2098816
BLAST score	89
E value	3.0e-42
Match length	160
% identity	94
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	174583
Seq. ID	jC-atXLIB327424P1c12a1
Method	BLASTX
NCBI GI	g1170897
BLAST score	155
E value	4.0e-10
Match length	61
% identity	54
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]

Seq. No.	174584
Seq. ID	jC-atXLIB327424P1c12b2
Method	BLASTN
NCBI GI	g3929650
BLAST score	48
E value	8.0e-18
Match length	180
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for microbody NAD-dependent malate dehydrogenase

Seq. No.	174585
Seq. ID	jC-atXLIB327424P1d02b2
Method	BLASTN
NCBI GI	g217856
BLAST score	82
E value	4.0e-38
Match length	236
% identity	90
NCBI Description	A. thaliana gene for metallothionein-like protein, complete cds

Seq. No.	174586
Seq. ID	jC-atXLIB327424P1d03a1
Method	BLASTN
NCBI GI	g3128143
BLAST score	77
E value	4.0e-35
Match length	240
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	174587
Seq. ID	jC-atXLIB327424P1d04b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	35
E value	4.0e-10
Match length	47
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174588
Seq. ID	jC-atXLIB327424P1d05b2
Method	BLASTX
NCBI GI	g3776025
BLAST score	357
E value	6.0e-62
Match length	149
% identity	89
NCBI Description	(AJ010474) RNA helicase [Arabidopsis thaliana]

Seq. No.	174589
Seq. ID	jC-atXLIB327424P1d10b2
Method	BLASTX
NCBI GI	g3335371
BLAST score	117
E value	1.0e-22
Match length	104
% identity	68
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	174590
Seq. ID	jC-atXLIB327424P1d11a1
Method	BLASTX
NCBI GI	g4090884
BLAST score	285
E value	2.0e-25
Match length	79
% identity	75
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	174591
Seq. ID	jC-atXLIB327424P1d11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	52
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174592
Seq. ID	jC-atXLIB327424P1e01a1
Method	BLASTN

NCBI GI	g2864607
BLAST score	153
E value	2.0e-80
Match length	307
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	174593
Seq. ID	jC-atXLIB327424P1e08a1
Method	BLASTN
NCBI GI	g4455348
BLAST score	315
E value	1.0e-177
Match length	412
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	174594
Seq. ID	jC-atXLIB327424P1e08b2
Method	BLASTN
NCBI GI	g4455348
BLAST score	79
E value	2.0e-36
Match length	237
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	174595
Seq. ID	jC-atXLIB327424P1f01b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	43
E value	9.0e-15
Match length	51
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174596
Seq. ID	jC-atXLIB327424P1f03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174597
Seq. ID	jC-atXLIB327424P1f05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	43
E value	9.0e-15

Match length	55
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174598
Seq. ID	jC-atXLIB327424P1f06a1
Method	BLASTX
NCBI GI	g4240116
BLAST score	318
E value	3.0e-29
Match length	65
% identity	88
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	174599
Seq. ID	jC-atXLIB327424P1f07a1
Method	BLASTX
NCBI GI	g4417300
BLAST score	510
E value	9.0e-52
Match length	103
% identity	91
NCBI Description	(AC006446) hypothetical protein [Arabidopsis thaliana] >gi_4733990_gb_AAD28670.1_AC007209_6 (AC007209) hypothetical protein [Arabidopsis thaliana]

Seq. No.	174600
Seq. ID	jC-atXLIB327424P1f08b2
Method	BLASTN
NCBI GI	g2564048
BLAST score	153
E value	1.0e-80
Match length	213
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	174601
Seq. ID	jC-atXLIB327424P1f10b2
Method	BLASTX
NCBI GI	g2829881
BLAST score	156
E value	3.0e-10
Match length	102
% identity	46
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	174602
Seq. ID	jC-atXLIB327424P1f12a1
Method	BLASTN
NCBI GI	g4678219
BLAST score	190
E value	1.0e-102
Match length	352

% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	174603
Seq. ID	jC-atXLIB327424P1g02a1
Method	BLASTX
NCBI GI	g4581146
BLAST score	241
E value	3.0e-20
Match length	56
% identity	84
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	174604
Seq. ID	jC-atXLIB327424P1g03b2
Method	BLASTX
NCBI GI	g2642157
BLAST score	438
E value	3.0e-43
Match length	151
% identity	60
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	174605
Seq. ID	jC-atXLIB327424P1g06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174606
Seq. ID	jC-atXLIB327424P1g06b2
Method	BLASTX
NCBI GI	g4218535
BLAST score	185
E value	1.0e-13
Match length	102
% identity	36
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	174607
Seq. ID	jC-atXLIB327424P1g08a1
Method	BLASTN
NCBI GI	g4741184
BLAST score	231
E value	1.0e-127
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	174608

Seq. ID	jC-atXLIB327424P1g09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174609
Seq. ID	jC-atXLIB327424P1g09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	9.0e-20
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174610
Seq. ID	jC-atXLIB327424P1g10a1
Method	BLASTX
NCBI GI	g2315463
BLAST score	183
E value	2.0e-13
Match length	111
% identity	41
NCBI Description	(AF016449) similar to enzymes that act through an ATP dependent binding of AMP; most similar to CoA ligases [Caenorhabditis elegans]

Seq. No.	174611
Seq. ID	jC-atXLIB327424P1g11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174612
Seq. ID	jC-atXLIB327424P1g11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174613
Seq. ID	jC-atXLIB327424P1g12a1
Method	BLASTX
NCBI GI	g3269287

BLAST score	214
E value	4.0e-17
Match length	70
% identity	57
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	174614
Seq. ID	jC-atXLIB327424P1h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	3.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174615
Seq. ID	jC-atXLIB327424P1h08a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	58
E value	9.0e-24
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	174616
Seq. ID	jC-atXLIB327424P1h10a1
Method	BLASTN
NCBI GI	g3894179
BLAST score	196
E value	1.0e-106
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174617
Seq. ID	jC-atXLIB327424P1h11a1
Method	BLASTX
NCBI GI	g3367536
BLAST score	489
E value	2.0e-49
Match length	131
% identity	82
NCBI Description	(AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana]

Seq. No.	174618
Seq. ID	jC-atXLIB327424P1h12a1
Method	BLASTN
NCBI GI	g2564049
BLAST score	96
E value	2.0e-46

Match length	155
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	174619
Seq. ID	jC-atXLIB327424P2a03b2
Method	BLASTN
NCBI GI	g4558586
BLAST score	60
E value	6.0e-25
Match length	165
% identity	85
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	174620
Seq. ID	jC-atXLIB327424P2a04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	57
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174621
Seq. ID	jC-atXLIB327424P2a06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174622
Seq. ID	jC-atXLIB327424P2a07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174623
Seq. ID	jC-atXLIB327424P2a07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	4.0e-25
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	174624
Seq. ID	jC-atXLIB327424P2a10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174625
Seq. ID	jC-atXLIB327424P2b02b2
Method	BLASTX
NCBI GI	g4249391
BLAST score	197
E value	4.0e-15
Match length	96
% identity	44
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	174626
Seq. ID	jC-atXLIB327424P2b09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	71
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174627
Seq. ID	jC-atXLIB327424P2b10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174628
Seq. ID	jC-atXLIB327424P2b10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	55
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174629

Seq. ID	jC-atXLIB327424P2b11b2
Method	BLASTX
NCBI GI	g2062169
BLAST score	182
E value	3.0e-13
Match length	106
% identity	36
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	174630
Seq. ID	jC-atXLIB327424P2b12b2
Method	BLASTN
NCBI GI	g3449322
BLAST score	351
E value	0.0e+00
Match length	427
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	174631
Seq. ID	jC-atXLIB327424P2c03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174632
Seq. ID	jC-atXLIB327424P2c07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14
Match length	70
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174633
Seq. ID	jC-atXLIB327424P2c09a2
Method	BLASTN
NCBI GI	g540252
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174634
Seq. ID	jC-atXLIB327424P2c09b2
Method	BLASTN
NCBI GI	g2582640

BLAST score	56
E value	2.0e-22
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174635
Seq. ID	jC-atXLIB327424P2c10b2
Method	BLASTN
NCBI GI	g3451055
BLAST score	67
E value	4.0e-29
Match length	151
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	174636
Seq. ID	jC-atXLIB327424P2c12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	49
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174637
Seq. ID	jC-atXLIB327424P2c12b2
Method	BLASTN
NCBI GI	g2262135
BLAST score	68
E value	1.0e-29
Match length	107
% identity	93
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	174638
Seq. ID	jC-atXLIB327424P2d10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174639
Seq. ID	jC-atXLIB327424P2d11a2
Method	BLASTN
NCBI GI	g3869065
BLAST score	405
E value	0.0e+00
Match length	405
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	174640
Seq. ID	jC-atXLIB327424P2e03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174641
Seq. ID	jC-atXLIB327424P2e06b2
Method	BLASTN
NCBI GI	g3860242
BLAST score	105
E value	1.0e-51
Match length	240
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	174642
Seq. ID	jC-atXLIB327424P2e07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	3.0e-18
Match length	57
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174643
Seq. ID	jC-atXLIB327424P2e08b2
Method	BLASTN
NCBI GI	g4713943
BLAST score	64
E value	3.0e-27
Match length	168
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	174644
Seq. ID	jC-atXLIB327424P2e09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174645
Seq. ID	jC-atXLIB327424P2e09b2
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	6.0e-10
Match length	71
% identity	87
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174646
Seq. ID	jC-atXLIB327424P2e10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	1.0e-09
Match length	42
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174647
Seq. ID	jC-atXLIB327424P2e11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	57
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174648
Seq. ID	jC-atXLIB327424P2e12a2
Method	BLASTN
NCBI GI	g531828
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174649
Seq. ID	jC-atXLIB327424P2e12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	2.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174650
Seq. ID	jC-atXLIB327424P2f02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	60

E value	6.0e-25
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174651
Seq. ID	jC-atXLIB327424P2f03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	1.0e-21
Match length	78
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174652
Seq. ID	jC-atXLIB327424P2f04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	6.0e-27
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174653
Seq. ID	jC-atXLIB327424P2f06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174654
Seq. ID	jC-atXLIB327424P2f07b2
Method	BLASTN
NCBI GI	g4733952
BLAST score	69
E value	3.0e-30
Match length	176
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	174655
Seq. ID	jC-atXLIB327424P2f08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	2.0e-09
Match length	70
% identity	87

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174656
Seq. ID	jC-atXLIB327424P2f09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174657
Seq. ID	jC-atXLIB327424P2f09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	59
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174658
Seq. ID	jC-atXLIB327424P2f10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	7.0e-18
Match length	56
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174659
Seq. ID	jC-atXLIB327424P2f12a2
Method	BLASTX
NCBI GI	g2129533
BLAST score	221
E value	3.0e-20
Match length	64
% identity	88
NCBI Description	adenine nucleotide translocase - Arabidopsis thaliana >gi_1051109_emb_CAA89201_ (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]

Seq. No.	174660
Seq. ID	jC-atXLIB327424P2g02b2
Method	BLASTX
NCBI GI	g2642157
BLAST score	364
E value	6.0e-42
Match length	96
% identity	89
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	174661
Seq. ID	jC-atXLIB327424P2g04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174662
Seq. ID	jC-atXLIB327424P2g09a2
Method	BLASTN
NCBI GI	g3985933
BLAST score	180
E value	1.0e-96
Match length	256
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9E15, complete sequence [Arabidopsis thaliana]

Seq. No.	174663
Seq. ID	jC-atXLIB327424P2g09b2
Method	BLASTN
NCBI GI	g3985933
BLAST score	141
E value	3.0e-73
Match length	221
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9E15, complete sequence [Arabidopsis thaliana]

Seq. No.	174664
Seq. ID	jC-atXLIB327424P2g10a2
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174665
Seq. ID	jC-atXLIB327424P2g10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	6.0e-19
Match length	70
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174666
Seq. ID	jC-atXLIB327424P2g12b2
Method	BLASTX

NCBI GI	g3738230
BLAST score	366
E value	7.0e-35
Match length	96
% identity	77
NCBI Description	(AB007790) DREB2A [Arabidopsis thaliana] >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis thaliana]

Seq. No.	174667
Seq. ID	jC-atXLIB327424P2h04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	4.0e-17
Match length	71
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174668
Seq. ID	jC-atXLIB327424P2h05a2
Method	BLASTX
NCBI GI	g1708313
BLAST score	369
E value	3.0e-35
Match length	77
% identity	96
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	174669
Seq. ID	jC-atXLIB327424P2h09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	6.0e-21
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174670
Seq. ID	jC-atXLIB327424P2h09b2
Method	BLASTX
NCBI GI	g127041
BLAST score	205
E value	5.0e-16
Match length	44
% identity	82
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	174671
Seq. ID	jC-atXLIB327424P2h10a2
Method	BLASTX
NCBI GI	g1711617
BLAST score	103
E value	1.0e-09
Match length	59
% identity	61
NCBI Description	HIGH AFFINITY SULPHATE TRANSPORTER 2 >gi_1085848_pir__S51764 high affinity sulphate transporter - Stylosanthes hamata >gi_607186_emb_CAA57711_ (X82256) high affinity sulphate transporter [Stylosanthes hamata]

Seq. No.	174672
Seq. ID	jC-atXLIB327424P2h11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	52
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174673
Seq. ID	jC-atXLIB327424P3a02b1
Method	BLASTN
NCBI GI	g3668073
BLAST score	122
E value	6.0e-62
Match length	220
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174674
Seq. ID	jC-atXLIB327424P3a09a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	76
E value	2.0e-34
Match length	174
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	174675
Seq. ID	jC-atXLIB327424P3b01a1
Method	BLASTN
NCBI GI	g3980374
BLAST score	46
E value	1.0e-16
Match length	30
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174676
Seq. ID	jC-atXLIB327424P3b01b1
Method	BLASTN
NCBI GI	g3980374
BLAST score	42
E value	3.0e-14
Match length	50
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174677
Seq. ID	jC-atXLIB327424P3b05b1
Method	BLASTN
NCBI GI	g3779020
BLAST score	65
E value	7.0e-28
Match length	101
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174678
Seq. ID	jC-atXLIB327424P3b10b1
Method	BLASTX
NCBI GI	g541816
BLAST score	247
E value	3.0e-26
Match length	135
% identity	55
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	174679
Seq. ID	jC-atXLIB327424P3b11b1
Method	BLASTN
NCBI GI	g3763944
BLAST score	43
E value	7.0e-15
Match length	108
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	174680
Seq. ID	jC-atXLIB327424P3c03b1
Method	BLASTN
NCBI GI	g2459406
BLAST score	50
E value	6.0e-19
Match length	85
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174681
Seq. ID	jC-atXLIB327424P3c05a1

Method	BLASTX
NCBI GI	g2565010
BLAST score	391
E value	8.0e-38
Match length	71
% identity	99
NCBI Description	(AC002983) putative microfibril-associated protein [Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm, score: 11.71) [Arabidopsis thaliana]

Seq. No.	174682
Seq. ID	jC-atXLIB327424P3c06b1
Method	BLASTX
NCBI GI	g2052510
BLAST score	308
E value	5.0e-28
Match length	143
% identity	54
NCBI Description	(U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No.	174683
Seq. ID	jC-atXLIB327424P3c08a1
Method	BLASTN
NCBI GI	g2264306
BLAST score	95
E value	7.0e-46
Match length	383
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	174684
Seq. ID	jC-atXLIB327424P3c09a1
Method	BLASTN
NCBI GI	g1644426
BLAST score	42
E value	3.0e-14
Match length	183
% identity	89
NCBI Description	Arabidopsis thaliana putative glyoxalase II mRNA, complete cds

Seq. No.	174685
Seq. ID	jC-atXLIB327424P3c09b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174686
Seq. ID	jC-atXLIB327424P3c11a1

Method	BLASTN
NCBI GI	g4581138
BLAST score	127
E value	6.0e-65
Match length	320
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	174687
Seq. ID	jC-atXLIB327424P3d02a1
Method	BLASTN
NCBI GI	g4567300
BLAST score	36
E value	1.0e-10
Match length	52
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	174688
Seq. ID	jC-atXLIB327424P3d02b1
Method	BLASTN
NCBI GI	g4567300
BLAST score	59
E value	2.0e-24
Match length	119
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	174689
Seq. ID	jC-atXLIB327424P3d03b1
Method	BLASTN
NCBI GI	g3402745
BLAST score	60
E value	6.0e-25
Match length	115
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	174690
Seq. ID	jC-atXLIB327424P3d05b1
Method	BLASTN
NCBI GI	g3985931
BLAST score	97
E value	5.0e-47
Match length	129
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	174691
Seq. ID	jC-atXLIB327424P3d07a1
Method	BLASTN
NCBI GI	g2924733

BLAST score	70
E value	6.0e-31
Match length	233
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	174692
Seq. ID	jC-atXLIB327424P3d07b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	76
E value	2.0e-34
Match length	100
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	174693
Seq. ID	jC-atXLIB327424P3d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174694
Seq. ID	jC-atXLIB327424P3d10b1
Method	BLASTN
NCBI GI	g3057149
BLAST score	63
E value	8.0e-27
Match length	132
% identity	92
NCBI Description	Arabidopsis thaliana chaperonin 10 (CPN10) mRNA, complete cds

Seq. No.	174695
Seq. ID	jC-atXLIB327424P3d12a1
Method	BLASTN
NCBI GI	g2827644
BLAST score	40
E value	3.0e-13
Match length	109
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	174696
Seq. ID	jC-atXLIB327424P3d12b1
Method	BLASTN
NCBI GI	g2827644
BLAST score	114
E value	3.0e-57

Match length	361
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	174697
Seq. ID	jC-atXLIB327424P3e01b1
Method	BLASTX
NCBI GI	g3482933
BLAST score	137
E value	4.0e-10
Match length	70
% identity	53
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	174698
Seq. ID	jC-atXLIB327424P3e02a1
Method	BLASTX
NCBI GI	g81601
BLAST score	244
E value	1.0e-20
Match length	71
% identity	70
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	174699
Seq. ID	jC-atXLIB327424P3e02b1
Method	BLASTX
NCBI GI	g81601
BLAST score	360
E value	3.0e-34
Match length	143
% identity	59
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	174700
Seq. ID	jC-atXLIB327424P3e08a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	94
E value	3.0e-45
Match length	343
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	174701
Seq. ID	jC-atXLIB327424P3e08b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	97
E value	5.0e-47
Match length	228
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	174702
Seq. ID	jC-atXLIB327424P3f01b1
Method	BLASTN
NCBI GI	g1871173
BLAST score	108
E value	1.0e-53
Match length	132
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	174703
Seq. ID	jC-atXLIB327424P3f04a1
Method	BLASTN
NCBI GI	g2924729
BLAST score	154
E value	3.0e-81
Match length	264
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	174704
Seq. ID	jC-atXLIB327424P3f05a1
Method	BLASTN
NCBI GI	g4490717
BLAST score	34
E value	2.0e-09
Match length	102
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	174705
Seq. ID	jC-atXLIB327424P3f05b1
Method	BLASTN
NCBI GI	g4490717
BLAST score	41
E value	1.0e-13
Match length	101
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	174706
Seq. ID	jC-atXLIB327424P3f06a1
Method	BLASTN
NCBI GI	g4159707
BLAST score	80
E value	6.0e-37
Match length	179
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No. 174707

Seq. ID	jC-atXLIB327424P3f06b1
Method	BLASTN
NCBI GI	g4159707
BLAST score	154
E value	4.0e-81
Match length	273
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	174708
Seq. ID	jC-atXLIB327424P3f07a1
Method	BLASTN
NCBI GI	g2739359
BLAST score	152
E value	7.0e-80
Match length	348
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174709
Seq. ID	jC-atXLIB327424P3f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174710
Seq. ID	jC-atXLIB327424P3f12b1
Method	BLASTN
NCBI GI	g861214
BLAST score	89
E value	3.0e-42
Match length	307
% identity	90
NCBI Description	Arabidopsis thaliana glycine decarboxylase complex H-protein precursor gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	174711
Seq. ID	jC-atXLIB327424P3g01a1
Method	BLASTN
NCBI GI	g4581138
BLAST score	212
E value	1.0e-115
Match length	397
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	174712
Seq. ID	jC-atXLIB327424P3g02b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174713
Seq. ID	jC-atXLIB327424P3g03a1
Method	BLASTN
NCBI GI	g16208
BLAST score	118
E value	1.0e-59
Match length	213
% identity	89
NCBI Description	A.thaliana mRNA for calcium binding protein

Seq. No.	174714
Seq. ID	jC-atXLIB327424P3g03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174715
Seq. ID	jC-atXLIB327424P3g06a1
Method	BLASTN
NCBI GI	g4220629
BLAST score	90
E value	7.0e-43
Match length	255
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24F5, complete sequence [Arabidopsis thaliana]

Seq. No.	174716
Seq. ID	jC-atXLIB327424P3g07b1
Method	BLASTN
NCBI GI	g2645198
BLAST score	60
E value	6.0e-25
Match length	119
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174717
Seq. ID	jC-atXLIB327424P3g08a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	147

E value	7.0e-77
Match length	293
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	174718
Seq. ID	jC-atXLIB327424P3g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	8.0e-09
Match length	45
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174719
Seq. ID	jC-atXLIB327424P3g11b1
Method	BLASTN
NCBI GI	g1865678
BLAST score	35
E value	4.0e-10
Match length	59
% identity	90
NCBI Description	A.thaliana ATB2 gene

Seq. No.	174720
Seq. ID	jC-atXLIB327424P3h01a1
Method	BLASTN
NCBI GI	g4455348
BLAST score	35
E value	4.0e-10
Match length	119
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	174721
Seq. ID	jC-atXLIB327424P3h02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174722
Seq. ID	jC-atXLIB327424P3h03a1
Method	BLASTN
NCBI GI	g4582444
BLAST score	100
E value	7.0e-49
Match length	296
% identity	82

NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	174723
Seq. ID	jC-atXLIB327424P4a01a1
Method	BLASTN
NCBI GI	g4757395
BLAST score	34
E value	1.0e-09
Match length	54
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	174724
Seq. ID	jC-atXLIB327424P4a02a1
Method	BLASTN
NCBI GI	g693691
BLAST score	64
E value	3.0e-27
Match length	132
% identity	88
NCBI Description	Arabidopsis thaliana aspartate aminotransferase (Asp3) mRNA, complete cds

Seq. No.	174725
Seq. ID	jC-atXLIB327424P4a08b1
Method	BLASTN
NCBI GI	g4218109
BLAST score	50
E value	4.0e-19
Match length	141
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	174726
Seq. ID	jC-atXLIB327424P4a09a1
Method	BLASTN
NCBI GI	g4220627
BLAST score	52
E value	2.0e-20
Match length	80
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	174727
Seq. ID	jC-atXLIB327424P4a09b1
Method	BLASTN
NCBI GI	g4220627
BLAST score	32
E value	1.0e-08
Match length	47
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	174728
Seq. ID	jC-atXLIB327424P4a10a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	96
E value	2.0e-46
Match length	194
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	174729
Seq. ID	jC-atXLIB327424P4a11a1
Method	BLASTN
NCBI GI	g3426033
BLAST score	107
E value	5.0e-53
Match length	215
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174730
Seq. ID	jC-atXLIB327424P4b01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	2.0e-23
Match length	61
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174731
Seq. ID	jC-atXLIB327424P4b10a1
Method	BLASTX
NCBI GI	g585421
BLAST score	214
E value	5.0e-17
Match length	84
% identity	54
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	174732
Seq. ID	jC-atXLIB327424P4c05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	9.0e-18
Match length	59
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174733
Seq. ID	jC-atXLIB327424P4c06b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	4.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174734
Seq. ID	jC-atXLIB327424P4d02a1
Method	BLASTX
NCBI GI	g4835233
BLAST score	398
E value	1.0e-38
Match length	103
% identity	80
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	174735
Seq. ID	jC-atXLIB327424P4d02b1
Method	BLASTN
NCBI GI	g4835223
BLAST score	93
E value	8.0e-45
Match length	179
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	174736
Seq. ID	jC-atXLIB327424P4d04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174737
Seq. ID	jC-atXLIB327424P4d04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	2.0e-23
Match length	65
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174738
Seq. ID	jC-atXLIB327424P4d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56

E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174739
Seq. ID	jC-atXLIB327424P4d09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	2.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174740
Seq. ID	jC-atXLIB327424P4d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174741
Seq. ID	jC-atXLIB327424P4e01a1
Method	BLASTN
NCBI GI	g2226430
BLAST score	35
E value	5.0e-10
Match length	47
% identity	94
NCBI Description	Mus saxicola haptoglobin mRNA, complete cds

Seq. No.	174742
Seq. ID	jC-atXLIB327424P4e02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	5.0e-21
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174743
Seq. ID	jC-atXLIB327424P4e02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	1.0e-13
Match length	57
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174744

Seq. ID	jC-atXLIB327424P4e04b1
Method	BLASTX
NCBI GI	g1575754
BLAST score	88
E value	4.0e-14
Match length	87
% identity	62
NCBI Description	(U70616) ADP glucose pyrophosphorylase small subunit [Arabidopsis thaliana]

Seq. No.	174745
Seq. ID	jC-atXLIB327424P4e06a1
Method	BLASTN
NCBI GI	g2351071
BLAST score	79
E value	3.0e-36
Match length	103
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	174746
Seq. ID	jC-atXLIB327424P4f01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174747
Seq. ID	jC-atXLIB327424P4f04a1
Method	BLASTN
NCBI GI	g2656026
BLAST score	73
E value	1.0e-32
Match length	264
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	174748
Seq. ID	jC-atXLIB327424P4f05a1
Method	BLASTN
NCBI GI	g3702729
BLAST score	85
E value	7.0e-40
Match length	270
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	174749
Seq. ID	jC-atXLIB327424P4f07b1
Method	BLASTN
NCBI GI	g3660464

BLAST score	48
E value	3.0e-18
Match length	84
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for Inositol 1,3,4-Trisphosphate 5/6 Kinase

Seq. No.	174750
Seq. ID	jC-atXLIB327424P4f08a1
Method	BLASTX
NCBI GI	g2498726
BLAST score	216
E value	3.0e-17
Match length	79
% identity	52
NCBI Description	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (OST5OP) >gi_1085153_pir__JC4132 oligosaccharyltransferase 50k chain - fruit fly (Drosophila melanogaster) >gi_1019386_emb_CAA57525_ (X81999) oligosaccharyltransferase subunit [Drosophila melanogaster]

Seq. No.	174751
Seq. ID	jC-atXLIB327424P4f08b1
Method	BLASTN
NCBI GI	g3702737
BLAST score	55
E value	4.0e-22
Match length	75
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	174752
Seq. ID	jC-atXLIB327424P4g02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174753
Seq. ID	jC-atXLIB327424P4g05b1
Method	BLASTN
NCBI GI	g4512656
BLAST score	59
E value	2.0e-24
Match length	163
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	174754
Seq. ID	jC-atXLIB327424P4g06a1

Method	BLASTN
NCBI GI	g2262135
BLAST score	83
E value	1.0e-38
Match length	135
% identity	91
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	174755
Seq. ID	jC-atXLIB327424P4g06b1
Method	BLASTN
NCBI GI	g2262135
BLAST score	56
E value	3.0e-22
Match length	240
% identity	89
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	174756
Seq. ID	jC-atXLIB327424P4g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	8.0e-15
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174757
Seq. ID	jC-atXLIB327424P4g12b1
Method	BLASTX
NCBI GI	g2982583
BLAST score	141
E value	5.0e-21
Match length	80
% identity	75
NCBI Description	(AJ003135) polygalacturonase [Arabidopsis thaliana] >gi_3152948_emb_CAA06610_ (AJ005584) polygalacturonase [Arabidopsis thaliana]

Seq. No.	174758
Seq. ID	jC-atXLIB327424P4h02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174759
Seq. ID	jC-atXLIB327424P4h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41

E value	1.0e-13
Match length	53
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174760
Seq. ID	jC-atXLIB327424P4h04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	61
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174761
Seq. ID	jC-atXLIB327424P4h06a1
Method	BLASTN
NCBI GI	g4544435
BLAST score	116
E value	2.0e-58
Match length	269
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	174762
Seq. ID	jC-atXLIB327424P4h07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174763
Seq. ID	jC-atXLIB327424P4h11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	8.0e-21
Match length	73
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174764
Seq. ID	jC-atXLIB327425P1a03b1
Method	BLASTX
NCBI GI	g1172538
BLAST score	232
E value	4.0e-19
Match length	135
% identity	44
NCBI Description	PROBABLE PECTINESTERASE PRECURSOR (PECTIN METHYLESTERASE) (PE) >gi_99823_pir__S14952 pectinesterase homolog - rape >gi_17784_emb_CAA39658_ (X56195) Bp19 [Brassica napus]

Seq. No.	174765
Seq. ID	jC-atXLIB327425P1a04b1
Method	BLASTX
NCBI GI	g3927825
BLAST score	131
E value	2.0e-14
Match length	139
% identity	44
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	174766
Seq. ID	jC-atXLIB327425P1a07b1
Method	BLASTN
NCBI GI	g4376087
BLAST score	54
E value	2.0e-21
Match length	90
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	174767
Seq. ID	jC-atXLIB327425P1a11b1
Method	BLASTN
NCBI GI	g2584720
BLAST score	37
E value	3.0e-11
Match length	99
% identity	90
NCBI Description	A.thaliana gene encoding sulfite reductase

Seq. No.	174768
Seq. ID	jC-atXLIB327425P1b02a1
Method	BLASTN
NCBI GI	g3355463
BLAST score	134
E value	5.0e-69
Match length	345
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174769
Seq. ID	jC-atXLIB327425P1b07b1
Method	BLASTX
NCBI GI	g3355480
BLAST score	48
E value	2.0e-09
Match length	70
% identity	51
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	174770
Seq. ID	jC-atXLIB327425P1b09a1

Method	BLASTN
NCBI GI	g3046853
BLAST score	52
E value	4.0e-20
Match length	226
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	174771
Seq. ID	jC-atXLIB327425P1b09b1
Method	BLASTN
NCBI GI	g3046853
BLAST score	251
E value	1.0e-139
Match length	433
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	174772
Seq. ID	jC-atXLIB327425P1b11b1
Method	BLASTX
NCBI GI	g1346215
BLAST score	81
E value	4.0e-15
Match length	95
% identity	55
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE PARC (AUXIN-REGULATED PROTEIN PARC) >gi_100350_pir__S19185 parC protein - common tobacco >gi_19906_emb_CAA45740_ (X64398) parC [Nicotiana tabacum]

Seq. No.	174773
Seq. ID	jC-atXLIB327425P1c01a1
Method	BLASTN
NCBI GI	g4455348
BLAST score	43
E value	9.0e-15
Match length	103
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	174774
Seq. ID	jC-atXLIB327425P1c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174775
Seq. ID	jC-atXLIB327425P1c10b1
Method	BLASTN

NCBI GI	g4757415
BLAST score	71
E value	2.0e-31
Match length	132
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	174776
Seq. ID	jC-atXLIB327425P1c12a1
Method	BLASTN
NCBI GI	g4531433
BLAST score	35
E value	5.0e-10
Match length	79
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	174777
Seq. ID	jC-atXLIB327425P1d02a1
Method	BLASTX
NCBI GI	g4335751
BLAST score	409
E value	7.0e-40
Match length	85
% identity	94
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	174778
Seq. ID	jC-atXLIB327425P1d03a1
Method	BLASTN
NCBI GI	g4589435
BLAST score	97
E value	5.0e-47
Match length	310
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	174779
Seq. ID	jC-atXLIB327425P1d06b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	42
E value	4.0e-14
Match length	50
% identity	96
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	174780
Seq. ID	jC-atXLIB327425P1d07b1
Method	BLASTX
NCBI GI	g1707412
BLAST score	236

E value	5.0e-21
Match length	153
% identity	43
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	174781
Seq. ID	jC-atXLIB327425P1d08a1
Method	BLASTX
NCBI GI	g629602
BLAST score	325
E value	5.0e-30
Match length	91
% identity	70
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	174782
Seq. ID	jC-atXLIB327425P1d09a1
Method	BLASTN
NCBI GI	g2191157
BLAST score	69
E value	3.0e-30
Match length	207
% identity	87
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	174783
Seq. ID	jC-atXLIB327425P1d09b1
Method	BLASTX
NCBI GI	g2191177
BLAST score	173
E value	3.0e-12
Match length	106
% identity	51
NCBI Description	(AF007270) belongs to the SPOU family of rRNA methylases. [Arabidopsis thaliana]

Seq. No.	174784
Seq. ID	jC-atXLIB327425P1d12b1
Method	BLASTN
NCBI GI	g2160132
BLAST score	50
E value	4.0e-19
Match length	254
% identity	88
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174785
Seq. ID	jC-atXLIB327425P1e07a1
Method	BLASTN
NCBI GI	g2351065
BLAST score	86
E value	2.0e-40
Match length	106

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	174786
Seq. ID	jC-atXLIB327425P1e07b1
Method	BLASTN
NCBI GI	g2351065
BLAST score	86
E value	2.0e-40
Match length	236
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	174787
Seq. ID	jC-atXLIB327425P1e11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174788
Seq. ID	jC-atXLIB327425P1e12a1
Method	BLASTX
NCBI GI	g3860277
BLAST score	239
E value	6.0e-20
Match length	82
% identity	62
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	174789
Seq. ID	jC-atXLIB327425P1e12b1
Method	BLASTX
NCBI GI	g1709970
BLAST score	242
E value	2.0e-20
Match length	98
% identity	49
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	174790
Seq. ID	jC-atXLIB327425P1f02a1
Method	BLASTN
NCBI GI	g3355463
BLAST score	99
E value	3.0e-48
Match length	275
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174791
Seq. ID	jC-atXLIB327425P1f03b1
Method	BLASTN
NCBI GI	g3702732
BLAST score	50
E value	2.0e-19
Match length	119
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	174792
Seq. ID	jC-atXLIB327425P1f04a1
Method	BLASTN
NCBI GI	g207740
BLAST score	39
E value	2.0e-12
Match length	161
% identity	80
NCBI Description	Cloning vector pHV100 DNA with partial lacI, lacZ and luxA genes, and polylinker regions

Seq. No.	174793
Seq. ID	jC-atXLIB327425P1f07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174794
Seq. ID	jC-atXLIB327425P1f08b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	36
E value	1.0e-10
Match length	52
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	174795
Seq. ID	jC-atXLIB327425P1f09a1
Method	BLASTX
NCBI GI	g3548802
BLAST score	154
E value	5.0e-10
Match length	69
% identity	51
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	174796
Seq. ID	jC-atXLIB327425P1f11a1
Method	BLASTX
NCBI GI	g4539459
BLAST score	202
E value	1.0e-15
Match length	73
% identity	59
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	174797
Seq. ID	jC-atXLIB327425P1f12a1
Method	BLASTX
NCBI GI	g2493495
BLAST score	294
E value	2.0e-26
Match length	89
% identity	58
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370 carboxypeptidase - garden pea (fragment) >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase [Pisum sativum]

Seq. No.	174798
Seq. ID	jC-atXLIB327425P1g03a1
Method	BLASTX
NCBI GI	g4455173
BLAST score	391
E value	4.0e-47
Match length	106
% identity	92
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	174799
Seq. ID	jC-atXLIB327425P1g06a1
Method	BLASTN
NCBI GI	g3297806
BLAST score	36
E value	1.0e-10
Match length	134
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	174800
Seq. ID	jC-atXLIB327425P1g09a1
Method	BLASTN
NCBI GI	g4589423
BLAST score	272
E value	1.0e-151
Match length	391
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No.	174801

Seq. ID	jC-atXLIB327425P1h02a1
Method	BLASTX
NCBI GI	g126962
BLAST score	164
E value	4.0e-11
Match length	56
% identity	59
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7 >gi_99747_pir__S13718 probable membrane channel protein - Arabidopsis thaliana >gi_16492_emb_CAA38633_ (X54854) possible membrane channel protein [Arabidopsis thaliana]

Seq. No.	174802
Seq. ID	jC-atXLIB327425P1h03a1
Method	BLASTX
NCBI GI	g3334409
BLAST score	260
E value	2.0e-22
Match length	72
% identity	74
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	174803
Seq. ID	jC-atXLIB327425P1h08a1
Method	BLASTX
NCBI GI	g2160142
BLAST score	166
E value	5.0e-61
Match length	146
% identity	84
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	174804
Seq. ID	jC-atXLIB327425P1h10a1
Method	BLASTX
NCBI GI	g1168260
BLAST score	318
E value	3.0e-29
Match length	68
% identity	87
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_629503_pir__S47490 aspartate transaminase (EC 2.6.1.1) - Arabidopsis thaliana >gi_1361984_pir__S56657 aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana >gi_531555_emb_CAA56932_ (X81026) aspartate aminotransferase [Arabidopsis thaliana] >gi_1017411_emb_CAA62972_ (X91865) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	174805
Seq. ID	jC-atXLIB327425P1h11a1

Method	BLASTN
NCBI GI	g3193282
BLAST score	165
E value	1.0e-87
Match length	308
% identity	92
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	174806
Seq. ID	jC-atXLIB327425P1h11b1
Method	BLASTN
NCBI GI	g3193282
BLAST score	74
E value	3.0e-33
Match length	101
% identity	93
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	174807
Seq. ID	jC-atXLIB327425P1h12b1
Method	BLASTN
NCBI GI	g2262135
BLAST score	35
E value	5.0e-10
Match length	93
% identity	91
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	174808
Seq. ID	jC-atXLIB327425P2b02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	1.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174809
Seq. ID	jC-atXLIB327425P2b07a1
Method	BLASTN
NCBI GI	g4191760
BLAST score	105
E value	8.0e-52
Match length	137
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	174810
Seq. ID	jC-atXLIB327425P2b11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	65

% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174811
Seq. ID	jC-atXLIB327425P2b12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174812
Seq. ID	jC-atXLIB327425P2c01a1
Method	BLASTN
NCBI GI	g2160155
BLAST score	139
E value	2.0e-72
Match length	175
% identity	95
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174813
Seq. ID	jC-atXLIB327425P2c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174814
Seq. ID	jC-atXLIB327425P2d06a1
Method	BLASTX
NCBI GI	g3688186
BLAST score	198
E value	3.0e-15
Match length	51
% identity	78
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	174815
Seq. ID	jC-atXLIB327425P2d12a1
Method	BLASTN
NCBI GI	g3367567
BLAST score	168
E value	1.0e-89
Match length	253
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	174816

Seq. ID	jC-atXLIB327425P2e12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174817
Seq. ID	jC-atXLIB327425P2g12a1
Method	BLASTN
NCBI GI	g4580454
BLAST score	106
E value	1.0e-52
Match length	184
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	174818
Seq. ID	jC-atXLIB327425P3a04a1
Method	BLASTN
NCBI GI	g2104523
BLAST score	36
E value	1.0e-10
Match length	68
% identity	90
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	174819
Seq. ID	jC-atXLIB327425P3a05b1
Method	BLASTN
NCBI GI	g2760361
BLAST score	66
E value	2.0e-28
Match length	122
% identity	90
NCBI Description	Arabidopsis thaliana 15.9 kDa subunit of RNA polymerase II (RPB15.9) mRNA, complete cds

Seq. No.	174820
Seq. ID	jC-atXLIB327425P3a06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	42
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174821
Seq. ID	jC-atXLIB327425P3a08a1
Method	BLASTX
NCBI GI	g2827548
BLAST score	157

E value	2.0e-10
Match length	72
% identity	46
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	174822
Seq. ID	jC-atXLIB327425P3b02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174823
Seq. ID	jC-atXLIB327425P3b02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	3.0e-18
Match length	72
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174824
Seq. ID	jC-atXLIB327425P3b03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174825
Seq. ID	jC-atXLIB327425P3b04b1
Method	BLASTN
NCBI GI	g4159709
BLAST score	135
E value	9.0e-70
Match length	297
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	174826
Seq. ID	jC-atXLIB327425P3b05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174827
Seq. ID	jC-atXLIB327425P3b07a1
Method	BLASTN
NCBI GI	g1817543
BLAST score	59
E value	2.0e-24
Match length	329
% identity	86
NCBI Description	Arabidopsis thaliana mRNA for proline oxidase precursor, complete cds

Seq. No.	174828
Seq. ID	jC-atXLIB327425P3b07b1
Method	BLASTN
NCBI GI	g1817543
BLAST score	67
E value	4.0e-29
Match length	189
% identity	85
NCBI Description	Arabidopsis thaliana mRNA for proline oxidase precursor, complete cds

Seq. No.	174829
Seq. ID	jC-atXLIB327425P3b08b1
Method	BLASTN
NCBI GI	g2224934
BLAST score	222
E value	1.0e-121
Match length	347
% identity	90
NCBI Description	Arabidopsis thaliana ethylene-insensitive3 (EIN3) gene, complete cds

Seq. No.	174830
Seq. ID	jC-atXLIB327425P3c03a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	125
E value	9.0e-64
Match length	278
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	174831
Seq. ID	jC-atXLIB327425P3c03b1
Method	BLASTN
NCBI GI	g4589434
BLAST score	127
E value	5.0e-65
Match length	147
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	174832

Seq. ID	jC-atXLIB327425P3c06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174833
Seq. ID	jC-atXLIB327425P3c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174834
Seq. ID	jC-atXLIB327425P3c08a1
Method	BLASTN
NCBI GI	g531832
BLAST score	35
E value	4.0e-10
Match length	63
% identity	89
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	174835
Seq. ID	jC-atXLIB327425P3c08b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	34
E value	2.0e-09
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	174836
Seq. ID	jC-atXLIB327425P3c09a1
Method	BLASTN
NCBI GI	g4757403
BLAST score	83
E value	1.0e-38
Match length	293
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	174837
Seq. ID	jC-atXLIB327425P3d02a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174838
Seq. ID	jC-atXLIB327425P3d03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174839
Seq. ID	jC-atXLIB327425P3d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174840
Seq. ID	jC-atXLIB327425P3d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174841
Seq. ID	jC-atXLIB327425P3d06b1
Method	BLASTX
NCBI GI	g3288821
BLAST score	239
E value	6.0e-20
Match length	133
% identity	43
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	174842
Seq. ID	jC-atXLIB327425P3d12a1
Method	BLASTN
NCBI GI	g4589950
BLAST score	66
E value	2.0e-28
Match length	346

% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	174843
Seq. ID	jC-atXLIB327425P3e06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174844
Seq. ID	jC-atXLIB327425P3e07b1
Method	BLASTN
NCBI GI	g16323
BLAST score	107
E value	6.0e-53
Match length	138
% identity	99
NCBI Description	A.thaliana H3 gene 1 and H3 gene 2 for H3.3-like histone variant

Seq. No.	174845
Seq. ID	jC-atXLIB327425P3e09a1
Method	BLASTX
NCBI GI	g4584525
BLAST score	326
E value	3.0e-30
Match length	63
% identity	98
NCBI Description	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	174846
Seq. ID	jC-atXLIB327425P3f02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174847
Seq. ID	jC-atXLIB327425P3f03a1
Method	BLASTN
NCBI GI	g3511222
BLAST score	80
E value	7.0e-37
Match length	256
% identity	89
NCBI Description	Arabidopsis thaliana plant adhesion molecule 1 (PAM1) mRNA, complete cds

Seq. No.	174848
Seq. ID	jC-atXLIB327425P3f06a1
Method	BLASTN
NCBI GI	g4589438
BLAST score	218
E value	1.0e-119
Match length	355
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	174849
Seq. ID	jC-atXLIB327425P3f07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174850
Seq. ID	jC-atXLIB327425P3f08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174851
Seq. ID	jC-atXLIB327425P3f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174852
Seq. ID	jC-atXLIB327425P3g02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174853
Seq. ID	jC-atXLIB327425P3g04b1
Method	BLASTX
NCBI GI	g4587569
BLAST score	357

E value	1.0e-55
Match length	135
% identity	83
NCBI Description	(AC006550) Identical to gb_U12536 3-methylcrotonyl-CoA carboxylase precursor protein from Arabidopsis thaliana. ESTs gb_H35836, gb_AA651295 and gb_AA721862 come from this gene

Seq. No.	174854
Seq. ID	jC-atXLIB327425P3g05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174855
Seq. ID	jC-atXLIB327425P3g06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174856
Seq. ID	jC-atXLIB327425P3g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14
Match length	62
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174857
Seq. ID	jC-atXLIB327425P3g07b1
Method	BLASTN
NCBI GI	g4455290
BLAST score	150
E value	1.0e-78
Match length	332
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	174858
Seq. ID	jC-atXLIB327425P3g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	7.0e-12
Match length	62

% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174859
Seq. ID	jC-atXLIB327425P3g11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	5.0e-22
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174860
Seq. ID	jC-atXLIB327425P3h02b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	174861
Seq. ID	jC-atXLIB327425P3h04b1
Method	BLASTX
NCBI GI	g2773270
BLAST score	132
E value	6.0e-23
Match length	141
% identity	57
NCBI Description	(AF039851) ferredoxin-dependent glutamate synthase [Glycine max]

Seq. No.	174862
Seq. ID	jC-atXLIB327425P3h06a1
Method	BLASTN
NCBI GI	g4519791
BLAST score	75
E value	7.0e-34
Match length	206
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for Asp1, complete cds

Seq. No.	174863
Seq. ID	jC-atXLIB327425P3h07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	51
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174864
Seq. ID	jC-atXLIB327425P3h08b1
Method	BLASTX
NCBI GI	g3608261
BLAST score	199
E value	3.0e-15
Match length	55
% identity	69
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	174865
Seq. ID	jC-atXLIB327425P3h09b1
Method	BLASTX
NCBI GI	g399091
BLAST score	73
E value	5.0e-15
Match length	87
% identity	60
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	174866
Seq. ID	jC-atXLIB327425P4e03b1
Method	BLASTX
NCBI GI	g3250738
BLAST score	182
E value	3.0e-19
Match length	71
% identity	75
NCBI Description	(AJ224338) shaggy-like kinase beta [Arabidopsis thaliana]

Seq. No.	174867
Seq. ID	jC-atXLIB327426P1a03a1
Method	BLASTN
NCBI GI	g540252
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174868
Seq. ID	jC-atXLIB327426P1a03b1
Method	BLASTN
NCBI GI	g886433
BLAST score	100
E value	9.0e-49
Match length	313
% identity	86
NCBI Description	A.thaliana mRNA for ARP protein

Seq. No.	174869
Seq. ID	jC-atXLIB327426P1a05b1

Method	BLASTN
NCBI GI	g2351069
BLAST score	33
E value	9.0e-09
Match length	101
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	174870
Seq. ID	jC-atXLIB327426P1a08a1
Method	BLASTN
NCBI GI	g2833627
BLAST score	47
E value	3.0e-17
Match length	75
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	174871
Seq. ID	jC-atXLIB327426P1b02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	46
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174872
Seq. ID	jC-atXLIB327426P1b05b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	38
E value	9.0e-12
Match length	70
% identity	51
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	174873
Seq. ID	jC-atXLIB327426P1b07a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	72
E value	4.0e-32
Match length	215
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	174874
Seq. ID	jC-atXLIB327426P1b08a1
Method	BLASTN
NCBI GI	g3849811
BLAST score	41
E value	1.0e-13

Match length	81
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174875
Seq. ID	jC-atXLIB327426P1b08b1
Method	BLASTN
NCBI GI	g3849811
BLAST score	116
E value	2.0e-58
Match length	371
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174876
Seq. ID	jC-atXLIB327426P1b10b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	54
E value	2.0e-21
Match length	82
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	174877
Seq. ID	jC-atXLIB327426P1c03a1
Method	BLASTN
NCBI GI	g540252
BLAST score	43
E value	8.0e-15
Match length	43
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174878
Seq. ID	jC-atXLIB327426P1c03b1
Method	BLASTX
NCBI GI	g2062164
BLAST score	83
E value	1.2e-01
Match length	100
% identity	26
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	174879
Seq. ID	jC-atXLIB327426P1c07a1
Method	BLASTX
NCBI GI	g4138855
BLAST score	245
E value	1.0e-20
Match length	76
% identity	64
NCBI Description	(AF098072) IMMUTANS [Arabidopsis thaliana]

Seq. No.	174880
Seq. ID	jC-atXLIB327426P1c07b1
Method	BLASTX
NCBI GI	g4138855
BLAST score	332
E value	1.0e-38
Match length	106
% identity	82
NCBI Description	(AF098072) IMMUTANS [Arabidopsis thaliana]

Seq. No.	174881
Seq. ID	jC-atXLIB327426P1c11a1
Method	BLASTN
NCBI GI	g4538918
BLAST score	99
E value	3.0e-48
Match length	278
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)

Seq. No.	174882
Seq. ID	jC-atXLIB327426P1c11b1
Method	BLASTN
NCBI GI	g4538918
BLAST score	182
E value	1.0e-97
Match length	283
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)

Seq. No.	174883
Seq. ID	jC-atXLIB327426P1d02a1
Method	BLASTX
NCBI GI	g1076675
BLAST score	389
E value	2.0e-37
Match length	87
% identity	80
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - potato

Seq. No.	174884
Seq. ID	jC-atXLIB327426P1d02b1
Method	BLASTX
NCBI GI	g586145
BLAST score	98
E value	6.0e-35
Match length	149
% identity	60
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur protein [Solanum tuberosum]

Seq. No.	174885
Seq. ID	jC-atXLIB327426P1d04a1
Method	BLASTN
NCBI GI	g540252
BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174886
Seq. ID	jC-atXLIB327426P1d07a1
Method	BLASTN
NCBI GI	g3402745
BLAST score	90
E value	7.0e-43
Match length	207
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	174887
Seq. ID	jC-atXLIB327426P1d07b1
Method	BLASTN
NCBI GI	g4455262
BLAST score	51
E value	2.0e-19
Match length	152
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	174888
Seq. ID	jC-atXLIB327426P1d08a1
Method	BLASTX
NCBI GI	g1172817
BLAST score	54
E value	2.0e-19
Match length	84
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	174889
Seq. ID	jC-atXLIB327426P1d09a1
Method	BLASTN
NCBI GI	g4835223
BLAST score	124
E value	4.0e-63
Match length	291
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	174890

Seq. ID	jC-atXLIB327426P1d11a1
Method	BLASTX
NCBI GI	g2262176
BLAST score	212
E value	9.0e-17
Match length	61
% identity	67
NCBI Description	(AC002329) putative RING zinc-finger protein [Arabidopsis thaliana] >gi_3790573 (AF078824) RING-H2 finger protein RHA3a [Arabidopsis thaliana]

Seq. No.	174891
Seq. ID	jC-atXLIB327426P1d11b1
Method	BLASTX
NCBI GI	g2262176
BLAST score	376
E value	4.0e-36
Match length	111
% identity	72
NCBI Description	(AC002329) putative RING zinc-finger protein [Arabidopsis thaliana] >gi_3790573 (AF078824) RING-H2 finger protein RHA3a [Arabidopsis thaliana]

Seq. No.	174892
Seq. ID	jC-atXLIB327426P1d12b1
Method	BLASTN
NCBI GI	g3766106
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174893
Seq. ID	jC-atXLIB327426P1e01b1
Method	BLASTN
NCBI GI	g4039151
BLAST score	37
E value	2.0e-11
Match length	81
% identity	88
NCBI Description	Arabidopsis thaliana low temperature and salt responsive protein LTI6B (lti6b) and low temperature and salt responsive protein LTI6A (lti6a) genes, complete cds

Seq. No.	174894
Seq. ID	jC-atXLIB327426P1e02a1
Method	BLASTN
NCBI GI	g2980757
BLAST score	49
E value	2.0e-18
Match length	353
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	174895
Seq. ID	jC-atXLIB327426P1e03a1
Method	BLASTN
NCBI GI	g4678291
BLAST score	76
E value	2.0e-34
Match length	243
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	174896
Seq. ID	jC-atXLIB327426P1e04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174897
Seq. ID	jC-atXLIB327426P1e06a1
Method	BLASTN
NCBI GI	g4589409
BLAST score	79
E value	2.0e-36
Match length	274
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	174898
Seq. ID	jC-atXLIB327426P1e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	47
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174899
Seq. ID	jC-atXLIB327426P1e07b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	73
E value	1.0e-32
Match length	154
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	174900
Seq. ID	jC-atXLIB327426P1e09a1

Method	BLASTN
NCBI GI	g4567237
BLAST score	127
E value	6.0e-65
Match length	367
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	174901
Seq. ID	jC-atXLIB327426P1f05b1
Method	BLASTN
NCBI GI	g16375
BLAST score	53
E value	1.0e-20
Match length	85
% identity	93
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	174902
Seq. ID	jC-atXLIB327426P1f06a1
Method	BLASTN
NCBI GI	g3849811
BLAST score	40
E value	6.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174903
Seq. ID	jC-atXLIB327426P1f08a1
Method	BLASTN
NCBI GI	g1019903
BLAST score	115
E value	9.0e-58
Match length	287
% identity	88
NCBI Description	Arabidopsis thaliana cell division cycle protein (CDC48) mRNA, complete cds

Seq. No.	174904
Seq. ID	jC-atXLIB327426P1f09a1
Method	BLASTN
NCBI GI	g3449321
BLAST score	206
E value	1.0e-112
Match length	369
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	174905
Seq. ID	jC-atXLIB327426P1g01b1
Method	BLASTN
NCBI GI	g3869065

BLAST score	60
E value	6.0e-25
Match length	84
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	174906
Seq. ID	jC-atXLIB327426P1g02a1
Method	BLASTX
NCBI GI	g1523796
BLAST score	361
E value	2.0e-34
Match length	81
% identity	86
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	174907
Seq. ID	jC-atXLIB327426P1g06a1
Method	BLASTN
NCBI GI	g2226430
BLAST score	33
E value	5.0e-09
Match length	37
% identity	97
NCBI Description	Mus saxicola haptoglobin mRNA, complete cds

Seq. No.	174908
Seq. ID	jC-atXLIB327426P1g06b1
Method	BLASTX
NCBI GI	g2244837
BLAST score	183
E value	1.0e-13
Match length	96
% identity	48
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	174909
Seq. ID	jC-atXLIB327426P1g10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174910
Seq. ID	jC-atXLIB327426P1h02a1
Method	BLASTN
NCBI GI	g2618677
BLAST score	148
E value	2.0e-77
Match length	362

% identity	98
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	174911
Seq. ID	jC-atXLIB327426P1h12b1
Method	BLASTN
NCBI GI	g2088638
BLAST score	89
E value	3.0e-42
Match length	325
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174912
Seq. ID	jC-atXLIB327426P2a06a1
Method	BLASTN
NCBI GI	g4220633
BLAST score	86
E value	1.0e-40
Match length	208
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	174913
Seq. ID	jC-atXLIB327426P2a07a1
Method	BLASTN
NCBI GI	g643089
BLAST score	152
E value	4.0e-80
Match length	255
% identity	89
NCBI Description	A.thaliana mRNA for NADH:ubiquinone oxidoreductase (complex I)

Seq. No.	174914
Seq. ID	jC-atXLIB327426P2a08b1
Method	BLASTX
NCBI GI	g3540185
BLAST score	239
E value	1.0e-19
Match length	108
% identity	51
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	174915
Seq. ID	jC-atXLIB327426P2a11a1
Method	BLASTN
NCBI GI	g2832667
BLAST score	110
E value	6.0e-55
Match length	192
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14

(ESSAII project)

Seq. No.	174916
Seq. ID	jC-atXLIB327426P2a12b1
Method	BLASTN
NCBI GI	g4678315
BLAST score	48
E value	1.0e-17
Match length	169
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	174917
Seq. ID	jC-atXLIB327426P2b06a1
Method	BLASTN
NCBI GI	g414340
BLAST score	133
E value	1.0e-68
Match length	203
% identity	90
NCBI Description	A.thaliana rd21A gene for thiol protease, complete cds

Seq. No.	174918
Seq. ID	jC-atXLIB327426P2b12a1
Method	BLASTN
NCBI GI	g3869069
BLAST score	255
E value	1.0e-141
Match length	267
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	174919
Seq. ID	jC-atXLIB327426P2c02b1
Method	BLASTX
NCBI GI	g3219267
BLAST score	115
E value	3.0e-34
Match length	166
% identity	59
NCBI Description	(AB015313) MAP kinase kinase 2 [Arabidopsis thaliana]

Seq. No.	174920
Seq. ID	jC-atXLIB327426P2d01b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	67
E value	2.0e-15
Match length	108
% identity	48
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	174921
Seq. ID	jC-atXLIB327426P2e01b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	9.0e-17
Match length	62
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174922
Seq. ID	jC-atXLIB327426P2e02a1
Method	BLASTN
NCBI GI	g540252
BLAST score	44
E value	1.0e-15
Match length	48
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174923
Seq. ID	jC-atXLIB327426P2e07a1
Method	BLASTN
NCBI GI	g1408472
BLAST score	214
E value	1.0e-117
Match length	234
% identity	98
NCBI Description	Arabidopsis thaliana actin depolymerizing factor 2 (AtADF2) mRNA, complete cds

Seq. No.	174924
Seq. ID	jC-atXLIB327426P2f01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	4.0e-16
Match length	49
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174925
Seq. ID	jC-atXLIB327426P2f02a1
Method	BLASTN
NCBI GI	g2288979
BLAST score	144
E value	3.0e-75
Match length	256
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174926
Seq. ID	jC-atXLIB327426P2g01b1
Method	BLASTX
NCBI GI	g1174162
BLAST score	152

E value	7.0e-63
Match length	141
% identity	82
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	174927
Seq. ID	jC-atXLIB327426P2g02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	5.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174928
Seq. ID	jC-atXLIB327426P2g02b1
Method	BLASTN
NCBI GI	g4519188
BLAST score	288
E value	1.0e-161
Match length	507
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	174929
Seq. ID	jC-atXLIB327426P2g07a1
Method	BLASTN
NCBI GI	g4757404
BLAST score	97
E value	3.0e-47
Match length	206
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	174930
Seq. ID	jC-atXLIB327426P2g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174931
Seq. ID	jC-atXLIB327426P2g09a1
Method	BLASTX
NCBI GI	g131398
BLAST score	149
E value	1.0e-09
Match length	43

% identity	72
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174932
Seq. ID	jC-atXLIB327426P2g09b1
Method	BLASTX
NCBI GI	g131398
BLAST score	283
E value	2.0e-35
Match length	105
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	174933
Seq. ID	jC-atXLIB327426P2h02a1
Method	BLASTN
NCBI GI	g2252848
BLAST score	95
E value	5.0e-46
Match length	147
% identity	93
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	174934
Seq. ID	jC-atXLIB327426P2h02b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	169
E value	6.0e-90
Match length	388
% identity	85
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	174935
Seq. ID	jC-atXLIB327426P2h03a1
Method	BLASTN
NCBI GI	g2739359
BLAST score	180
E value	1.0e-96
Match length	244
% identity	95

NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174936
Seq. ID	jC-atXLIB327426P2h06a1
Method	BLASTN
NCBI GI	g3510341
BLAST score	170
E value	9.0e-91
Match length	226
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	174937
Seq. ID	jC-atXLIB327426P3a01a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	376
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	174938
Seq. ID	jC-atXLIB327426P3a06a1
Method	BLASTN
NCBI GI	g3894179
BLAST score	101
E value	2.0e-49
Match length	335
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174939
Seq. ID	jC-atXLIB327426P3b01a1
Method	BLASTN
NCBI GI	g3043414
BLAST score	91
E value	2.0e-43
Match length	209
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for At-hsc70-3 protein

Seq. No.	174940
Seq. ID	jC-atXLIB327426P3b06a1
Method	BLASTX
NCBI GI	g4544409
BLAST score	257
E value	4.0e-22
Match length	51
% identity	96
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana] >gi_4585920_gb_AAD25580.1_AC007211_2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana]

Seq. No.	174941
Seq. ID	jC-atXLIB327426P3c04a1
Method	BLASTX
NCBI GI	g2252825
BLAST score	346
E value	2.0e-32
Match length	64
% identity	100
NCBI Description	(AF013293) Similar to transmembrane protein; coded for by A. thaliana cDNA H37637; coded for by A. thaliana cDNA T41850; coded for by A. thaliana cDNA T13717; coded for by A. thaliana cDNA T04371; coded for by A. thaliana cDNA T43789; coded

Seq. No.	174942
Seq. ID	jC-atXLIB327426P3c05a1
Method	BLASTN
NCBI GI	g4105695
BLAST score	313
E value	1.0e-176
Match length	384
% identity	96
NCBI Description	Arabidopsis thaliana beta tubulin 1, thaumatin-like protein (TL1), small hydrophobic protein, receptor kinase (CLAVATA1), and antifungal protein (PDF1.1) genes, complete cds

Seq. No.	174943
Seq. ID	jC-atXLIB327426P3d06a1
Method	BLASTN
NCBI GI	g3928074
BLAST score	341
E value	0.0e+00
Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174944
Seq. ID	jC-atXLIB327426P3d09a1
Method	BLASTN
NCBI GI	g540252
BLAST score	46
E value	1.0e-16
Match length	58
% identity	95
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174945
Seq. ID	jC-atXLIB327426P3f01a1
Method	BLASTX
NCBI GI	g2347192
BLAST score	149
E value	1.0e-25
Match length	69
% identity	87

NCBI Description	(AC002338) spliceosomal protein U2B isolog [Arabidopsis thaliana]

Seq. No.	174946
Seq. ID	jC-atXLIB327426P3f02a1
Method	BLASTX
NCBI GI	g4506635
BLAST score	258
E value	3.0e-22
Match length	76
% identity	66
NCBI Description	ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32 ribosomal protein L32 - human >gi_71336_pir__R5MS32 ribosomal protein L32 - mouse >gi_71337_pir__R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048_ (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777_ (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal protein L32-3A [Mus musculus] >gi_226004_prf__1405339A ribosomal protein L32 [Rattus norvegicus]

Seq. No.	174947
Seq. ID	jC-atXLIB327426P3f03a1
Method	BLASTN
NCBI GI	g540252
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174948
Seq. ID	jC-atXLIB327426P3f04a1
Method	BLASTN
NCBI GI	g540252
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	174949
Seq. ID	jC-atXLIB327426P3h02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	2.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174950
Seq. ID	jC-atXLIB327426P3h05a1
Method	BLASTN
NCBI GI	g2656031
BLAST score	189

E value	1.0e-102
Match length	252
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	174951
Seq. ID	jC-atXLIB327426P3h06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	5.0e-22
Match length	63
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174952
Seq. ID	jC-atXLIB327426P3h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174953
Seq. ID	jC-atXLIB327426P3h07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174954
Seq. ID	jC-atXLIB327426P3h09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	5.0e-22
Match length	63
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174955
Seq. ID	jC-atXLIB327426P4a05a1
Method	BLASTN
NCBI GI	g3766106
BLAST score	65
E value	6.0e-28
Match length	105
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174956
Seq. ID	jC-atXLIB327426P4a10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	6.0e-13
Match length	52
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174957
Seq. ID	jC-atXLIB327426P4b07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174958
Seq. ID	jC-atXLIB327426P4b08a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	73
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174959
Seq. ID	jC-atXLIB327426P4b09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	5.0e-19
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174960
Seq. ID	jC-atXLIB327426P4c01a1
Method	BLASTN
NCBI GI	g16266
BLAST score	64
E value	3.0e-27
Match length	183
% identity	91
NCBI Description	A.thaliana mRNA for Eli3-1

Seq. No.	174961
Seq. ID	jC-atXLIB327426P4c02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17

Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174962
Seq. ID	jC-atXLIB327426P4c10a1
Method	BLASTN
NCBI GI	g2252471
BLAST score	106
E value	2.0e-52
Match length	222
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for argininosuccinate lyase

Seq. No.	174963
Seq. ID	jC-atXLIB327426P4d01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174964
Seq. ID	jC-atXLIB327426P4d02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	47
E value	3.0e-17
Match length	51
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174965
Seq. ID	jC-atXLIB327426P4d03a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	61
E value	2.0e-25
Match length	133
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	174966
Seq. ID	jC-atXLIB327426P4d05a1
Method	BLASTN
NCBI GI	g3510344
BLAST score	78
E value	1.0e-35
Match length	321
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	174967
Seq. ID	jC-atXLIB327426P4d06a1
Method	BLASTN
NCBI GI	g3928074
BLAST score	95
E value	7.0e-46
Match length	135
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174968
Seq. ID	jC-atXLIB327426P4d08a1
Method	BLASTN
NCBI GI	g2529657
BLAST score	60
E value	6.0e-25
Match length	64
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174969
Seq. ID	jC-atXLIB327426P4d09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	6.0e-19
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174970
Seq. ID	jC-atXLIB327426P4e01a1
Method	BLASTN
NCBI GI	g4691223
BLAST score	74
E value	3.0e-33
Match length	133
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	174971
Seq. ID	jC-atXLIB327426P4e03a1
Method	BLASTN
NCBI GI	g2252823
BLAST score	113
E value	2.0e-56
Match length	189
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	174972
Seq. ID	jC-atXLIB327426P4e06a1
Method	BLASTN

NCBI GI	g3241923
BLAST score	109
E value	4.0e-54
Match length	137
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	174973
Seq. ID	jC-atXLIB327426P4e08a1
Method	BLASTN
NCBI GI	g4519188
BLAST score	67
E value	4.0e-29
Match length	123
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	174974
Seq. ID	jC-atXLIB327426P4e09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174975
Seq. ID	jC-atXLIB327426P4e10a1
Method	BLASTN
NCBI GI	g4559344
BLAST score	158
E value	2.0e-83
Match length	226
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	174976
Seq. ID	jC-atXLIB327426P4f03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	9.0e-18
Match length	52
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174977
Seq. ID	jC-atXLIB327426P4f08a1
Method	BLASTN
NCBI GI	g606969
BLAST score	110
E value	9.0e-55

Match length	258
% identity	91
NCBI Description	Arabidopsis thaliana cytoplasmic ribosomal protein L18 mRNA, complete cds

Seq. No.	174978
Seq. ID	jC-atXLIB327426P4f09a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	87
E value	5.0e-41
Match length	119
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	174979
Seq. ID	jC-atXLIB327426P4g03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	2.0e-16
Match length	65
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174980
Seq. ID	jC-atXLIB327426P4g05a1
Method	BLASTN
NCBI GI	g1405439
BLAST score	74
E value	3.0e-33
Match length	105
% identity	93
NCBI Description	A.thaliana mRNA for SRG3 protein, 5'

Seq. No.	174981
Seq. ID	jC-atXLIB327426P4g08a1
Method	BLASTN
NCBI GI	g4678340
BLAST score	100
E value	8.0e-49
Match length	160
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	174982
Seq. ID	jC-atXLIB327426P4g12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174983
Seq. ID	jC-atXLIB327426P4h01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	2.0e-12
Match length	47
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174984
Seq. ID	jC-atXLIB327426P4h02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	4.0e-14
Match length	61
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174985
Seq. ID	jC-atXLIB327426P4h03a1
Method	BLASTN
NCBI GI	g343501
BLAST score	117
E value	6.0e-59
Match length	246
% identity	87
NCBI Description	Tobacco chloroplast 23S and 4.5S rRNA genes

Seq. No.	174986
Seq. ID	jC-atXLIB327426P4h05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	40
E value	6.0e-13
Match length	44
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	174987
Seq. ID	jC-atXLIB327426P4h06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174988
Seq. ID	jC-atXLIB327426P4h08a1
Method	BLASTN
NCBI GI	g2529657

BLAST score	100
E value	8.0e-49
Match length	128
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	174989
Seq. ID	jC-atXLIB327426P4h09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	174990
Seq. ID	jC-atXLIB327426P4h12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	174991
Seq. ID	jC-atXLIB327427P1a02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	80
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174992
Seq. ID	jC-atXLIB327427P1a04a2
Method	BLASTN
NCBI GI	g4589435
BLAST score	170
E value	1.0e-90
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	174993
Seq. ID	jC-atXLIB327427P1a07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	1.0e-17
Match length	76
% identity	91

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174994
Seq. ID	jC-atXLIB327427P1a10a2
Method	BLASTX
NCBI GI	g2459421
BLAST score	273
E value	5.0e-24
Match length	72
% identity	76
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	174995
Seq. ID	jC-atXLIB327427P1a11b1
Method	BLASTN
NCBI GI	g3402747
BLAST score	64
E value	2.0e-27
Match length	92
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)

Seq. No.	174996
Seq. ID	jC-atXLIB327427P1a12a2
Method	BLASTX
NCBI GI	g16374
BLAST score	357
E value	8.0e-34
Match length	84
% identity	80
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	174997
Seq. ID	jC-atXLIB327427P1a12b1
Method	BLASTN
NCBI GI	g16367
BLAST score	65
E value	6.0e-28
Match length	77
% identity	96
NCBI Description	A.thaliana gene (LHCP AB 165) for chlorophyll a/b binding protein

Seq. No.	174998
Seq. ID	jC-atXLIB327427P1b08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	3.0e-23
Match length	81
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	174999
Seq. ID	jC-atXLIB327427P1c01b1
Method	BLASTX
NCBI GI	g3150416
BLAST score	216
E value	3.0e-17
Match length	89
% identity	56
NCBI Description	(AC004165) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	175000
Seq. ID	jC-atXLIB327427P1c03a2
Method	BLASTN
NCBI GI	g540252
BLAST score	50
E value	5.0e-19
Match length	50
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	175001
Seq. ID	jC-atXLIB327427P1c04a2
Method	BLASTN
NCBI GI	g2264317
BLAST score	268
E value	1.0e-149
Match length	280
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	175002
Seq. ID	jC-atXLIB327427P1d08b1
Method	BLASTN
NCBI GI	g540558
BLAST score	33
E value	6.0e-09
Match length	111
% identity	86
NCBI Description	A.thaliana RCI1A mRNA

Seq. No.	175003
Seq. ID	jC-atXLIB327427P1e01b1
Method	BLASTN
NCBI GI	g16228
BLAST score	89
E value	3.0e-42
Match length	112
% identity	96
NCBI Description	A.thaliana cor47 mRNA

Seq. No.	175004
Seq. ID	jC-atXLIB327427P1e04b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	63
E value	1.0e-26
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175005
Seq. ID	jC-atXLIB327427P1e10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	2.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175006
Seq. ID	jC-atXLIB327427P1f03b1
Method	BLASTN
NCBI GI	g4220635
BLAST score	141
E value	3.0e-73
Match length	245
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	175007
Seq. ID	jC-atXLIB327427P1f12a2
Method	BLASTX
NCBI GI	g2494610
BLAST score	329
E value	1.0e-30
Match length	92
% identity	74
NCBI Description	CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR >gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]

Seq. No.	175008
Seq. ID	jC-atXLIB327427P1g03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175009
Seq. ID	jC-atXLIB327427P1g05b1
Method	BLASTN
NCBI GI	g4757662
BLAST score	115
E value	1.0e-57
Match length	331

% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	175010
Seq. ID	jC-atXLIB327427P1g07b1
Method	BLASTX
NCBI GI	g3193320
BLAST score	308
E value	5.0e-28
Match length	158
% identity	51
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	175011
Seq. ID	jC-atXLIB327427P1g09b1
Method	BLASTN
NCBI GI	g3860243
BLAST score	103
E value	8.0e-51
Match length	127
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175012
Seq. ID	jC-atXLIB327427P1h01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175013
Seq. ID	jC-atXLIB327427P1h06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175014
Seq. ID	jC-atXLIB327427P1h11a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175015
Seq. ID	jC-atXLIB327427P2a08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175016
Seq. ID	jC-atXLIB327427P2a09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	8.0e-18
Match length	63
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175017
Seq. ID	jC-atXLIB327427P2a09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	2.0e-18
Match length	72
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175018
Seq. ID	jC-atXLIB327427P2a10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	66
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175019
Seq. ID	jC-atXLIB327427P2a11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	3.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175020
Seq. ID	jC-atXLIB327427P2b01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54

E value	2.0e-21
Match length	66
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175021
Seq. ID	jC-atXLIB327427P2b03a1
Method	BLASTN
NCBI GI	g540252
BLAST score	38
E value	8.0e-12
Match length	38
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	175022
Seq. ID	jC-atXLIB327427P2b08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	59
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175023
Seq. ID	jC-atXLIB327427P2c01a1
Method	BLASTX
NCBI GI	g1170215
BLAST score	207
E value	3.0e-16
Match length	44
% identity	91
NCBI Description	DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR (PORPHOBILINOGEN SYNTHASE) (ALDH) (ALAD) >gi_805062_emb_CAA40974_ (X57842) porphobilinogen synthase [Spinacia oleracea]

Seq. No.	175024
Seq. ID	jC-atXLIB327427P2c03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	9.0e-21
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175025
Seq. ID	jC-atXLIB327427P2c08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	6.0e-22

Match length	67
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175026
Seq. ID	jC-atXLIB327427P2e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	5.0e-25
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175027
Seq. ID	jC-atXLIB327427P2g05b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	96
E value	2.0e-46
Match length	340
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	175028
Seq. ID	jC-atXLIB327427P2g10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	6.0e-22
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175029
Seq. ID	jC-atXLIB327427P2g12a1
Method	BLASTN
NCBI GI	g217850
BLAST score	321
E value	1.0e-180
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana CDC2b gene for p34 protein serine/threonine kinase-related protein

Seq. No.	175030
Seq. ID	jC-atXLIB327427P2h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	51
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175031
Seq. ID	jC-atXLIB327427P2h02a1
Method	BLASTN
NCBI GI	g3096946
BLAST score	280
E value	1.0e-156
Match length	404
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for putative cyclic nucleotide-regulated ion channel, cngc1

Seq. No.	175032
Seq. ID	jC-atXLIB327427P2h02b1
Method	BLASTN
NCBI GI	g3096946
BLAST score	56
E value	1.0e-22
Match length	318
% identity	80
NCBI Description	Arabidopsis thaliana mRNA for putative cyclic nucleotide-regulated ion channel, cngc1

Seq. No.	175033
Seq. ID	jC-atXLIB327427P2h03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	5.0e-22
Match length	67
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175034
Seq. ID	jC-atXLIB327427P2h03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175035
Seq. ID	jC-atXLIB327427P2h04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175036
Seq. ID	jC-atXLIB327427P2h05b1

Method	BLASTN
NCBI GI	g2618602
BLAST score	37
E value	3.0e-11
Match length	159
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	175037
Seq. ID	jC-atXLIB327427P2h06a1
Method	BLASTX
NCBI GI	g730526
BLAST score	154
E value	5.0e-10
Match length	81
% identity	44
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	175038
Seq. ID	jC-atXLIB327427P2h08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	7.0e-11
Match length	60
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175039
Seq. ID	jC-atXLIB327427P2h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175040
Seq. ID	jC-atXLIB327427P2h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	9.0e-26
Match length	81
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175041
Seq. ID	jC-atXLIB327427P2h11a1
Method	BLASTN

NCBI GI	g2264314
BLAST score	60
E value	6.0e-25
Match length	128
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	175042
Seq. ID	jC-atXLIB327427P3a03b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	2.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175043
Seq. ID	jC-atXLIB327427P3a06a2
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	7.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175044
Seq. ID	jC-atXLIB327427P3a07b2
Method	BLASTN
NCBI GI	g4159705
BLAST score	71
E value	2.0e-31
Match length	237
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	175045
Seq. ID	jC-atXLIB327427P3a12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	46
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175046
Seq. ID	jC-atXLIB327427P3b03b1
Method	BLASTX
NCBI GI	g4678349
BLAST score	211
E value	1.0e-16
Match length	105

% identity	25
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	175047
Seq. ID	jC-atXLIB327427P3b08a2
Method	BLASTX
NCBI GI	g4512709
BLAST score	206
E value	4.0e-16
Match length	66
% identity	67
NCBI Description	(AC006569) putative photosystem I reaction center subunit IV precursor [Arabidopsis thaliana]

Seq. No.	175048
Seq. ID	jC-atXLIB327427P3b08b2
Method	BLASTN
NCBI GI	g16131
BLAST score	135
E value	9.0e-70
Match length	341
% identity	88
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment

Seq. No.	175049
Seq. ID	jC-atXLIB327427P3b10b2
Method	BLASTN
NCBI GI	g3132469
BLAST score	156
E value	3.0e-82
Match length	357
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175050
Seq. ID	jC-atXLIB327427P3b11b2
Method	BLASTX
NCBI GI	g2129597
BLAST score	180
E value	6.0e-13
Match length	99
% identity	45
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	175051
Seq. ID	jC-atXLIB327427P3c07b1
Method	BLASTN
NCBI GI	g2739359
BLAST score	62
E value	2.0e-26
Match length	90
% identity	91

NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	175052
Seq. ID	jC-atXLIB327427P3c08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	175053
Seq. ID	jC-atXLIB327427P3c09b1
Method	BLASTN
NCBI GI	g16316
BLAST score	108
E value	1.0e-53
Match length	284
% identity	84
NCBI Description	A.thaliana gene for histone H1-1
Seq. No.	175054
Seq. ID	jC-atXLIB327427P3c11b1
Method	BLASTN
NCBI GI	g3869075
BLAST score	66
E value	2.0e-28
Match length	80
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.	175055
Seq. ID	jC-atXLIB327427P3c12a2
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	3.0e-14
Match length	68
% identity	93
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175056
Seq. ID	jC-atXLIB327427P3d01a2
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175057
Seq. ID	jC-atXLIB327427P3d01b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	5.0e-17
Match length	58
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175058
Seq. ID	jC-atXLIB327427P3d02a2
Method	BLASTN
NCBI GI	g531828
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175059
Seq. ID	jC-atXLIB327427P3d03a1
Method	BLASTX
NCBI GI	g1076314
BLAST score	440
E value	2.0e-43
Match length	91
% identity	95
NCBI Description	cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis thaliana (fragment) >gi_499166_emb_CAA56143_ (X79707) CYS1 [Arabidopsis thaliana]

Seq. No.	175060
Seq. ID	jC-atXLIB327427P3d04a1
Method	BLASTN
NCBI GI	g2341023
BLAST score	71
E value	2.0e-31
Match length	377
% identity	84
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	175061
Seq. ID	jC-atXLIB327427P3d04b1
Method	BLASTN
NCBI GI	g2341023
BLAST score	40
E value	5.0e-13
Match length	235
% identity	83
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	175062
Seq. ID	jC-atXLIB327427P3d06b1
Method	BLASTN
NCBI GI	g2244901

BLAST score	45
E value	6.0e-16
Match length	56
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175063
Seq. ID	jC-atXLIB327427P3d09a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175064
Seq. ID	jC-atXLIB327427P3d10a1
Method	BLASTN
NCBI GI	g4713943
BLAST score	44
E value	2.0e-15
Match length	88
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	175065
Seq. ID	jC-atXLIB327427P3d10b1
Method	BLASTN
NCBI GI	g4713943
BLAST score	49
E value	2.0e-18
Match length	228
% identity	83
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	175066
Seq. ID	jC-atXLIB327427P3d12a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	41
E value	1.0e-13
Match length	68
% identity	91
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175067
Seq. ID	jC-atXLIB327427P3e01a2
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13

Match length	48
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175068
Seq. ID	jC-atXLIB327427P3e02b2
Method	BLASTN
NCBI GI	g4581161
BLAST score	153
E value	2.0e-80
Match length	305
% identity	55
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	175069
Seq. ID	jC-atXLIB327427P3e03b1
Method	BLASTN
NCBI GI	g4581161
BLAST score	47
E value	2.0e-17
Match length	125
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	175070
Seq. ID	jC-atXLIB327427P3e05b1
Method	BLASTN
NCBI GI	g510237
BLAST score	36
E value	9.0e-11
Match length	88
% identity	90
NCBI Description	Arabadopsis thaliana Landsberg NT1 mRNA

Seq. No.	175071
Seq. ID	jC-atXLIB327427P3e06a1
Method	BLASTN
NCBI GI	g3603425
BLAST score	37
E value	1.0e-11
Match length	65
% identity	89
NCBI Description	Arabidopsis thaliana rac-like GTP binding protein Arac11 (Arac11) gene, complete cds

Seq. No.	175072
Seq. ID	jC-atXLIB327427P3e06b1
Method	BLASTX
NCBI GI	g2435519
BLAST score	63
E value	2.0e-17
Match length	90
% identity	65
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110)

[Arabidopsis thaliana]

Seq. No.	175073
Seq. ID	jC-atXLIB327427P3f01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175074
Seq. ID	jC-atXLIB327427P3f01b2
Method	BLASTX
NCBI GI	g2642159
BLAST score	373
E value	8.0e-36
Match length	118
% identity	70
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	175075
Seq. ID	jC-atXLIB327427P3f02a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175076
Seq. ID	jC-atXLIB327427P3f02b2
Method	BLASTX
NCBI GI	g2642159
BLAST score	234
E value	3.0e-19
Match length	148
% identity	35
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	175077
Seq. ID	jC-atXLIB327427P3f03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	7.0e-11
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175078
Seq. ID	jC-atXLIB327427P3f06a1
Method	BLASTN
NCBI GI	g2696018
BLAST score	126
E value	2.0e-64
Match length	263
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	175079
Seq. ID	jC-atXLIB327427P3f06b1
Method	BLASTN
NCBI GI	g2696018
BLAST score	86
E value	2.0e-40
Match length	370
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	175080
Seq. ID	jC-atXLIB327427P3f07a1
Method	BLASTN
NCBI GI	g3396078
BLAST score	160
E value	1.0e-84
Match length	356
% identity	93
NCBI Description	Arabidopsis thaliana inositol 1,3,4-trisphosphate 5/6-kinase mRNA, complete cds

Seq. No.	175081
Seq. ID	jC-atXLIB327427P3f07b1
Method	BLASTX
NCBI GI	g3660465
BLAST score	482
E value	2.0e-48
Match length	146
% identity	68
NCBI Description	(AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana]

Seq. No.	175082
Seq. ID	jC-atXLIB327427P3f08a1
Method	BLASTN
NCBI GI	g4589428
BLAST score	38
E value	8.0e-12
Match length	82
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	175083

Seq. ID	jC-atXLIB327427P3f10a1
Method	BLASTN
NCBI GI	g468770
BLAST score	45
E value	6.0e-16
Match length	97
% identity	87
NCBI Description	A.thaliana genes for chloroplast ribosomal protein L12 and tRNA-Pro

Seq. No.	175084
Seq. ID	jC-atXLIB327427P3f10b1
Method	BLASTN
NCBI GI	g468770
BLAST score	47
E value	3.0e-17
Match length	82
% identity	66
NCBI Description	A.thaliana genes for chloroplast ribosomal protein L12 and tRNA-Pro

Seq. No.	175085
Seq. ID	jC-atXLIB327427P3f12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	8.0e-21
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175086
Seq. ID	jC-atXLIB327427P3f12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	4.0e-17
Match length	78
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175087
Seq. ID	jC-atXLIB327427P3g04a1
Method	BLASTX
NCBI GI	g2738998
BLAST score	90
E value	1.4e-02
Match length	83
% identity	42
NCBI Description	(AF022458) CYP98A2p [Glycine max]

Seq. No.	175088
Seq. ID	jC-atXLIB327427P3g04b1
Method	BLASTX
NCBI GI	g2623303
BLAST score	551

E value	1.0e-56
Match length	124
% identity	87
NCBI Description	(AC002409) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	175089
Seq. ID	jC-atXLIB327427P3g05a2
Method	BLASTX
NCBI GI	g4249409
BLAST score	314
E value	9.0e-29
Match length	88
% identity	73
NCBI Description	(AC006072) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	175090
Seq. ID	jC-atXLIB327427P3g09b1
Method	BLASTX
NCBI GI	g3164140
BLAST score	132
E value	4.0e-18
Match length	109
% identity	50
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	175091
Seq. ID	jC-atXLIB327427P3h01b2
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	3.0e-17
Match length	67
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175092
Seq. ID	jC-atXLIB327427P3h03a1
Method	BLASTN
NCBI GI	g2244747
BLAST score	38
E value	5.0e-12
Match length	127
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175093
Seq. ID	jC-atXLIB327427P3h03b1
Method	BLASTX
NCBI GI	g4455318
BLAST score	130
E value	1.0e-20
Match length	72
% identity	77
NCBI Description	(AL035528) glycine hydroxymethyltransferase-like protein

[Arabidopsis thaliana]

Seq. No.	175094
Seq. ID	jC-atXLIB327427P3h08a2
Method	BLASTN
NCBI GI	g3341671
BLAST score	133
E value	2.0e-68
Match length	408
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175095
Seq. ID	jC-atXLIB327427P3h08b2
Method	BLASTN
NCBI GI	g3420042
BLAST score	291
E value	1.0e-163
Match length	471
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175096
Seq. ID	jC-atXLIB327427P3h10b1
Method	BLASTX
NCBI GI	g2129597
BLAST score	205
E value	2.0e-18
Match length	79
% identity	71
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	175097
Seq. ID	jC-atXLIB327427P3h11a2
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175098
Seq. ID	jC-atXLIB327427P3h11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	7.0e-22
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175099
Seq. ID	jC-atXLIB327427P3h12b1
Method	BLASTX
NCBI GI	g4210332
BLAST score	161
E value	6.0e-11
Match length	117
% identity	39
NCBI Description	(AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]

Seq. No.	175100
Seq. ID	jC-atXLIB327427P4a04a2
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175101
Seq. ID	jC-atXLIB327427P4a09a1
Method	BLASTN
NCBI GI	g2351069
BLAST score	94
E value	3.0e-45
Match length	259
% identity	61
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	175102
Seq. ID	jC-atXLIB327427P4a09b1
Method	BLASTN
NCBI GI	g2351069
BLAST score	62
E value	1.0e-26
Match length	108
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	175103
Seq. ID	jC-atXLIB327427P4a12a1
Method	BLASTX
NCBI GI	g2494417
BLAST score	148
E value	2.0e-09
Match length	76
% identity	50
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_1364071_pir__S57717 fructose-1, 6-bisphosphatase (EC 3.1.3.11) - sugarcane hybrid H65-7052 >gi_895909_emb_CAA61409.1_ (X89006) fructose-1,

6-bisphosphatase [Saccharum hybrid cultivar H65-7052]

Seq. No.	175104
Seq. ID	jC-atXLIB327427P4b01a2
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	8.0e-09
Match length	45
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175105
Seq. ID	jC-atXLIB327427P4b01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	3.0e-20
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175106
Seq. ID	jC-atXLIB327427P4b02a2
Method	BLASTX
NCBI GI	g3269284
BLAST score	264
E value	6.0e-23
Match length	69
% identity	78
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	175107
Seq. ID	jC-atXLIB327427P4b05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	47
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175108
Seq. ID	jC-atXLIB327427P4b06a2
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	175109
Seq. ID	jC-atXLIB327427P4b07a1
Method	BLASTN

NCBI GI	g4056429
BLAST score	46
E value	1.0e-16
Match length	101
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175110
Seq. ID	jC-atXLIB327427P4b08a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175111
Seq. ID	jC-atXLIB327427P4b12a2
Method	BLASTX
NCBI GI	g4587988
BLAST score	143
E value	1.0e-08
Match length	64
% identity	50
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	175112
Seq. ID	jC-atXLIB327427P4c01a2
Method	BLASTX
NCBI GI	g1388084
BLAST score	44
E value	7.0e-35
Match length	112
% identity	70
NCBI Description	(U35829) thioredoxin h [Arabidopsis thaliana]

Seq. No.	175113
Seq. ID	jC-atXLIB327427P4c03a2
Method	BLASTN
NCBI GI	g3426059
BLAST score	139
E value	4.0e-72
Match length	329
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for src2-like protein

Seq. No.	175114
Seq. ID	jC-atXLIB327427P4c03b2
Method	BLASTN
NCBI GI	g2342673
BLAST score	342
E value	0.0e+00
Match length	368
% identity	98
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No.	175115
Seq. ID	jC-atXLIB327427P4c07a2
Method	BLASTN
NCBI GI	g598848
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	175116
Seq. ID	jC-atXLIB327427P4c10a1
Method	BLASTN
NCBI GI	g4544435
BLAST score	134
E value	4.0e-69
Match length	233
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	175117
Seq. ID	jC-atXLIB327427P4c12a2
Method	BLASTN
NCBI GI	g2264312
BLAST score	93
E value	1.0e-44
Match length	155
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	175118
Seq. ID	jC-atXLIB327427P4d01a2
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	4.0e-17
Match length	58
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175119
Seq. ID	jC-atXLIB327427P4d02a2
Method	BLASTN
NCBI GI	g4220628
BLAST score	91
E value	2.0e-43
Match length	214
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24C1, complete sequence [Arabidopsis thaliana]

Seq. No.	175120
Seq. ID	jC-atXLIB327427P4d03b2

Method	BLASTX
NCBI GI	g4490314
BLAST score	172
E value	4.0e-12
Match length	105
% identity	44
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	175121
Seq. ID	jC-atXLIB327427P4d05b2
Method	BLASTX
NCBI GI	g4006853
BLAST score	81
E value	8.0e-33
Match length	114
% identity	75
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	175122
Seq. ID	jC-atXLIB327427P4d12b2
Method	BLASTN
NCBI GI	g1079731
BLAST score	58
E value	9.0e-24
Match length	154
% identity	85
NCBI Description	Arabidopsis thaliana cpFtsZ (cpFtsZ) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	175123
Seq. ID	jC-atXLIB327427P4e01b2
Method	BLASTN
NCBI GI	g2264321
BLAST score	73
E value	1.0e-32
Match length	285
% identity	41
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	175124
Seq. ID	jC-atXLIB327427P4e07a1
Method	BLASTN
NCBI GI	g4204173
BLAST score	69
E value	2.0e-30
Match length	121
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175125
Seq. ID	jC-atXLIB327427P4e09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36

E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175126
Seq. ID	jC-atXLIB327427P4e09b1
Method	BLASTN
NCBI GI	g4713943
BLAST score	84
E value	3.0e-39
Match length	346
% identity	93
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	175127
Seq. ID	jC-atXLIB327427P4e11a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	46
E value	1.0e-16
Match length	74
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	175128
Seq. ID	jC-atXLIB327427P4e11a2
Method	BLASTN
NCBI GI	g3241916
BLAST score	227
E value	1.0e-124
Match length	367
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	175129
Seq. ID	jC-atXLIB327427P4e11b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	46
E value	1.0e-16
Match length	94
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	175130
Seq. ID	jC-atXLIB327427P4e12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175131
Seq. ID	jC-atXLIB327427P4e12b1
Method	BLASTN
NCBI GI	g1079731
BLAST score	128
E value	1.0e-65
Match length	384
% identity	89
NCBI Description	Arabidopsis thaliana cpFtsZ (cpFtsZ) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	175132
Seq. ID	jC-atXLIB327427P4f05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175133
Seq. ID	jC-atXLIB327427P4f07a2
Method	BLASTN
NCBI GI	g836895
BLAST score	34
E value	2.0e-09
Match length	49
% identity	94
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	175134
Seq. ID	jC-atXLIB327427P4f08b1
Method	BLASTN
NCBI GI	g3510345
BLAST score	75
E value	6.0e-34
Match length	137
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	175135
Seq. ID	jC-atXLIB327427P4f09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175136
Seq. ID	jC-atXLIB327427P4f10a1
Method	BLASTX

NCBI GI	g1871503
BLAST score	112
E value	1.0e-13
Match length	61
% identity	67
NCBI Description	(Y11559) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	175137
Seq. ID	jC-atXLIB327427P4f10b1
Method	BLASTX
NCBI GI	g2129544
BLAST score	154
E value	1.0e-10
Match length	28
% identity	100
NCBI Description	beta-fructosidase, vacuolar form - Arabidopsis thaliana (fragment) >gi_1321684_emb_CAA66330_ (X97749) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	175138
Seq. ID	jC-atXLIB327427P4f10b2
Method	BLASTX
NCBI GI	g2129544
BLAST score	630
E value	8.0e-66
Match length	154
% identity	81
NCBI Description	beta-fructosidase, vacuolar form - Arabidopsis thaliana (fragment) >gi_1321684_emb_CAA66330_ (X97749) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	175139
Seq. ID	jC-atXLIB327427P4f11a1
Method	BLASTX
NCBI GI	g4539383
BLAST score	300
E value	3.0e-27
Match length	71
% identity	85
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	175140
Seq. ID	jC-atXLIB327427P4f11a2
Method	BLASTX
NCBI GI	g4539383
BLAST score	414
E value	2.0e-40
Match length	81
% identity	100
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	175141
Seq. ID	jC-atXLIB327427P4f12a2
Method	BLASTN
NCBI GI	g4102599

BLAST score	148
E value	2.0e-77
Match length	260
% identity	89
NCBI Description	Arabidopsis thaliana ARF6 (ARF6) mRNA, complete cds

Seq. No.	175142
Seq. ID	jC-atXLIB327427P4f12b2
Method	BLASTN
NCBI GI	g4102599
BLAST score	304
E value	1.0e-170
Match length	336
% identity	97
NCBI Description	Arabidopsis thaliana ARF6 (ARF6) mRNA, complete cds

Seq. No.	175143
Seq. ID	jC-atXLIB327427P4g01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	3.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175144
Seq. ID	jC-atXLIB327427P4g02a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	48
E value	9.0e-18
Match length	68
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175145
Seq. ID	jC-atXLIB327427P4g03b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	33
E value	7.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	175146
Seq. ID	jC-atXLIB327427P4g05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175147
Seq. ID	jC-atXLIB327427P4g06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175148
Seq. ID	jC-atXLIB327427P4g07a1
Method	BLASTN
NCBI GI	g4432847
BLAST score	62
E value	4.0e-26
Match length	210
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175149
Seq. ID	jC-atXLIB327427P4g12a1
Method	BLASTN
NCBI GI	g4490734
BLAST score	71
E value	2.0e-31
Match length	176
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	175150
Seq. ID	jC-atXLIB327427P4g12b1
Method	BLASTX
NCBI GI	g1066283
BLAST score	186
E value	2.0e-14
Match length	39
% identity	92
NCBI Description	(U38920) 1L-myo-inositol 1-phosphate synthase [Phaseolus vulgaris]

Seq. No.	175151
Seq. ID	jC-atXLIB327427P4h03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	55
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175152
Seq. ID	jC-atXLIB327427P4h09a2

Method	BLASTN
NCBI GI	g398601
BLAST score	406
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	A.thaliana ATAF2 mRNA

Seq. No.	175153
Seq. ID	jC-atXLIB327427P4h10a1
Method	BLASTN
NCBI GI	g2252848
BLAST score	100
E value	7.0e-49
Match length	259
% identity	96
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	175154
Seq. ID	jC-atXLIB327427P4h10a2
Method	BLASTN
NCBI GI	g2252848
BLAST score	215
E value	1.0e-117
Match length	281
% identity	97
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	175155
Seq. ID	jC-atXLIB327427P4h11a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	3.0e-14
Match length	58
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175156
Seq. ID	jC-atXLIB327428P1a01b2
Method	BLASTN
NCBI GI	g4538990
BLAST score	98
E value	1.0e-47
Match length	359
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	175157
Seq. ID	jC-atXLIB327428P1a02a2
Method	BLASTN
NCBI GI	g2584827
BLAST score	51
E value	1.0e-19
Match length	197

% identity	84
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175158
Seq. ID	jC-atXLIB327428P1a03b2
Method	BLASTN
NCBI GI	g3059018
BLAST score	115
E value	9.0e-58
Match length	200
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	175159
Seq. ID	jC-atXLIB327428P1a04a2
Method	BLASTN
NCBI GI	g4467094
BLAST score	48
E value	8.0e-18
Match length	202
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	175160
Seq. ID	jC-atXLIB327428P1a04b2
Method	BLASTX
NCBI GI	g4539340
BLAST score	68
E value	3.0e-32
Match length	90
% identity	75
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	175161
Seq. ID	jC-atXLIB327428P1a06a2
Method	BLASTN
NCBI GI	g397481
BLAST score	48
E value	4.0e-18
Match length	106
% identity	84
NCBI Description	A.thaliana hsc70 mRNA for heat shock cognate protein

Seq. No.	175162
Seq. ID	jC-atXLIB327428P1a10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175163
Seq. ID	jC-atXLIB327428P1a12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	48
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175164
Seq. ID	jC-atXLIB327428P1b01a2
Method	BLASTN
NCBI GI	g2618602
BLAST score	65
E value	4.0e-28
Match length	134
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	175165
Seq. ID	jC-atXLIB327428P1b02a2
Method	BLASTN
NCBI GI	g2494106
BLAST score	95
E value	5.0e-46
Match length	115
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175166
Seq. ID	jC-atXLIB327428P1b02b2
Method	BLASTX
NCBI GI	g1762150
BLAST score	601
E value	2.0e-62
Match length	146
% identity	80
NCBI Description	(U49919) lupeol synthase [Arabidopsis thaliana]

Seq. No.	175167
Seq. ID	jC-atXLIB327428P1b04a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175168
Seq. ID	jC-atXLIB327428P1b06b2
Method	BLASTX
NCBI GI	g1168739
BLAST score	233

E value	4.0e-76
Match length	144
% identity	100
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	175169
Seq. ID	jC-atXLIB327428P1b07a2
Method	BLASTX
NCBI GI	g4115377
BLAST score	322
E value	1.0e-29
Match length	82
% identity	74
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	175170
Seq. ID	jC-atXLIB327428P1b12b2
Method	BLASTX
NCBI GI	g3219273
BLAST score	251
E value	2.0e-21
Match length	144
% identity	41
NCBI Description	(AB015316) MAP kinase kinase 5 [Arabidopsis thaliana]

Seq. No.	175171
Seq. ID	jC-atXLIB327428P1c03b2
Method	BLASTX
NCBI GI	g4314378
BLAST score	360
E value	3.0e-34
Match length	91
% identity	70
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	175172
Seq. ID	jC-atXLIB327428P1c05b2
Method	BLASTN
NCBI GI	g531832
BLAST score	43
E value	8.0e-15
Match length	51
% identity	96
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175173
Seq. ID	jC-atXLIB327428P1c10b2
Method	BLASTX
NCBI GI	g2058280
BLAST score	732
E value	9.0e-78
Match length	151
% identity	90
NCBI Description	(X97381) atran3 [Arabidopsis thaliana]

Seq. No.	175174

Seq. ID	jC-atXLIB327428P1c11a2
Method	BLASTN
NCBI GI	g2924652
BLAST score	64
E value	2.0e-27
Match length	132
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	175175
Seq. ID	jC-atXLIB327428P1d08a2
Method	BLASTN
NCBI GI	g4662609
BLAST score	231
E value	1.0e-127
Match length	442
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	175176
Seq. ID	jC-atXLIB327428P1d09a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	5.0e-16
Match length	45
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175177
Seq. ID	jC-atXLIB327428P1d10b2
Method	BLASTX
NCBI GI	g1362007
BLAST score	774
E value	1.0e-82
Match length	145
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	175178
Seq. ID	jC-atXLIB327428P1d12b2
Method	BLASTX
NCBI GI	g4218128
BLAST score	72
E value	5.0e-35
Match length	120
% identity	68
NCBI Description	(AL035353) ammonium transporter-like protein [Arabidopsis thaliana]

Seq. No.	175179
Seq. ID	jC-atXLIB327428P1e04a2

Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	60
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175180
Seq. ID	jC-atXLIB327428P1e05b2
Method	BLASTX
NCBI GI	g2983997
BLAST score	145
E value	6.0e-09
Match length	55
% identity	45
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	175181
Seq. ID	jC-atXLIB327428P1e06a2
Method	BLASTN
NCBI GI	g3510337
BLAST score	66
E value	5.0e-29
Match length	93
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	175182
Seq. ID	jC-atXLIB327428P1e09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	2.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175183
Seq. ID	jC-atXLIB327428P1f01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	7.0e-10
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175184
Seq. ID	jC-atXLIB327428P1f09b2
Method	BLASTX
NCBI GI	g3869253
BLAST score	727
E value	3.0e-77
Match length	146
% identity	99

NCBI Description	(U39288) ferredoxin-dependent glutamate synthase precursor [Arabidopsis thaliana]

Seq. No.	175185
Seq. ID	jC-atXLIB327428P1g01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175186
Seq. ID	jC-atXLIB327428P1g02a2
Method	BLASTN
NCBI GI	g3449330
BLAST score	396
E value	0.0e+00
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	175187
Seq. ID	jC-atXLIB327428P1g02b2
Method	BLASTN
NCBI GI	g3449330
BLAST score	221
E value	1.0e-121
Match length	265
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	175188
Seq. ID	jC-atXLIB327428P1g08b2
Method	BLASTN
NCBI GI	g2961335
BLAST score	76
E value	6.0e-35
Match length	140
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	175189
Seq. ID	jC-atXLIB327428P1g10a2
Method	BLASTX
NCBI GI	g3367522
BLAST score	228
E value	1.0e-18
Match length	56
% identity	73
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	175190
Seq. ID	jC-atXLIB327428P1g11a2
Method	BLASTN
NCBI GI	g3695372
BLAST score	396
E value	0.0e+00
Match length	423
% identity	45
NCBI Description	Arabidopsis thaliana BAC F11O4

Seq. No.	175191
Seq. ID	jC-atXLIB327428P1h01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175192
Seq. ID	jC-atXLIB327428P1h01b2
Method	BLASTX
NCBI GI	g4455199
BLAST score	321
E value	1.0e-30
Match length	105
% identity	72
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	175193
Seq. ID	jC-atXLIB327428P1h02a2
Method	BLASTX
NCBI GI	g4510405
BLAST score	303
E value	2.0e-27
Match length	77
% identity	77
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	175194
Seq. ID	jC-atXLIB327428P1h03a2
Method	BLASTX
NCBI GI	g3193287
BLAST score	331
E value	9.0e-31
Match length	71
% identity	82
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	175195
Seq. ID	jC-atXLIB327428P1h04a2
Method	BLASTN
NCBI GI	g1046224
BLAST score	70
E value	4.0e-31

Match length	121
% identity	91
NCBI Description	Arabidopsis thaliana ethylene response sensor (ERS) gene, complete cds

Seq. No.	175196
Seq. ID	jC-atXLIB327428P1h06b2
Method	BLASTN
NCBI GI	g4454022
BLAST score	45
E value	2.0e-16
Match length	128
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	175197
Seq. ID	jC-atXLIB327428P1h07b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	5.0e-09
Match length	48
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175198
Seq. ID	jC-atXLIB327428P1h10b2
Method	BLASTX
NCBI GI	g2129670
BLAST score	712
E value	2.0e-75
Match length	146
% identity	92
NCBI Description	phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana]

Seq. No.	175199
Seq. ID	jC-atXLIB327428P1h11b2
Method	BLASTX
NCBI GI	g4510363
BLAST score	66
E value	5.0e-26
Match length	119
% identity	56
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	175200
Seq. ID	jC-atXLIB327428P2c07a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	60
E value	5.0e-25
Match length	83

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	175201
Seq. ID	jC-atXLIB327428P2c10a1
Method	BLASTN
NCBI GI	g4217996
BLAST score	74
E value	3.0e-33
Match length	114
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175202
Seq. ID	jC-atXLIB327428P2d07a1
Method	BLASTN
NCBI GI	g4585896
BLAST score	34
E value	2.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F13I13 genomic sequence, complete sequence

Seq. No.	175203
Seq. ID	jC-atXLIB327428P2d09a1
Method	BLASTN
NCBI GI	g2264305
BLAST score	57
E value	2.0e-23
Match length	89
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	175204
Seq. ID	jC-atXLIB327428P2e10a1
Method	BLASTN
NCBI GI	g4519191
BLAST score	78
E value	1.0e-35
Match length	122
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	175205
Seq. ID	jC-atXLIB327428P2f05a1
Method	BLASTN
NCBI GI	g3337347
BLAST score	34
E value	2.0e-09
Match length	123
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175206
Seq. ID	jC-atXLIB327428P4a03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175207
Seq. ID	jC-atXLIB327428P4a04a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175208
Seq. ID	jC-atXLIB327428P4a06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175209
Seq. ID	jC-atXLIB327428P4a06b2
Method	BLASTX
NCBI GI	g2224927
BLAST score	102
E value	2.0e-12
Match length	104
% identity	46
NCBI Description	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No.	175210
Seq. ID	jC-atXLIB327428P4a08a2
Method	BLASTN
NCBI GI	g2656028
BLAST score	66
E value	1.0e-28
Match length	105
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	175211
Seq. ID	jC-atXLIB327428P4a12a2
Method	BLASTN

NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175212
Seq. ID	jC-atXLIB327428P4b01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175213
Seq. ID	jC-atXLIB327428P4b01b2
Method	BLASTN
NCBI GI	g4589438
BLAST score	159
E value	4.0e-84
Match length	231
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	175214
Seq. ID	jC-atXLIB327428P4b03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	60
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175215
Seq. ID	jC-atXLIB327428P4b03b2
Method	BLASTN
NCBI GI	g4589438
BLAST score	237
E value	1.0e-130
Match length	292
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	175216
Seq. ID	jC-atXLIB327428P4b05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	175217
Seq. ID	jC-atXLIB327428P4b05b2
Method	BLASTN
NCBI GI	g2828278
BLAST score	97
E value	4.0e-47
Match length	296
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
Seq. No.	175218
Seq. ID	jC-atXLIB327428P4b06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	1.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	175219
Seq. ID	jC-atXLIB327428P4b07a1
Method	BLASTN
NCBI GI	g2980787
BLAST score	83
E value	1.0e-38
Match length	131
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)
Seq. No.	175220
Seq. ID	jC-atXLIB327428P4b07a2
Method	BLASTX
NCBI GI	g2980805
BLAST score	438
E value	3.0e-43
Match length	96
% identity	97
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	175221
Seq. ID	jC-atXLIB327428P4b08a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	67
E value	4.0e-29
Match length	156
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	175222
Seq. ID	jC-atXLIB327428P4b10a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175223
Seq. ID	jC-atXLIB327428P4b11a2
Method	BLASTX
NCBI GI	g3426048
BLAST score	456
E value	2.0e-45
Match length	92
% identity	100
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	175224
Seq. ID	jC-atXLIB327428P4b12a2
Method	BLASTN
NCBI GI	g2828187
BLAST score	163
E value	2.0e-86
Match length	385
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	175225
Seq. ID	jC-atXLIB327428P4c01b2
Method	BLASTN
NCBI GI	g4115352
BLAST score	230
E value	1.0e-126
Match length	418
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175226
Seq. ID	jC-atXLIB327428P4c03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175227
Seq. ID	jC-atXLIB327428P4c06b2
Method	BLASTX
NCBI GI	g231586
BLAST score	47
E value	2.0e-39

Match length	115
% identity	87
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	175228
Seq. ID	jC-atXLIB327428P4c07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175229
Seq. ID	jC-atXLIB327428P4c08b2
Method	BLASTN
NCBI GI	g2618602
BLAST score	97
E value	2.0e-47
Match length	101
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	175230
Seq. ID	jC-atXLIB327428P4c10b2
Method	BLASTX
NCBI GI	g2462763
BLAST score	584
E value	2.0e-60
Match length	133
% identity	87
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	175231
Seq. ID	jC-atXLIB327428P4c11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	5.0e-16
Match length	77
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175232
Seq. ID	jC-atXLIB327428P4c12a2
Method	BLASTN
NCBI GI	g2264307
BLAST score	50
E value	6.0e-19

Match length	161
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	175233
Seq. ID	jC-atXLIB327428P4d03a2
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	5.0e-16
Match length	45
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175234
Seq. ID	jC-atXLIB327428P4d04b2
Method	BLASTX
NCBI GI	g2062161
BLAST score	50
E value	4.0e-66
Match length	130
% identity	51
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	175235
Seq. ID	jC-atXLIB327428P4d05a1
Method	BLASTN
NCBI GI	g4468976
BLAST score	101
E value	2.0e-49
Match length	309
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	175236
Seq. ID	jC-atXLIB327428P4d07a1
Method	BLASTN
NCBI GI	g4079614
BLAST score	154
E value	5.0e-81
Match length	333
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175237
Seq. ID	jC-atXLIB327428P4d10a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	51
E value	1.0e-19
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig

fragment No

Seq. No.	175238
Seq. ID	jC-atXLIB327428P4d10b1
Method	BLASTN
NCBI GI	g4006885
BLAST score	114
E value	3.0e-57
Match length	317
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	175239
Seq. ID	jC-atXLIB327428P4e01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175240
Seq. ID	jC-atXLIB327428P4e04b2
Method	BLASTX
NCBI GI	g2880051
BLAST score	49
E value	5.0e-15
Match length	74
% identity	62
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	175241
Seq. ID	jC-atXLIB327428P4e09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175242
Seq. ID	jC-atXLIB327428P4f01b2
Method	BLASTX
NCBI GI	g2673920
BLAST score	196
E value	6.0e-15
Match length	89
% identity	47
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	175243
Seq. ID	jC-atXLIB327428P4f02a1
Method	BLASTN

NCBI GI	g3789706
BLAST score	86
E value	2.0e-40
Match length	146
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175244
Seq. ID	jC-atXLIB327428P4f04b2
Method	BLASTN
NCBI GI	g2494110
BLAST score	61
E value	1.0e-25
Match length	240
% identity	87
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	175245
Seq. ID	jC-atXLIB327428P4f08a1
Method	BLASTN
NCBI GI	g2264311
BLAST score	130
E value	1.0e-66
Match length	324
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	175246
Seq. ID	jC-atXLIB327428P4g01a2
Method	BLASTX
NCBI GI	g3805849
BLAST score	328
E value	2.0e-30
Match length	63
% identity	100
NCBI Description	(AL031986) cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana]

Seq. No.	175247
Seq. ID	jC-atXLIB327428P4h02a2
Method	BLASTX
NCBI GI	g4115925
BLAST score	249
E value	4.0e-21
Match length	71
% identity	38
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	175248
Seq. ID	jC-atXLIB327428P4h06b1
Method	BLASTN

NCBI GI	g4490324
BLAST score	95
E value	6.0e-46
Match length	121
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	175249
Seq. ID	jC-atXLIB327428P4h08a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175250
Seq. ID	jC-atXLIB327428P4h10b2
Method	BLASTN
NCBI GI	g3176701
BLAST score	41
E value	1.0e-13
Match length	62
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175251
Seq. ID	jC-atXLIB327428P4h11a2
Method	BLASTX
NCBI GI	g1076398
BLAST score	351
E value	4.0e-33
Match length	84
% identity	77
NCBI Description	ribosomal protein L2 - Arabidopsis thaliana >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	175252
Seq. ID	jC-atXLIB327429P1a02b2
Method	BLASTN
NCBI GI	g3800746
BLAST score	36
E value	5.0e-11
Match length	48
% identity	94
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	175253
Seq. ID	jC-atXLIB327429P1a05a2
Method	BLASTN
NCBI GI	g4757394
BLAST score	34

E value	2.0e-09
Match length	82
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence

Seq. No.	175254
Seq. ID	jC-atXLIB327429P1a05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	63
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175255
Seq. ID	jC-atXLIB327429P1b03a2
Method	BLASTN
NCBI GI	g4220643
BLAST score	295
E value	1.0e-165
Match length	351
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	175256
Seq. ID	jC-atXLIB327429P1b04a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	46
E value	1.0e-16
Match length	70
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175257
Seq. ID	jC-atXLIB327429P1b07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175258
Seq. ID	jC-atXLIB327429P1c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	1.0e-23
Match length	61

% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175259
Seq. ID	jC-atXLIB327429P1c09b1
Method	BLASTX
NCBI GI	g1168530
BLAST score	702
E value	3.0e-74
Match length	165
% identity	81
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase [Arabidopsis thaliana]

Seq. No.	175260
Seq. ID	jC-atXLIB327429P1d01b2
Method	BLASTN
NCBI GI	g3168605
BLAST score	44
E value	2.0e-15
Match length	181
% identity	90
NCBI Description	Arabidopsis thaliana catalase 3 (CAT3) and catalase 1 (CAT1) genes, complete cds

Seq. No.	175261
Seq. ID	jC-atXLIB327429P1d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	59
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175262
Seq. ID	jC-atXLIB327429P1d05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	4.0e-16
Match length	45
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175263
Seq. ID	jC-atXLIB327429P1e06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	4.0e-19
Match length	58

% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175264
Seq. ID	jC-atXLIB327429P1f06a1
Method	BLASTN
NCBI GI	g4519193
BLAST score	116
E value	2.0e-58
Match length	128
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	175265
Seq. ID	jC-atXLIB327429P1f07b1
Method	BLASTN
NCBI GI	g1488266
BLAST score	70
E value	6.0e-31
Match length	106
% identity	93
NCBI Description	Arabidopsis thaliana low affinity calcium antiporter CAX2 mRNA, complete cds

Seq. No.	175266
Seq. ID	jC-atXLIB327429P1f08b2
Method	BLASTN
NCBI GI	g1488266
BLAST score	51
E value	1.0e-19
Match length	137
% identity	91
NCBI Description	Arabidopsis thaliana low affinity calcium antiporter CAX2 mRNA, complete cds

Seq. No.	175267
Seq. ID	jC-atXLIB327429P2b08b2
Method	BLASTX
NCBI GI	g464444
BLAST score	152
E value	9.0e-10
Match length	108
% identity	43
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome [Arabidopsis thaliana]

Seq. No.	175268
Seq. ID	jC-atXLIB327429P2b09b2
Method	BLASTX
NCBI GI	g1168257
BLAST score	615
E value	4.0e-64
Match length	128

% identity	96
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1 (TRANSAMINASE A) >gi_693690 (U15033) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	175269
Seq. ID	jC-atXLIB327429P2d10b1
Method	BLASTN
NCBI GI	g3869074
BLAST score	123
E value	1.0e-62
Match length	297
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	175270
Seq. ID	jC-atXLIB327429P2h02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	73
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175271
Seq. ID	jC-atXLIB327429P3a06a2
Method	BLASTN
NCBI GI	g4159707
BLAST score	296
E value	1.0e-165
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	175272
Seq. ID	jC-atXLIB327429P3b09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175273
Seq. ID	jC-atXLIB327429P3b10b2
Method	BLASTX
NCBI GI	g2351374
BLAST score	227
E value	1.0e-18
Match length	103
% identity	62

NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]
Seq. No.	175274
Seq. ID	jC-atXLIB327429P3c01b2
Method	BLASTX
NCBI GI	g3142289
BLAST score	242
E value	2.0e-20
Match length	132
% identity	48
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.	175275
Seq. ID	jC-atXLIB327429P3c08a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	39
E value	2.0e-12
Match length	50
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	175276
Seq. ID	jC-atXLIB327429P3c12a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	9.0e-09
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	175277
Seq. ID	jC-atXLIB327429P3c12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	175278
Seq. ID	jC-atXLIB327429P3d01b2
Method	BLASTX
NCBI GI	g2129575
BLAST score	346
E value	1.0e-32
Match length	132
% identity	59
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana
Seq. No.	175279

Seq. ID	jC-atXLIB327429P3d06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	63
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175280
Seq. ID	jC-atXLIB327429P3e06b2
Method	BLASTN
NCBI GI	g1785729
BLAST score	42
E value	2.0e-14
Match length	78
% identity	88
NCBI Description	A.thaliana mitochondrial genome, part B

Seq. No.	175281
Seq. ID	jC-atXLIB327429P3f01b2
Method	BLASTX
NCBI GI	g2829902
BLAST score	118
E value	2.0e-16
Match length	111
% identity	50
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	175282
Seq. ID	jC-atXLIB327429P3f03a2
Method	BLASTX
NCBI GI	g110072
BLAST score	90
E value	2.2e-02
Match length	210
% identity	6
NCBI Description	proline-rich protein MP4 - mouse >gi_53182_emb_CAA41344_ (X58438) proline rich protein [Mus musculus]

Seq. No.	175283
Seq. ID	jC-atXLIB327429P3f07b2
Method	BLASTX
NCBI GI	g1488267
BLAST score	529
E value	6.0e-54
Match length	138
% identity	80
NCBI Description	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]

Seq. No.	175284
Seq. ID	jC-atXLIB327429P3f12a2
Method	BLASTX
NCBI GI	g2144912

BLAST score	154
E value	6.0e-10
Match length	188
% identity	7
NCBI Description	salivary proline-rich glycoprotein precursor PRB4 (large allele) - human

Seq. No.	175285
Seq. ID	jC-atXLIB327429P3g05a2
Method	BLASTN
NCBI GI	g4678231
BLAST score	195
E value	1.0e-105
Match length	361
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F23I14 genomic sequence, complete sequence

Seq. No.	175286
Seq. ID	jC-atXLIB327429P3h05a2
Method	BLASTX
NCBI GI	g1155261
BLAST score	770
E value	4.0e-82
Match length	173
% identity	90
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	175287
Seq. ID	jC-atXLIB327429P4a04b2
Method	BLASTX
NCBI GI	g2181180
BLAST score	198
E value	3.0e-15
Match length	144
% identity	29
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	175288
Seq. ID	jC-atXLIB327429P4a05a2
Method	BLASTN
NCBI GI	g4589440
BLAST score	119
E value	5.0e-60
Match length	217
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	175289
Seq. ID	jC-atXLIB327429P4a05b2
Method	BLASTN
NCBI GI	g4589440
BLAST score	99
E value	3.0e-48
Match length	119

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	175290
Seq. ID	jC-atXLIB327429P4a06b2
Method	BLASTX
NCBI GI	g122003
BLAST score	196
E value	6.0e-17
Match length	72
% identity	72
NCBI Description	HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato

Seq. No.	175291
Seq. ID	jC-atXLIB327429P4a07b2
Method	BLASTN
NCBI GI	g4589445
BLAST score	67
E value	4.0e-29
Match length	319
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	175292
Seq. ID	jC-atXLIB327429P4a08b2
Method	BLASTN
NCBI GI	g2252639
BLAST score	67
E value	4.0e-29
Match length	143
% identity	88
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	175293
Seq. ID	jC-atXLIB327429P4a11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	9.0e-21
Match length	53
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175294
Seq. ID	jC-atXLIB327429P4a12b2
Method	BLASTX
NCBI GI	g2497738
BLAST score	190
E value	3.0e-14
Match length	74
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN A PRECURSOR (LTP A) (WAX-ASSOCIATED PROTEIN 9A) >gi_500841 (L33904) lipid

transfer protein [Brassica oleracea]

Seq. No.	175295
Seq. ID	jC-atXLIB327429P4b03a2
Method	BLASTX
NCBI GI	g2317731
BLAST score	77
E value	3.0e-17
Match length	134
% identity	44
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	175296
Seq. ID	jC-atXLIB327429P4b12a2
Method	BLASTN
NCBI GI	g2288979
BLAST score	33
E value	9.0e-09
Match length	93
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175297
Seq. ID	jC-atXLIB327429P4b12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	5.0e-12
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175298
Seq. ID	jC-atXLIB327429P4d12b2
Method	BLASTX
NCBI GI	g2191152
BLAST score	176
E value	1.0e-12
Match length	89
% identity	53
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	175299
Seq. ID	jC-atXLIB327429P4e02b2
Method	BLASTX
NCBI GI	g399091
BLAST score	320
E value	2.0e-29
Match length	98
% identity	68
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase

(EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi 166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	175300
Seq. ID	jC-atXLIB327429P4f03a2
Method	BLASTX
NCBI GI	g1495251
BLAST score	57
E value	4.0e-70
Match length	152
% identity	87
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	175301
Seq. ID	jC-atXLIB327429P4f07a2
Method	BLASTN
NCBI GI	g1488266
BLAST score	52
E value	4.0e-20
Match length	118
% identity	87
NCBI Description	Arabidopsis thaliana low affinity calcium antiporter CAX2 mRNA, complete cds

Seq. No.	175302
Seq. ID	jC-atXLIB327429P4g03a2
Method	BLASTX
NCBI GI	g100753
BLAST score	157
E value	3.0e-10
Match length	195
% identity	10
NCBI Description	hydroxyproline-rich glycoprotein - sorghum >gi_228939_prf__1814452D Hyp-rich glycoprotein [Sorghum bicolor]

Seq. No.	175303
Seq. ID	jC-atXLIB327429P4h02b2
Method	BLASTX
NCBI GI	g2645971
BLAST score	228
E value	1.0e-18
Match length	44
% identity	100
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	175304
Seq. ID	jC-atXLIB327429P4h10b2
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	68
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175305
Seq. ID	jC-atXLIB327429P4h11b2
Method	BLASTN
NCBI GI	g2262135
BLAST score	273
E value	1.0e-152
Match length	438
% identity	91
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	175306
Seq. ID	jC-atXLIB327430P1c01b1
Method	BLASTX
NCBI GI	g1621268
BLAST score	214
E value	4.0e-17
Match length	91
% identity	43
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	175307
Seq. ID	jC-atXLIB327430P1d10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175308
Seq. ID	jC-atXLIB327430P1f05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	9.0e-24
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175309
Seq. ID	jC-atXLIB327430P1g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	6.0e-22
Match length	63
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175310
Seq. ID	jC-atXLIB327430P1g12b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	41
E value	1.0e-13
Match length	67
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175311
Seq. ID	jC-atXLIB327430P1h03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	5.0e-25
Match length	72
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175312
Seq. ID	jC-atXLIB327430P1h06b1
Method	BLASTN
NCBI GI	g3702724
BLAST score	63
E value	4.0e-27
Match length	150
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	175313
Seq. ID	jC-atXLIB327430P1h08a1
Method	BLASTN
NCBI GI	g1155260
BLAST score	130
E value	1.0e-66
Match length	359
% identity	84
NCBI Description	Arabidopsis thaliana eukaryotic release factor 1 homolog (eRF1) mRNA, complete cds

Seq. No.	175314
Seq. ID	jC-atXLIB327430P1h11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	9.0e-18
Match length	63
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175315
Seq. ID	jC-atXLIB327430P2a03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	37

% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175316
Seq. ID	jC-atXLIB327430P2a07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175317
Seq. ID	jC-atXLIB327430P2b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18
Match length	48
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175318
Seq. ID	jC-atXLIB327430P2b05a1
Method	BLASTN
NCBI GI	g2264316
BLAST score	54
E value	3.0e-21
Match length	162
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	175319
Seq. ID	jC-atXLIB327430P2b06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175320
Seq. ID	jC-atXLIB327430P2b06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	7.0e-09
Match length	57
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175321

Seq. ID	jC-atXLIB327430P2b07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	62
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175322
Seq. ID	jC-atXLIB327430P2b07b1
Method	BLASTN
NCBI GI	g1877523
BLAST score	40
E value	6.0e-13
Match length	54
% identity	95
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	175323
Seq. ID	jC-atXLIB327430P2b09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	6.0e-22
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175324
Seq. ID	jC-atXLIB327430P2b09b1
Method	BLASTN
NCBI GI	g2781393
BLAST score	72
E value	5.0e-32
Match length	99
% identity	94
NCBI Description	Arabidopsis thaliana O-methyltransferase 1 (OMT1) mRNA, complete cds

Seq. No.	175325
Seq. ID	jC-atXLIB327430P2b10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	61
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175326
Seq. ID	jC-atXLIB327430P2c04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42

E value	3.0e-14
Match length	61
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175327
Seq. ID	jC-atXLIB327430P2c05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	48
E value	9.0e-18
Match length	64
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175328
Seq. ID	jC-atXLIB327430P2c08a1
Method	BLASTN
NCBI GI	g2262155
BLAST score	180
E value	1.0e-96
Match length	304
% identity	89
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	175329
Seq. ID	jC-atXLIB327430P2c11b1
Method	BLASTN
NCBI GI	g2351071
BLAST score	100
E value	8.0e-49
Match length	140
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	175330
Seq. ID	jC-atXLIB327430P2c12b1
Method	BLASTN
NCBI GI	g4558586
BLAST score	50
E value	6.0e-19
Match length	110
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	175331
Seq. ID	jC-atXLIB327430P2d04a1
Method	BLASTX
NCBI GI	g3122387
BLAST score	186
E value	6.0e-14
Match length	42

% identity	79
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394229 (AF016846) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	175332
Seq. ID	jC-atXLIB327430P2d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	9.0e-09
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175333
Seq. ID	jC-atXLIB327430P2d07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175334
Seq. ID	jC-atXLIB327430P2d08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	4.0e-15
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175335
Seq. ID	jC-atXLIB327430P2d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	2.0e-29
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175336
Seq. ID	jC-atXLIB327430P2d09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	9.0e-12
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175337

Seq. ID	jC-atXLIB327430P2d10a1
Method	BLASTN
NCBI GI	g4733952
BLAST score	58
E value	9.0e-24
Match length	110
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	175338
Seq. ID	jC-atXLIB327430P2d10b1
Method	BLASTN
NCBI GI	g4733952
BLAST score	83
E value	1.0e-38
Match length	132
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	175339
Seq. ID	jC-atXLIB327430P2d11b1
Method	BLASTN
NCBI GI	g4580744
BLAST score	122
E value	6.0e-62
Match length	142
% identity	97
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	175340
Seq. ID	jC-atXLIB327430P2e01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	57
% identity	91
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175341
Seq. ID	jC-atXLIB327430P2e01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	1.0e-20
Match length	80
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175342
Seq. ID	jC-atXLIB327430P2e02b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	40
E value	4.0e-13
Match length	52
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175343
Seq. ID	jC-atXLIB327430P2e03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175344
Seq. ID	jC-atXLIB327430P2e07b1
Method	BLASTN
NCBI GI	g4468103
BLAST score	35
E value	6.0e-10
Match length	63
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	175345
Seq. ID	jC-atXLIB327430P2e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	4.0e-14
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175346
Seq. ID	jC-atXLIB327430P2f01b1
Method	BLASTN
NCBI GI	g3688169
BLAST score	62
E value	4.0e-26
Match length	145
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	175347
Seq. ID	jC-atXLIB327430P2f04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	67

% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175348
Seq. ID	jC-atXLIB327430P2f06a1
Method	BLASTN
NCBI GI	g3702732
BLAST score	119
E value	3.0e-60
Match length	295
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	175349
Seq. ID	jC-atXLIB327430P2f06b1
Method	BLASTN
NCBI GI	g3702732
BLAST score	96
E value	2.0e-46
Match length	120
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	175350
Seq. ID	jC-atXLIB327430P2f07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175351
Seq. ID	jC-atXLIB327430P2f08b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	109
E value	3.0e-54
Match length	179
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	175352
Seq. ID	jC-atXLIB327430P2f09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175353
Seq. ID	jC-atXLIB327430P2f11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	61
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175354
Seq. ID	jC-atXLIB327430P2f12a1
Method	BLASTN
NCBI GI	g3292807
BLAST score	126
E value	2.0e-64
Match length	162
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	175355
Seq. ID	jC-atXLIB327430P2g01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175356
Seq. ID	jC-atXLIB327430P2g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	43
E value	8.0e-15
Match length	70
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175357
Seq. ID	jC-atXLIB327430P2g03a1
Method	BLASTX
NCBI GI	g2760834
BLAST score	244
E value	1.0e-20
Match length	135
% identity	33
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	175358
Seq. ID	jC-atXLIB327430P2g03b1
Method	BLASTN

NCBI GI	g2760829
BLAST score	61
E value	2.0e-25
Match length	69
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175359
Seq. ID	jC-atXLIB327430P2g07a1
Method	BLASTN
NCBI GI	g4204173
BLAST score	61
E value	1.0e-25
Match length	200
% identity	85
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175360
Seq. ID	jC-atXLIB327430P2g07b1
Method	BLASTN
NCBI GI	g4204173
BLAST score	94
E value	3.0e-45
Match length	257
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175361
Seq. ID	jC-atXLIB327430P2g08a1
Method	BLASTX
NCBI GI	g1352458
BLAST score	312
E value	2.0e-33
Match length	114
% identity	72
NCBI Description	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD) >gi_2117507_pir__JC4999 IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana >gi_1100063 (L34684) IMP dehydrogenase [Arabidopsis thaliana]

Seq. No.	175362
Seq. ID	jC-atXLIB327430P2g09a1
Method	BLASTN
NCBI GI	g2335089
BLAST score	115
E value	9.0e-58
Match length	290
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175363
Seq. ID	jC-atXLIB327430P2g10a1
Method	BLASTN

NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175364
Seq. ID	jC-atXLIB327430P2h03a1
Method	BLASTN
NCBI GI	g4185120
BLAST score	113
E value	1.0e-56
Match length	267
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175365
Seq. ID	jC-atXLIB327430P2h04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175366
Seq. ID	jC-atXLIB327430P2h04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	6.0e-13
Match length	56
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175367
Seq. ID	jC-atXLIB327430P2h06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175368
Seq. ID	jC-atXLIB327430P3a07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	67
% identity	94

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175369
Seq. ID	jC-atXLIB327430P3c06b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	172
E value	1.0e-91
Match length	280
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	175370
Seq. ID	jC-atXLIB327430P3c11b1
Method	BLASTN
NCBI GI	g2760172
BLAST score	64
E value	2.0e-27
Match length	300
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	175371
Seq. ID	jC-atXLIB327430P3d04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	59
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175372
Seq. ID	jC-atXLIB327430P3d05b1
Method	BLASTX
NCBI GI	g4455329
BLAST score	295
E value	2.0e-26
Match length	111
% identity	59
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	175373
Seq. ID	jC-atXLIB327430P3d07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	56
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175374
Seq. ID	jC-atXLIB327430P3d11b1
Method	BLASTX
NCBI GI	g2642157
BLAST score	278
E value	2.0e-24
Match length	139
% identity	45
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	175375
Seq. ID	jC-atXLIB327430P3e05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175376
Seq. ID	jC-atXLIB327430P3e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	63
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175377
Seq. ID	jC-atXLIB327430P3f02b1
Method	BLASTN
NCBI GI	g3449311
BLAST score	67
E value	4.0e-29
Match length	110
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15I22, complete sequence [Arabidopsis thaliana]

Seq. No.	175378
Seq. ID	jC-atXLIB327430P3f04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	8.0e-09
Match length	53
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175379
Seq. ID	jC-atXLIB327430P3f06b1

Method	BLASTN
NCBI GI	g2244829
BLAST score	102
E value	6.0e-50
Match length	212
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175380
Seq. ID	jC-atXLIB327430P3f07b1
Method	BLASTN
NCBI GI	g16491
BLAST score	64
E value	3.0e-27
Match length	119
% identity	88
NCBI Description	A. thaliana mRNA for root-specific gene

Seq. No.	175381
Seq. ID	jC-atXLIB327430P3g06b1
Method	BLASTX
NCBI GI	g1174718
BLAST score	325
E value	1.0e-32
Match length	146
% identity	63
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	175382
Seq. ID	jC-atXLIB327430P3g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175383
Seq. ID	jC-atXLIB327430P4a02b1
Method	BLASTX
NCBI GI	g2129657
BLAST score	159
E value	6.0e-12
Match length	110
% identity	47
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	175384

Seq. ID	jC-atXLIB327430P4a03b1
Method	BLASTN
NCBI GI	g4756963
BLAST score	102
E value	2.0e-50
Match length	102
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	175385
Seq. ID	jC-atXLIB327430P4a11b1
Method	BLASTX
NCBI GI	g1173104
BLAST score	552
E value	1.0e-56
Match length	115
% identity	89
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	175386
Seq. ID	jC-atXLIB327430P4c06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	53
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175387
Seq. ID	jC-atXLIB327430P4c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175388
Seq. ID	jC-atXLIB327430P4d01b1
Method	BLASTN
NCBI GI	g3228389
BLAST score	33
E value	6.0e-09
Match length	37
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	175389
Seq. ID	jC-atXLIB327430P4d05a1
Method	BLASTN

NCBI GI	g3128476
BLAST score	86
E value	2.0e-40
Match length	134
% identity	92
NCBI Description	Arabidopsis thaliana metalloproteinase mRNA, complete cds

Seq. No.	175390
Seq. ID	jC-atXLIB327430P4d08a1
Method	BLASTN
NCBI GI	g2618601
BLAST score	57
E value	4.0e-23
Match length	82
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	175391
Seq. ID	jC-atXLIB327430P4f05a1
Method	BLASTN
NCBI GI	g3319339
BLAST score	43
E value	1.0e-14
Match length	87
% identity	91
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	175392
Seq. ID	jC-atXLIB327430P4g12b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	35
E value	5.0e-10
Match length	140
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175393
Seq. ID	jC-atXLIB327431P1a11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	71
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175394
Seq. ID	jC-atXLIB327431P1d06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	3.0e-14
Match length	49

% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175395
Seq. ID	jC-atXLIB327431P1e02a1
Method	BLASTX
NCBI GI	g2827634
BLAST score	496
E value	4.0e-50
Match length	98
% identity	100
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	175396
Seq. ID	jC-atXLIB327431P1f12a1
Method	BLASTN
NCBI GI	g304040
BLAST score	175
E value	1.0e-93
Match length	368
% identity	88
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	175397
Seq. ID	jC-atXLIB327431P1g03a1
Method	BLASTN
NCBI GI	g3434972
BLAST score	253
E value	1.0e-140
Match length	361
% identity	93
NCBI Description	Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive element binding factor 4, complete cds

Seq. No.	175398
Seq. ID	jC-atXLIB327431P1h01a1
Method	BLASTN
NCBI GI	g2182287
BLAST score	43
E value	8.0e-15
Match length	79
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	175399
Seq. ID	jC-atXLIB327431P1h03a1
Method	BLASTN
NCBI GI	g3492855
BLAST score	76
E value	2.0e-34
Match length	156
% identity	88
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	175400
Seq. ID	jC-atXLIB327431P1h03b1
Method	BLASTN
NCBI GI	g531828
BLAST score	34
E value	2.0e-09
Match length	71
% identity	87
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175401
Seq. ID	jC-atXLIB327431P1h09a1
Method	BLASTN
NCBI GI	g3687221
BLAST score	99
E value	1.0e-48
Match length	144
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175402
Seq. ID	jC-atXLIB327431P2b05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175403
Seq. ID	jC-atXLIB327431P2d03a1
Method	BLASTN
NCBI GI	g1871173
BLAST score	223
E value	1.0e-122
Match length	357
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	175404
Seq. ID	jC-atXLIB327431P2d05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	39
E value	2.0e-12
Match length	66
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175405
Seq. ID	jC-atXLIB327431P2f02a1
Method	BLASTN

NCBI GI	g1460048
BLAST score	408
E value	0.0e+00
Match length	474
% identity	96
NCBI Description	A.thaliana mitochondrial tRNA-Tyr pseudogene & nad2 gene, exon 3,4 &

Seq. No.	175406
Seq. ID	jC-atXLIB327431P2f06a1
Method	BLASTN
NCBI GI	g4079631
BLAST score	66
E value	1.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for hypothetical protein, partial

Seq. No.	175407
Seq. ID	jC-atXLIB327431P2f10a1
Method	BLASTN
NCBI GI	g4519188
BLAST score	221
E value	1.0e-121
Match length	457
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	175408
Seq. ID	jC-atXLIB327431P2g03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	43
E value	9.0e-15
Match length	43
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175409
Seq. ID	jC-atXLIB327431P2g06a1
Method	BLASTX
NCBI GI	g1169598
BLAST score	872
E value	4.0e-94
Match length	161
% identity	100
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	175410
Seq. ID	jC-atXLIB327431P2h11a1
Method	BLASTX
NCBI GI	g3024871
BLAST score	383

E value	8.0e-37
Match length	152
% identity	49
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	175411
Seq. ID	jC-atXLIB327431P3a03a1
Method	BLASTX
NCBI GI	g3335516
BLAST score	791
E value	1.0e-84
Match length	158
% identity	77
NCBI Description	(AF053941) nonphototropic hypocotyl 2 [Arabidopsis thaliana]

Seq. No.	175412
Seq. ID	jC-atXLIB327431P3b01a1
Method	BLASTN
NCBI GI	g4757392
BLAST score	251
E value	1.0e-139
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	175413
Seq. ID	jC-atXLIB327431P3b09a1
Method	BLASTX
NCBI GI	g2129578
BLAST score	259
E value	2.0e-22
Match length	72
% identity	72
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	175414
Seq. ID	jC-atXLIB327431P3b12a1
Method	BLASTX
NCBI GI	g729479
BLAST score	398
E value	1.0e-38
Match length	98
% identity	77
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	175415
Seq. ID	jC-atXLIB327431P3c03a1
Method	BLASTN

NCBI GI	g887938
BLAST score	30
E value	5.0e-07
Match length	136
% identity	93
NCBI Description	Arabidopsis thaliana clone YAP317 GAST1 protein homolog mRNA, complete cds

Seq. No.	175416
Seq. ID	jC-atXLIB327431P3e07a1
Method	BLASTX
NCBI GI	g430947
BLAST score	526
E value	1.0e-53
Match length	135
% identity	76
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	175417
Seq. ID	jC-atXLIB327431P3e08b1
Method	BLASTX
NCBI GI	g3808062
BLAST score	100
E value	1.0e-03
Match length	185
% identity	6
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	175418
Seq. ID	jC-atXLIB327431P3f06a1
Method	BLASTN
NCBI GI	g3582315
BLAST score	73
E value	1.0e-32
Match length	81
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175419
Seq. ID	jC-atXLIB327431P3f09a1
Method	BLASTX
NCBI GI	g2827546
BLAST score	711
E value	3.0e-75
Match length	136
% identity	99
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	175420
Seq. ID	jC-atXLIB327431P3g04a1
Method	BLASTX
NCBI GI	g3660467
BLAST score	658
E value	4.0e-69

Match length	147
% identity	90
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No.	175421
Seq. ID	jC-atXLIB327431P4a05b1
Method	BLASTN
NCBI GI	g2098816
BLAST score	52
E value	4.0e-20
Match length	80
% identity	93
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	175422
Seq. ID	jC-atXLIB327431P4a08a1
Method	BLASTN
NCBI GI	g4325216
BLAST score	112
E value	6.0e-56
Match length	323
% identity	86
NCBI Description	Arabidopsis thaliana hydrophobic protein (RCI2A) mRNA, complete cds

Seq. No.	175423
Seq. ID	jC-atXLIB327431P4c11b1
Method	BLASTX
NCBI GI	g3335371
BLAST score	196
E value	6.0e-15
Match length	92
% identity	34
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	175424
Seq. ID	jC-atXLIB327431P4e02a1
Method	BLASTX
NCBI GI	g2914700
BLAST score	598
E value	5.0e-62
Match length	118
% identity	100
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	175425
Seq. ID	jC-atXLIB327431P4e05a1
Method	BLASTX
NCBI GI	g2129613
BLAST score	571
E value	7.0e-59
Match length	159
% identity	70
NCBI Description	homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No.	175426
Seq. ID	jC-atXLIB327431P4f03a1
Method	BLASTX
NCBI GI	g4091806
BLAST score	371
E value	2.0e-35
Match length	95
% identity	68
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	175427
Seq. ID	jC-atXLIB327431P4g08a1
Method	BLASTX
NCBI GI	g1653702
BLAST score	256
E value	6.0e-22
Match length	73
% identity	71
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	175428
Seq. ID	jC-atXLIB327431P4h02a1
Method	BLASTX
NCBI GI	g1749546
BLAST score	228
E value	1.0e-18
Match length	81
% identity	57
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	175429
Seq. ID	jC-atXLIB327431P4h03a1
Method	BLASTN
NCBI GI	g531832
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175430
Seq. ID	jC-atXLIB327431P4h06a1
Method	BLASTX
NCBI GI	g4587549
BLAST score	332
E value	8.0e-31
Match length	132
% identity	43
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	175431
Seq. ID	jC-atXLIB327431P4h09a1
Method	BLASTX
NCBI GI	g3641868
BLAST score	308
E value	5.0e-28
Match length	108
% identity	56
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]

Seq. No.	175432
Seq. ID	jC-atXLIB327432P1a02a1
Method	BLASTN
NCBI GI	g3434970
BLAST score	72
E value	5.0e-32
Match length	161
% identity	88
NCBI Description	Arabidopsis thaliana AtERF-3 mRNA for ethylene responsive element binding factor 3, complete cds

Seq. No.	175433
Seq. ID	jC-atXLIB327432P1a09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175434
Seq. ID	jC-atXLIB327432P1a10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	1.0e-22
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175435
Seq. ID	jC-atXLIB327432P1a11a1
Method	BLASTX
NCBI GI	g3138972
BLAST score	149
E value	2.0e-09
Match length	114
% identity	41
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	175436
Seq. ID	jC-atXLIB327432P1b04a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175437
Seq. ID	jC-atXLIB327432P1b09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175438
Seq. ID	jC-atXLIB327432P1b10a1
Method	BLASTN
NCBI GI	g3738313
BLAST score	110
E value	8.0e-55
Match length	382
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175439
Seq. ID	jC-atXLIB327432P1b10b1
Method	BLASTX
NCBI GI	g3738339
BLAST score	59
E value	2.0e-28
Match length	147
% identity	60
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	175440
Seq. ID	jC-atXLIB327432P1b12b1
Method	BLASTN
NCBI GI	g3282170
BLAST score	41
E value	1.0e-13
Match length	53
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175441
Seq. ID	jC-atXLIB327432P1c01b1
Method	BLASTN
NCBI GI	g4432847
BLAST score	99
E value	4.0e-48
Match length	203
% identity	88

NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175442
Seq. ID	jC-atXLIB327432P1c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175443
Seq. ID	jC-atXLIB327432P1c03b1
Method	BLASTN
NCBI GI	g3193282
BLAST score	76
E value	5.0e-35
Match length	99
% identity	94
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	175444
Seq. ID	jC-atXLIB327432P1c06a1
Method	BLASTN
NCBI GI	g3128141
BLAST score	64
E value	2.0e-27
Match length	125
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	175445
Seq. ID	jC-atXLIB327432P1c06b1
Method	BLASTN
NCBI GI	g3128141
BLAST score	45
E value	2.0e-16
Match length	61
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	175446
Seq. ID	jC-atXLIB327432P1c08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175447

Seq. ID	jC-atXLIB327432P1c09a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	1.0e-16
Match length	61
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175448
Seq. ID	jC-atXLIB327432P1c12a1
Method	BLASTN
NCBI GI	g4263586
BLAST score	247
E value	1.0e-136
Match length	435
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F28K20 sequence, complete sequence

Seq. No.	175449
Seq. ID	jC-atXLIB327432P1d02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175450
Seq. ID	jC-atXLIB327432P1d04a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	52
E value	3.0e-20
Match length	84
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175451
Seq. ID	jC-atXLIB327432P1d04b1
Method	BLASTN
NCBI GI	g3212846
BLAST score	123
E value	1.0e-62
Match length	249
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175452
Seq. ID	jC-atXLIB327432P1d06a1
Method	BLASTN
NCBI GI	g2264316
BLAST score	139

E value	4.0e-72
Match length	294
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	175453
Seq. ID	jC-atXLIB327432P1d07b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	38
E value	2.0e-12
Match length	57
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	175454
Seq. ID	jC-atXLIB327432P1d10b1
Method	BLASTN
NCBI GI	g531832
BLAST score	34
E value	2.0e-09
Match length	46
% identity	93
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175455
Seq. ID	jC-atXLIB327432P1d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	51
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175456
Seq. ID	jC-atXLIB327432P1e01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	2.0e-11
Match length	57
% identity	91
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175457
Seq. ID	jC-atXLIB327432P1e03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175458
Seq. ID	jC-atXLIB327432P1e03b1
Method	BLASTX
NCBI GI	g135406
BLAST score	266
E value	6.0e-34
Match length	104
% identity	78
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	175459
Seq. ID	jC-atXLIB327432P1f01b1
Method	BLASTX
NCBI GI	g4539327
BLAST score	283
E value	2.0e-27
Match length	88
% identity	74
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	175460
Seq. ID	jC-atXLIB327432P1f04a1
Method	BLASTN
NCBI GI	g4580528
BLAST score	58
E value	9.0e-24
Match length	139
% identity	86
NCBI Description	Arabidopsis thaliana scarecrow-like 13 (SCL13) mRNA, partial cds

Seq. No.	175461
Seq. ID	jC-atXLIB327432P1f04b1
Method	BLASTN
NCBI GI	g2245073
BLAST score	83
E value	1.0e-38
Match length	239
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175462
Seq. ID	jC-atXLIB327432P1f05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 175463

Seq. ID	jC-atXLIB327432P1f07a1
Method	BLASTN
NCBI GI	g4006815
BLAST score	63
E value	1.0e-26
Match length	103
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175464
Seq. ID	jC-atXLIB327432P1f08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175465
Seq. ID	jC-atXLIB327432P1g03a1
Method	BLASTN
NCBI GI	g4678705
BLAST score	85
E value	7.0e-40
Match length	129
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	175466
Seq. ID	jC-atXLIB327432P1h01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	9.0e-12
Match length	61
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175467
Seq. ID	jC-atXLIB327432P1h02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175468
Seq. ID	jC-atXLIB327432P1h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16

Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175469
Seq. ID	jC-atXLIB327432P1h04a1
Method	BLASTN
NCBI GI	g531832
BLAST score	39
E value	2.0e-12
Match length	58
% identity	93
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175470
Seq. ID	jC-atXLIB327432P1h04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175471
Seq. ID	jC-atXLIB327432P1h07a1
Method	BLASTN
NCBI GI	g2264367
BLAST score	139
E value	5.0e-72
Match length	298
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	175472
Seq. ID	jC-atXLIB327432P1h08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175473
Seq. ID	jC-atXLIB327432P1h09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175474

Seq. ID	jC-atXLIB327432P1h12a1
Method	BLASTX
NCBI GI	g3201554
BLAST score	257
E value	4.0e-22
Match length	59
% identity	76
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	175475
Seq. ID	jC-atXLIB327432P2a05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	9.0e-12
Match length	54
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175476
Seq. ID	jC-atXLIB327432P2a09a2
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175477
Seq. ID	jC-atXLIB327432P2b08a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	115
E value	4.0e-58
Match length	139
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	175478
Seq. ID	jC-atXLIB327432P2b11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	3.0e-13
Match length	40
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175479
Seq. ID	jC-atXLIB327432P2b12a1
Method	BLASTN
NCBI GI	g2924734
BLAST score	63
E value	7.0e-27
Match length	94

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	175480
Seq. ID	jC-atXLIB327432P2c08a1
Method	BLASTN
NCBI GI	g1483219
BLAST score	121
E value	2.0e-61
Match length	189
% identity	94
NCBI Description	A.thaliana mRNA for peroxidase ATP1a, clone EST 103m21t7

Seq. No.	175481
Seq. ID	jC-atXLIB327432P2c09b1
Method	BLASTN
NCBI GI	g4432829
BLAST score	52
E value	2.0e-20
Match length	154
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175482
Seq. ID	jC-atXLIB327432P2c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	7.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175483
Seq. ID	jC-atXLIB327432P2d02b1
Method	BLASTN
NCBI GI	g4589424
BLAST score	59
E value	2.0e-24
Match length	164
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	175484
Seq. ID	jC-atXLIB327432P2d04a1
Method	BLASTN
NCBI GI	g2088638
BLAST score	82
E value	3.0e-38
Match length	263
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175485
Seq. ID	jC-atXLIB327432P2d07a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	52
E value	3.0e-20
Match length	76
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175486
Seq. ID	jC-atXLIB327432P2d08b1
Method	BLASTX
NCBI GI	g902586
BLAST score	483
E value	8.0e-49
Match length	105
% identity	18
NCBI Description	(U29162) ubiquitin [Zea mays]

Seq. No.	175487
Seq. ID	jC-atXLIB327432P2d09a2
Method	BLASTN
NCBI GI	g531828
BLAST score	34
E value	2.0e-09
Match length	50
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175488
Seq. ID	jC-atXLIB327432P2d10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	7.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175489
Seq. ID	jC-atXLIB327432P2d11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175490
Seq. ID	jC-atXLIB327432P2e03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	3.0e-14

Match length	46
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175491
Seq. ID	jC-atXLIB327432P2e06b2
Method	BLASTN
NCBI GI	g3775986
BLAST score	411
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase,RH3

Seq. No.	175492
Seq. ID	jC-atXLIB327432P2e12a2
Method	BLASTN
NCBI GI	g4519193
BLAST score	121
E value	2.0e-61
Match length	376
% identity	77
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	175493
Seq. ID	jC-atXLIB327432P2f02a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	161
E value	2.0e-85
Match length	288
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175494
Seq. ID	jC-atXLIB327432P2f02b1
Method	BLASTN
NCBI GI	g2281081
BLAST score	83
E value	9.0e-39
Match length	147
% identity	74
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175495
Seq. ID	jC-atXLIB327432P2f03a1
Method	BLASTN
NCBI GI	g3132469
BLAST score	94
E value	2.0e-45
Match length	259
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175496
Seq. ID	jC-atXLIB327432P2f04a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	37
E value	3.0e-11
Match length	45
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175497
Seq. ID	jC-atXLIB327432P2f05b2
Method	BLASTX
NCBI GI	g112205
BLAST score	122
E value	3.0e-06
Match length	169
% identity	7
NCBI Description	proline-rich protein 15 - rat

Seq. No.	175498
Seq. ID	jC-atXLIB327432P2f10b1
Method	BLASTN
NCBI GI	g4586019
BLAST score	33
E value	4.0e-09
Match length	73
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T3P4 genomic sequence, complete sequence

Seq. No.	175499
Seq. ID	jC-atXLIB327432P2f12a1
Method	BLASTN
NCBI GI	g4220468
BLAST score	191
E value	1.0e-103
Match length	300
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175500
Seq. ID	jC-atXLIB327432P2g01b2
Method	BLASTN
NCBI GI	g4519194
BLAST score	137
E value	7.0e-71
Match length	433
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	175501
Seq. ID	jC-atXLIB327432P2g04a1

Method	BLASTN
NCBI GI	g3292807
BLAST score	61
E value	1.0e-25
Match length	200
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	175502
Seq. ID	jC-atXLIB327432P2g07a2
Method	BLASTX
NCBI GI	g1628622
BLAST score	114
E value	3.0e-15
Match length	93
% identity	48
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	175503
Seq. ID	jC-atXLIB327432P2g10b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	211
E value	1.0e-115
Match length	260
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	175504
Seq. ID	jC-atXLIB327432P2g12b2
Method	BLASTX
NCBI GI	g4220476
BLAST score	280
E value	7.0e-25
Match length	84
% identity	74
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	175505
Seq. ID	jC-atXLIB327432P2h02a1
Method	BLASTN
NCBI GI	g4757399
BLAST score	55
E value	5.0e-22
Match length	267
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	175506
Seq. ID	jC-atXLIB327432P2h03b2

Method	BLASTN
NCBI GI	g4757399
BLAST score	141
E value	3.0e-73
Match length	384
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	175507
Seq. ID	jC-atXLIB327432P2h05b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175508
Seq. ID	jC-atXLIB327432P2h06a1
Method	BLASTN
NCBI GI	g2191126
BLAST score	71
E value	1.0e-31
Match length	130
% identity	91
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	175509
Seq. ID	jC-atXLIB327432P2h06a2
Method	BLASTN
NCBI GI	g2191126
BLAST score	196
E value	1.0e-106
Match length	429
% identity	91
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	175510
Seq. ID	jC-atXLIB327432P2h07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	9.0e-11
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175511
Seq. ID	jC-atXLIB327432P2h07b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	34
E value	2.0e-09
Match length	48

% identity	92
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175512
Seq. ID	jC-atXLIB327432P2h09a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	1.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175513
Seq. ID	jC-atXLIB327432P2h10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	1.0e-16
Match length	70
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175514
Seq. ID	jC-atXLIB327432P3a01a1
Method	BLASTN
NCBI GI	g4589410
BLAST score	50
E value	5.0e-19
Match length	70
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	175515
Seq. ID	jC-atXLIB327432P3a01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	67
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175516
Seq. ID	jC-atXLIB327432P3a05b1
Method	BLASTN
NCBI GI	g1785673
BLAST score	128
E value	2.0e-65
Match length	144
% identity	97
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	175517
Seq. ID	jC-atXLIB327432P3a06b1
Method	BLASTX
NCBI GI	g2108252
BLAST score	133
E value	1.0e-07
Match length	78
% identity	31
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	175518
Seq. ID	jC-atXLIB327432P3a08a1
Method	BLASTN
NCBI GI	g4586024
BLAST score	164
E value	5.0e-87
Match length	333
% identity	70
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic sequence, complete sequence

Seq. No.	175519
Seq. ID	jC-atXLIB327432P3a08b1
Method	BLASTN
NCBI GI	g4586024
BLAST score	126
E value	2.0e-64
Match length	138
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic sequence, complete sequence

Seq. No.	175520
Seq. ID	jC-atXLIB327432P3b07b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	80
E value	7.0e-37
Match length	136
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	175521
Seq. ID	jC-atXLIB327432P3c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175522
Seq. ID	jC-atXLIB327432P3c06b1
Method	BLASTX
NCBI GI	g3281858
BLAST score	273
E value	5.0e-24
Match length	131
% identity	55
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	175523
Seq. ID	jC-atXLIB327432P3d01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	62
E value	4.0e-26
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175524
Seq. ID	jC-atXLIB327432P3d04b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	165
E value	1.0e-87
Match length	361
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	175525
Seq. ID	jC-atXLIB327432P3e08b1
Method	BLASTX
NCBI GI	g4582488
BLAST score	309
E value	3.0e-28
Match length	75
% identity	79
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	175526
Seq. ID	jC-atXLIB327432P3f04b1
Method	BLASTX
NCBI GI	g4314363
BLAST score	608
E value	3.0e-63
Match length	149
% identity	54
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	175527
Seq. ID	jC-atXLIB327432P3h03b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	59
E value	2.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175528
Seq. ID	jC-atXLIB327432P3h06b1
Method	BLASTX
NCBI GI	g829213
BLAST score	474
E value	2.0e-47
Match length	120
% identity	55
NCBI Description	(X81050) beta-tubulin [Naegleria gruberi]

Seq. No.	175529
Seq. ID	jC-atXLIB327432P4a03a1
Method	BLASTN
NCBI GI	g3869067
BLAST score	119
E value	4.0e-60
Match length	245
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	175530
Seq. ID	jC-atXLIB327432P4a06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175531
Seq. ID	jC-atXLIB327432P4a06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175532
Seq. ID	jC-atXLIB327432P4a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	72
% identity	94

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175533
Seq. ID	jC-atXLIB327432P4a10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	60
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175534
Seq. ID	jC-atXLIB327432P4b01a1
Method	BLASTN
NCBI GI	g4760411
BLAST score	142
E value	7.0e-74
Match length	270
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	175535
Seq. ID	jC-atXLIB327432P4b04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175536
Seq. ID	jC-atXLIB327432P4b06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175537
Seq. ID	jC-atXLIB327432P4c04b1
Method	BLASTN
NCBI GI	g2281081
BLAST score	421
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175538
Seq. ID	jC-atXLIB327432P4c07a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175539
Seq. ID	jC-atXLIB327432P4c12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175540
Seq. ID	jC-atXLIB327432P4d01a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	8.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175541
Seq. ID	jC-atXLIB327432P4e05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	3.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175542
Seq. ID	jC-atXLIB327432P4e07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	5.0e-16
Match length	61
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175543
Seq. ID	jC-atXLIB327432P4f01a1
Method	BLASTN
NCBI GI	g2281632
BLAST score	60
E value	6.0e-25
Match length	311

% identity	78
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.4 mRNA, partial cds

Seq. No.	175544
Seq. ID	jC-atXLIB327432P4g05a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175545
Seq. ID	jC-atXLIB327432P4g06a1
Method	BLASTX
NCBI GI	g4559372
BLAST score	219
E value	1.0e-17
Match length	71
% identity	63
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	175546
Seq. ID	jC-atXLIB327432P4g09a1
Method	BLASTX
NCBI GI	g481132
BLAST score	169
E value	9.0e-12
Match length	49
% identity	67
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	175547
Seq. ID	jC-atXLIB327432P4h01a1
Method	BLASTN
NCBI GI	g4220510
BLAST score	168
E value	2.0e-89
Match length	281
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	175548
Seq. ID	jC-atXLIB327432P4h04a1
Method	BLASTN
NCBI GI	g2618602
BLAST score	95
E value	7.0e-46
Match length	158
% identity	94

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	175549
Seq. ID	jC-atXLIB327432P4h06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175550
Seq. ID	jC-atXLIB327432P4h11a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	9.0e-21
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175551
Seq. ID	jC-atXLIB327432P4h12a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	195
E value	1.0e-105
Match length	247
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence
Seq. No.	175552
Seq. ID	jC-atXLIB327433P1b01a1
Method	BLASTN
NCBI GI	g4468976
BLAST score	185
E value	2.0e-99
Match length	261
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)
Seq. No.	175553
Seq. ID	jC-atXLIB327433P1c06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	9.0e-24
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	175554

Seq. ID	jC-atXLIB327433P1c07a1
Method	BLASTN
NCBI GI	g2529657
BLAST score	112
E value	6.0e-56
Match length	196
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175555
Seq. ID	jC-atXLIB327433P1d06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175556
Seq. ID	jC-atXLIB327433P1d07a1
Method	BLASTN
NCBI GI	g4454022
BLAST score	246
E value	1.0e-136
Match length	432
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	175557
Seq. ID	jC-atXLIB327433P1e07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175558
Seq. ID	jC-atXLIB327433P1e09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18
Match length	60
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175559
Seq. ID	jC-atXLIB327433P1f11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18

Match length	48
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175560
Seq. ID	jC-atXLIB327433P1g01a1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	9.0e-15
Match length	66
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175561
Seq. ID	jC-atXLIB327433P1g03a1
Method	BLASTN
NCBI GI	g3869066
BLAST score	105
E value	8.0e-52
Match length	208
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	175562
Seq. ID	jC-atXLIB327433P1g07a1
Method	BLASTN
NCBI GI	g4589435
BLAST score	98
E value	1.0e-47
Match length	174
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	175563
Seq. ID	jC-atXLIB327433P1g08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175564
Seq. ID	jC-atXLIB327433P1h02a1
Method	BLASTN
NCBI GI	g2924651
BLAST score	79
E value	3.0e-36
Match length	119
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	175565
Seq. ID	jC-atXLIB327433P1h06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175566
Seq. ID	jC-atXLIB327433P1h11a1
Method	BLASTN
NCBI GI	g3218549
BLAST score	75
E value	5.0e-34
Match length	79
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for Cdk-activating kinase 1At, complete cds

Seq. No.	175567
Seq. ID	jC-atXLIB327433P2a01a1
Method	BLASTN
NCBI GI	g4662609
BLAST score	121
E value	2.0e-61
Match length	274
% identity	87
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	175568
Seq. ID	jC-atXLIB327433P2a07a1
Method	BLASTN
NCBI GI	g531832
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175569
Seq. ID	jC-atXLIB327433P2a08a1
Method	BLASTN
NCBI GI	g4093156
BLAST score	252
E value	1.0e-139
Match length	356
% identity	93
NCBI Description	Arabidopsis thaliana phytochrome-associated protein 2 (PAP2) mRNA, complete cds

Seq. No.	175570
Seq. ID	jC-atXLIB327433P2c02a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175571
Seq. ID	jC-atXLIB327433P2c06a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175572
Seq. ID	jC-atXLIB327433P2c07a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175573
Seq. ID	jC-atXLIB327433P2d03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175574
Seq. ID	jC-atXLIB327433P2d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175575
Seq. ID	jC-atXLIB327433P2e02a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175576
Seq. ID	jC-atXLIB327433P2e03a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	2.0e-21
Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175577
Seq. ID	jC-atXLIB327433P2e07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175578
Seq. ID	jC-atXLIB327433P2f03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	61
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175579
Seq. ID	jC-atXLIB327433P2f11a1
Method	BLASTN
NCBI GI	g4159703
BLAST score	61
E value	1.0e-25
Match length	251
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	175580
Seq. ID	jC-atXLIB327433P3e04a1
Method	BLASTN
NCBI GI	g3445196
BLAST score	44
E value	1.0e-15
Match length	155
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175581
Seq. ID	jC-atXLIB327433P3f10b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	48
E value	9.0e-18
Match length	55
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175582
Seq. ID	jC-atXLIB327437P2a05b2
Method	BLASTX
NCBI GI	g2760086
BLAST score	100
E value	6.0e-17
Match length	59
% identity	52
NCBI Description	(Y16046) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	175583
Seq. ID	jC-atXLIB327437P2a06a2
Method	BLASTN
NCBI GI	g2760085
BLAST score	65
E value	5.0e-28
Match length	342
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for leucine rich repeat protein (G8B7T7)

Seq. No.	175584
Seq. ID	jC-atXLIB327437P2a07b2
Method	BLASTN
NCBI GI	g540252
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	175585
Seq. ID	jC-atXLIB327437P2a11b2
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	5.0e-18
Match length	67
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175586
Seq. ID	jC-atXLIB327437P2a12b2
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	4.0e-17
Match length	63
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175587
Seq. ID	jC-atXLIB327437P2b03a2
Method	BLASTN
NCBI GI	g2582640
BLAST score	43
E value	9.0e-15
Match length	51
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175588
Seq. ID	jC-atXLIB327437P2b03b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175589
Seq. ID	jC-atXLIB327437P2b04a1
Method	BLASTX
NCBI GI	g643469
BLAST score	201
E value	1.0e-15
Match length	58
% identity	60
NCBI Description	(U19886) unknown [Lycopersicon esculentum]

Seq. No.	175590
Seq. ID	jC-atXLIB327437P2b05b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	136
E value	3.0e-70
Match length	394
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	175591
Seq. ID	jC-atXLIB327437P2b06a2
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175592
Seq. ID	jC-atXLIB327437P2b06b2
Method	BLASTN

NCBI GI	g531828
BLAST score	48
E value	9.0e-18
Match length	59
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175593
Seq. ID	jC-atXLIB327437P2b07a2
Method	BLASTX
NCBI GI	g4759100
BLAST score	149
E value	2.0e-09
Match length	144
% identity	18
NCBI Description	splicing factor, arginine/serine-rich 11 >gi_105148_pir__A40988 54K arginine-rich nuclear protein - human >gi_178997 (M74002) arginine-rich nuclear protein [Homo sapiens]

Seq. No.	175594
Seq. ID	jC-atXLIB327437P2b10a2
Method	BLASTN
NCBI GI	g3800746
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	175595
Seq. ID	jC-atXLIB327437P2b12a2
Method	BLASTN
NCBI GI	g3241917
BLAST score	80
E value	7.0e-37
Match length	206
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	175596
Seq. ID	jC-atXLIB327437P2c01b2
Method	BLASTN
NCBI GI	g3449334
BLAST score	102
E value	5.0e-50
Match length	328
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	175597
Seq. ID	jC-atXLIB327437P2c02b2
Method	BLASTN
NCBI GI	g2462264

BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175598
Seq. ID	jC-atXLIB327437P2c04b2
Method	BLASTN
NCBI GI	g2290120
BLAST score	48
E value	9.0e-18
Match length	59
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175599
Seq. ID	jC-atXLIB327437P2c07b1
Method	BLASTN
NCBI GI	g4539309
BLAST score	96
E value	1.0e-46
Match length	151
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	175600
Seq. ID	jC-atXLIB327437P2c10a2
Method	BLASTN
NCBI GI	g3941523
BLAST score	42
E value	3.0e-14
Match length	46
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175601
Seq. ID	jC-atXLIB327437P2c11a2
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	8.0e-09
Match length	45
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175602
Seq. ID	jC-atXLIB327437P2d01b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	52

% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175603
Seq. ID	jC-atXLIB327437P2d05a2
Method	BLASTN
NCBI GI	g3941523
BLAST score	35
E value	6.0e-10
Match length	47
% identity	94
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175604
Seq. ID	jC-atXLIB327437P2d12a2
Method	BLASTN
NCBI GI	g3241917
BLAST score	63
E value	9.0e-27
Match length	187
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	175605
Seq. ID	jC-atXLIB327437P2d12b2
Method	BLASTN
NCBI GI	g531828
BLAST score	44
E value	2.0e-15
Match length	55
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175606
Seq. ID	jC-atXLIB327437P2f01a2
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	7.0e-17
Match length	50
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175607
Seq. ID	jC-atXLIB327437P2f01b2
Method	BLASTX
NCBI GI	g1872521
BLAST score	491
E value	2.0e-49
Match length	99
% identity	70
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	175608
Seq. ID	jC-atXLIB327437P2f03a1
Method	BLASTN
NCBI GI	g3132469
BLAST score	53
E value	9.0e-21
Match length	107
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175609
Seq. ID	jC-atXLIB327437P2f03b2
Method	BLASTN
NCBI GI	g3132469
BLAST score	84
E value	3.0e-39
Match length	307
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175610
Seq. ID	jC-atXLIB327437P2f07a1
Method	BLASTX
NCBI GI	g3688191
BLAST score	481
E value	2.0e-48
Match length	136
% identity	73
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	175611
Seq. ID	jC-atXLIB327437P2f10b2
Method	BLASTX
NCBI GI	g2133919
BLAST score	143
E value	1.0e-08
Match length	132
% identity	33
NCBI Description	neurofilament medium protein - goldfish >gi_213020 (L09742) [Carassius auratus gene, complete cds.], gene product [Carassius auratus]

Seq. No.	175612
Seq. ID	jC-atXLIB327437P2f12b2
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175613

Seq. ID	jC-atXLIB327437P2g01a2
Method	BLASTN
NCBI GI	g2582640
BLAST score	33
E value	8.0e-09
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175614
Seq. ID	jC-atXLIB327437P2g01b2
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	5.0e-10
Match length	43
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175615
Seq. ID	jC-atXLIB327437P2g04a2
Method	BLASTN
NCBI GI	g4191771
BLAST score	35
E value	5.0e-10
Match length	109
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175616
Seq. ID	jC-atXLIB327437P2g04b2
Method	BLASTN
NCBI GI	g4191771
BLAST score	48
E value	9.0e-18
Match length	239
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175617
Seq. ID	jC-atXLIB327437P2g12a2
Method	BLASTN
NCBI GI	g3241917
BLAST score	85
E value	6.0e-40
Match length	173
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	175618
Seq. ID	jC-atXLIB327437P2h02a1
Method	BLASTN
NCBI GI	g4741959

BLAST score	70
E value	6.0e-31
Match length	239
% identity	85
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	175619
Seq. ID	jC-atXLIB327437P2h04b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175620
Seq. ID	jC-atXLIB327437P2h08a2
Method	BLASTN
NCBI GI	g2582640
BLAST score	35
E value	5.0e-10
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175621
Seq. ID	jC-atXLIB327437P2h08b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175622
Seq. ID	jC-atXLIB327437P2h11b2
Method	BLASTN
NCBI GI	g2290120
BLAST score	34
E value	2.0e-09
Match length	46
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175623
Seq. ID	jC-atXLIB327437P3a02a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	2.0e-15
Match length	60
% identity	95

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	175624
Seq. ID	jC-atXLIB327437P3a02b3
Method	BLASTX
NCBI GI	g3402672
BLAST score	438
E value	2.0e-43
Match length	142
% identity	68
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]
Seq. No.	175625
Seq. ID	jC-atXLIB327437P3a08a2
Method	BLASTN
NCBI GI	g3402671
BLAST score	50
E value	4.0e-19
Match length	90
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	175626
Seq. ID	jC-atXLIB327437P3a12a2
Method	BLASTX
NCBI GI	g1946367
BLAST score	392
E value	6.0e-38
Match length	131
% identity	64
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]
Seq. No.	175627
Seq. ID	jC-atXLIB327437P3b02b2
Method	BLASTN
NCBI GI	g2244788
BLAST score	70
E value	2.0e-31
Match length	78
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	175628
Seq. ID	jC-atXLIB327437P3b06a1
Method	BLASTN
NCBI GI	g4557061
BLAST score	191
E value	1.0e-103
Match length	199
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence
Seq. No.	175629

Seq. ID	jC-atXLIB327437P3b08b2
Method	BLASTX
NCBI GI	g3402689
BLAST score	494
E value	7.0e-50
Match length	99
% identity	96
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	175630
Seq. ID	jC-atXLIB327437P3b10b3
Method	BLASTN
NCBI GI	g4757413
BLAST score	154
E value	5.0e-81
Match length	376
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	175631
Seq. ID	jC-atXLIB327437P3d01a2
Method	BLASTX
NCBI GI	g2493144
BLAST score	292
E value	3.0e-26
Match length	146
% identity	37
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	175632
Seq. ID	jC-atXLIB327437P3d04a2
Method	BLASTX
NCBI GI	g464711
BLAST score	99
E value	5.0e-21
Match length	84
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN S15A (YS24) >gi_320167_pir__S30003 ribosomal protein S15a.e - yeast (Kluyveromyces marxianus) >gi_263484_bbs_122433 (S53434) S24-1=ribosomal protein [Kluyveromyces marxianus, Peptide, 130 aa] [Kluyveromyces marxianus]

Seq. No.	175633
Seq. ID	jC-atXLIB327437P3d12a1
Method	BLASTX
NCBI GI	g1710530
BLAST score	385
E value	4.0e-37
Match length	144
% identity	60

NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]
Seq. No.	175634
Seq. ID	jC-atXLIB327437P3e01a2
Method	BLASTN
NCBI GI	g4581084
BLAST score	119
E value	3.0e-60
Match length	274
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	175635
Seq. ID	jC-atXLIB327437P3e07a2
Method	BLASTX
NCBI GI	g2373401
BLAST score	147
E value	3.0e-09
Match length	63
% identity	54
NCBI Description	(D85192) transmembrane protein [Arabidopsis thaliana]
Seq. No.	175636
Seq. ID	jC-atXLIB327437P3e07b3
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	2.0e-10
Match length	61
% identity	90
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175637
Seq. ID	jC-atXLIB327437P3f08a1
Method	BLASTX
NCBI GI	g444790
BLAST score	293
E value	4.0e-36
Match length	101
% identity	83
NCBI Description	nucleotide translocator [Arabidopsis thaliana]
Seq. No.	175638
Seq. ID	jC-atXLIB327437P3f10b3
Method	BLASTN
NCBI GI	g540252
BLAST score	36
E value	1.0e-10
Match length	62
% identity	90
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.	175639

Seq. ID	jC-atXLIB327437P3f12a2
Method	BLASTX
NCBI GI	g1710530
BLAST score	68
E value	2.0e-25
Match length	109
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	175640
Seq. ID	jC-atXLIB327437P3g11a2
Method	BLASTN
NCBI GI	g1086462
BLAST score	35
E value	2.0e-10
Match length	55
% identity	91
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT2b) gene, complete cds

Seq. No.	175641
Seq. ID	jC-atXLIB327437P3g12a2
Method	BLASTN
NCBI GI	g2564046
BLAST score	101
E value	2.0e-49
Match length	186
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	175642
Seq. ID	jC-atXLIB327437P3h08a2
Method	BLASTX
NCBI GI	g444790
BLAST score	188
E value	1.0e-16
Match length	70
% identity	73
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	175643
Seq. ID	jC-atXLIB327437P3h10a2
Method	BLASTX
NCBI GI	g543751
BLAST score	176
E value	1.0e-12
Match length	55
% identity	67
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir__JT0755 ethylene-forming enzyme - Arabidopsis thaliana >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme [Arabidopsis thaliana]

Seq. No.	175644
Seq. ID	jC-atXLIB327437P3h11a1
Method	BLASTX
NCBI GI	g4056424
BLAST score	63
E value	4.0e-29
Match length	77
% identity	76
NCBI Description	(AC005322) Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb_X66719 (EAT1). ESTs gb_T43073, gb_T5714, gb_R90435, gb_R44023, gb_AA597926, gb_AI099676, gb_AA650810 and gb_29725 come from this gene. [Arabidopsis thaliana]

Seq. No.	175645
Seq. ID	jC-atXLIB327437P3h12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	9.0e-18
Match length	55
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175646
Seq. ID	jC-atXLIB327437P4a03a2
Method	BLASTN
NCBI GI	g3402671
BLAST score	43
E value	8.0e-15
Match length	75
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175647
Seq. ID	jC-atXLIB327437P4a06b2
Method	BLASTN
NCBI GI	g3800746
BLAST score	47
E value	2.0e-17
Match length	47
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	175648
Seq. ID	jC-atXLIB327437P4a10a2
Method	BLASTN
NCBI GI	g4757413
BLAST score	173
E value	2.0e-92
Match length	335
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	175649
Seq. ID	jC-atXLIB327437P4a10b2
Method	BLASTN
NCBI GI	g4757413
BLAST score	107
E value	3.0e-53
Match length	187
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	175650
Seq. ID	jC-atXLIB327437P4b01b2
Method	BLASTN
NCBI GI	g3386593
BLAST score	206
E value	1.0e-112
Match length	206
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175651
Seq. ID	jC-atXLIB327437P4b02b2
Method	BLASTN
NCBI GI	g3985932
BLAST score	93
E value	7.0e-45
Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	175652
Seq. ID	jC-atXLIB327437P4b12a2
Method	BLASTX
NCBI GI	g131398
BLAST score	537
E value	6.0e-55
Match length	136
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	175653
Seq. ID	jC-atXLIB327437P4c01a2
Method	BLASTN
NCBI GI	g3386593
BLAST score	332

E value	0.0e+00
Match length	415
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175654
Seq. ID	jC-atXLIB327437P4c02a2
Method	BLASTX
NCBI GI	g3402672
BLAST score	160
E value	9.0e-11
Match length	90
% identity	43
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]

Seq. No.	175655
Seq. ID	jC-atXLIB327437P4d02a2
Method	BLASTX
NCBI GI	g3287862
BLAST score	313
E value	1.0e-28
Match length	73
% identity	84
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]

Seq. No.	175656
Seq. ID	jC-atXLIB327437P4d06b2
Method	BLASTX
NCBI GI	g2353173
BLAST score	158
E value	4.0e-11
Match length	47
% identity	68
NCBI Description	(AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No.	175657
Seq. ID	jC-atXLIB327437P4e05a2
Method	BLASTX
NCBI GI	g2252830
BLAST score	319
E value	2.0e-29
Match length	402
% identity	54
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	175658
Seq. ID	jC-atXLIB327437P4e06a2
Method	BLASTX
NCBI GI	g2252830
BLAST score	382
E value	9.0e-37
Match length	130
% identity	65

NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	175659
Seq. ID	jC-atXLIB327437P4e06b2
Method	BLASTN
NCBI GI	g2252823
BLAST score	119
E value	2.0e-60
Match length	189
% identity	90
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	175660
Seq. ID	jC-atXLIB327437P4e07a2
Method	BLASTX
NCBI GI	g1175012
BLAST score	86
E value	5.1e-02
Match length	136
% identity	62
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	175661
Seq. ID	jC-atXLIB327437P4f01a2
Method	BLASTN
NCBI GI	g4581084
BLAST score	250
E value	1.0e-138
Match length	327
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	175662
Seq. ID	jC-atXLIB327437P4f02a2
Method	BLASTN
NCBI GI	g2288979
BLAST score	145
E value	1.0e-75
Match length	193
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175663
Seq. ID	jC-atXLIB327437P4f04a2
Method	BLASTN
NCBI GI	g2150129
BLAST score	48
E value	7.0e-18
Match length	135
% identity	84
NCBI Description	Arabidopsis thaliana cytoplasmic ribosomal protein S15a mRNA, complete cds

Seq. No.	175664
Seq. ID	jC-atXLIB327437P4f05a2
Method	BLASTX
NCBI GI	g4585881
BLAST score	128
E value	4.0e-14
Match length	96
% identity	44
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	175665
Seq. ID	jC-atXLIB327437P4g11b2
Method	BLASTN
NCBI GI	g2494106
BLAST score	94
E value	2.0e-45
Match length	167
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175666
Seq. ID	jC-atXLIB327437P4h06b2
Method	BLASTX
NCBI GI	g4759160
BLAST score	139
E value	1.0e-08
Match length	71
% identity	42
NCBI Description	small nuclear ribonucleoprotein D3 polypeptide (18kD) >gi_1173456_sp_P43331_SMD3_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	175667
Seq. ID	jC-atXLIB327438P1a01a1
Method	BLASTX
NCBI GI	g1076416
BLAST score	206
E value	4.0e-16
Match length	140
% identity	40
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]

Seq. No.	175668
Seq. ID	jC-atXLIB327438P1a02a1
Method	BLASTX
NCBI GI	g3834312
BLAST score	143
E value	2.0e-27
Match length	174
% identity	49

NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an

Seq. No.	175669
Seq. ID	jC-atXLIB327438P1a07a1
Method	BLASTX
NCBI GI	g1174718
BLAST score	438
E value	2.0e-43
Match length	123
% identity	68
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	175670
Seq. ID	jC-atXLIB327438P1b02a1
Method	BLASTX
NCBI GI	g552857
BLAST score	172
E value	8.0e-13
Match length	46
% identity	74
NCBI Description	(M31464) atpB gene product [Oryza sativa]

Seq. No.	175671
Seq. ID	jC-atXLIB327438P1b09a1
Method	BLASTX
NCBI GI	g1944518
BLAST score	666
E value	6.0e-70
Match length	125
% identity	99
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	175672
Seq. ID	jC-atXLIB327438P1c02a1
Method	BLASTN
NCBI GI	g531832
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175673
Seq. ID	jC-atXLIB327438P1c05a1
Method	BLASTX
NCBI GI	g4725946
BLAST score	322
E value	9.0e-30

Match length	69
% identity	91
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana]

Seq. No.	175674
Seq. ID	jC-atXLIB327438P1c06a1
Method	BLASTN
NCBI GI	g3738313
BLAST score	64
E value	3.0e-27
Match length	154
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175675
Seq. ID	jC-atXLIB327438P1c12a1
Method	BLASTX
NCBI GI	g3123188
BLAST score	267
E value	1.0e-72
Match length	149
% identity	86
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	175676
Seq. ID	jC-atXLIB327438P1d02a1
Method	BLASTN
NCBI GI	g3449331
BLAST score	129
E value	2.0e-66
Match length	236
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	175677
Seq. ID	jC-atXLIB327438P1d05a1
Method	BLASTN
NCBI GI	g3928074
BLAST score	328
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175678
Seq. ID	jC-atXLIB327438P1e05a1
Method	BLASTN
NCBI GI	g4388816
BLAST score	69
E value	3.0e-30
Match length	133
% identity	91

NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175679
Seq. ID	jC-atXLIB327438P1e07a1
Method	BLASTX
NCBI GI	g1103322
BLAST score	283
E value	4.0e-25
Match length	114
% identity	56
NCBI Description	(X78820) casein kinase I [Arabidopsis thaliana]

Seq. No.	175680
Seq. ID	jC-atXLIB327438P1e09a1
Method	BLASTX
NCBI GI	g3434967
BLAST score	447
E value	2.0e-44
Match length	107
% identity	83
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	175681
Seq. ID	jC-atXLIB327438P1e12a1
Method	BLASTX
NCBI GI	g417383
BLAST score	281
E value	5.0e-25
Match length	64
% identity	89
NCBI Description	NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958) nitrilase [Arabidopsis thaliana]

Seq. No.	175682
Seq. ID	jC-atXLIB327438P1f03a1
Method	BLASTN
NCBI GI	g16440
BLAST score	44
E value	1.0e-15
Match length	52
% identity	96
NCBI Description	A.thaliana PRKase gene for Ribulose-5-phosphate kinase

Seq. No.	175683
Seq. ID	jC-atXLIB327438P1h05a1
Method	BLASTX
NCBI GI	g4510348
BLAST score	360
E value	3.0e-34
Match length	155
% identity	48
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	175684
Seq. ID	jC-atXLIB327438P1h06a1
Method	BLASTN
NCBI GI	g2245377
BLAST score	322
E value	0.0e+00
Match length	399
% identity	95
NCBI Description	Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA, complete cds

Seq. No.	175685
Seq. ID	jC-atXLIB327438P1h10a1
Method	BLASTN
NCBI GI	g4519191
BLAST score	97
E value	5.0e-47
Match length	317
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	175686
Seq. ID	jC-atXLIB327438P1h11a1
Method	BLASTN
NCBI GI	g258157
BLAST score	46
E value	1.0e-16
Match length	62
% identity	94
NCBI Description	psbD=reaction center protein D2 {5'region} [peas, Chloroplast, 90 nt]

Seq. No.	175687
Seq. ID	jC-atXLIB327438P2a03a1
Method	BLASTN
NCBI GI	g3176695
BLAST score	133
E value	1.0e-68
Match length	187
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	175688
Seq. ID	jC-atXLIB327438P2b04a1
Method	BLASTX
NCBI GI	g1813887
BLAST score	207
E value	3.0e-16
Match length	110
% identity	54
NCBI Description	(Y10864) hypothetical protein (cDNA194) [Arabidopsis thaliana] >gi_1834355_emb_CAA71880_ (Y10987) hypothetical protein 194 [Arabidopsis thaliana]

Seq. No.	175689
Seq. ID	jC-atXLIB327438P2b09a1
Method	BLASTX
NCBI GI	g4455214
BLAST score	108
E value	5.0e-57
Match length	142
% identity	94
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	175690
Seq. ID	jC-atXLIB327438P2c03a1
Method	BLASTN
NCBI GI	g3269280
BLAST score	92
E value	5.0e-44
Match length	120
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	175691
Seq. ID	jC-atXLIB327438P2c09a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	232
E value	1.0e-127
Match length	309
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	175692
Seq. ID	jC-atXLIB327438P2c10a1
Method	BLASTX
NCBI GI	g1170028
BLAST score	516
E value	2.0e-64
Match length	146
% identity	80
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	175693
Seq. ID	jC-atXLIB327438P2d01a1
Method	BLASTX
NCBI GI	g3164126
BLAST score	446
E value	2.0e-44
Match length	122
% identity	74
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	175694
Seq. ID	jC-atXLIB327438P2d07a1
Method	BLASTN
NCBI GI	g2264304
BLAST score	201
E value	1.0e-109
Match length	379
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	175695
Seq. ID	jC-atXLIB327438P2e05a1
Method	BLASTN
NCBI GI	g2696018
BLAST score	44
E value	2.0e-15
Match length	112
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	175696
Seq. ID	jC-atXLIB327438P2e12a1
Method	BLASTX
NCBI GI	g3415117
BLAST score	690
E value	6.0e-73
Match length	146
% identity	49
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	175697
Seq. ID	jC-atXLIB327438P2f03a1
Method	BLASTN
NCBI GI	g304040
BLAST score	276
E value	1.0e-154
Match length	396
% identity	93
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	175698
Seq. ID	jC-atXLIB327438P2f04a1
Method	BLASTX
NCBI GI	g2924779
BLAST score	331
E value	9.0e-31
Match length	157
% identity	54
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	175699
Seq. ID	jC-atXLIB327438P2f06a1
Method	BLASTN
NCBI GI	g4585890
BLAST score	125
E value	1.0e-63
Match length	253
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	175700
Seq. ID	jC-atXLIB327438P2g01a1
Method	BLASTX
NCBI GI	g4406816
BLAST score	504
E value	5.0e-51
Match length	96
% identity	96
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	175701
Seq. ID	jC-atXLIB327438P2g03a1
Method	BLASTN
NCBI GI	g2618683
BLAST score	38
E value	6.0e-12
Match length	86
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175702
Seq. ID	jC-atXLIB327438P2h01a1
Method	BLASTX
NCBI GI	g2829862
BLAST score	179
E value	6.0e-13
Match length	123
% identity	43
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	175703
Seq. ID	jC-atXLIB327438P2h06a1
Method	BLASTN
NCBI GI	g4406805
BLAST score	93
E value	1.0e-44
Match length	145
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175704
Seq. ID	jC-atXLIB327438P2h09a1
Method	BLASTN

NCBI GI	g4519191
BLAST score	97
E value	5.0e-47
Match length	243
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	175705
Seq. ID	jC-atXLIB327438P2h10a1
Method	BLASTN
NCBI GI	g972910
BLAST score	148
E value	2.0e-77
Match length	335
% identity	88
NCBI Description	Arabidopsis thaliana IAA3 (IAA3) gene, complete cds

Seq. No.	175706
Seq. ID	jC-atXLIB327438P3a02a2
Method	BLASTN
NCBI GI	g3859840
BLAST score	334
E value	0.0e+00
Match length	420
% identity	95
NCBI Description	Plastid transformation vector pGS31A 16S ribosomal RNA gene, partial sequence; aminoglycoside 3'-adenyltransferase (aadA) gene, complete cds

Seq. No.	175707
Seq. ID	jC-atXLIB327438P3a04a2
Method	BLASTN
NCBI GI	g4490324
BLAST score	68
E value	7.0e-30
Match length	169
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	175708
Seq. ID	jC-atXLIB327438P3a09a2
Method	BLASTN
NCBI GI	g4704539
BLAST score	36
E value	1.0e-10
Match length	165
% identity	86
NCBI Description	Alluaudiopsis marnieriana ribosomal protein L16 (rpl16) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.	175709
Seq. ID	jC-atXLIB327438P3a09b1
Method	BLASTX
NCBI GI	g132714

BLAST score	235
E value	2.0e-19
Match length	92
% identity	54
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 (RIBOSOMAL PROTEIN CS-L24) >gi_71248_pir__R5SP16 ribosomal protein L16 - spinach chloroplast >gi_12311_emb_CAA31716_ (X13336) ribosomal protein L16 [Spinacia oleracea]

Seq. No.	175710
Seq. ID	jC-atXLIB327438P3a11a2
Method	BLASTX
NCBI GI	g120675
BLAST score	451
E value	1.0e-55
Match length	147
% identity	80
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	175711
Seq. ID	jC-atXLIB327438P3b07a2
Method	BLASTN
NCBI GI	g2262097
BLAST score	248
E value	1.0e-137
Match length	380
% identity	92
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	175712
Seq. ID	jC-atXLIB327438P3b10b1
Method	BLASTN
NCBI GI	g540252
BLAST score	35
E value	5.0e-10
Match length	35
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	175713
Seq. ID	jC-atXLIB327438P3b11b1
Method	BLASTX
NCBI GI	g4580467
BLAST score	201
E value	2.0e-15
Match length	69
% identity	55
NCBI Description	(AC006081) putative protein phosphatase; similar to protein phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]

Seq. No.	175714
Seq. ID	jC-atXLIB327438P3b12a2

Method	BLASTN
NCBI GI	g3702736
BLAST score	195
E value	1.0e-105
Match length	411
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	175715
Seq. ID	jC-atXLIB327438P3c04a2
Method	BLASTN
NCBI GI	g3600029
BLAST score	170
E value	1.0e-90
Match length	399
% identity	87
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	175716
Seq. ID	jC-atXLIB327438P3c04b1
Method	BLASTN
NCBI GI	g430946
BLAST score	34
E value	2.0e-09
Match length	50
% identity	92
NCBI Description	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds

Seq. No.	175717
Seq. ID	jC-atXLIB327438P3c09a2
Method	BLASTX
NCBI GI	g2146746
BLAST score	270
E value	1.0e-23
Match length	99
% identity	57
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	175718
Seq. ID	jC-atXLIB327438P3c09b1
Method	BLASTN
NCBI GI	g166818
BLAST score	173
E value	2.0e-92
Match length	241
% identity	93
NCBI Description	Arabidopsis thaliana protein kinase mRNA, complete cds

Seq. No.	175719
Seq. ID	jC-atXLIB327438P3d07b1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	2.0e-11

Match length	62
% identity	90
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175720
Seq. ID	jC-atXLIB327438P3e01a2
Method	BLASTX
NCBI GI	g3790569
BLAST score	603
E value	1.0e-62
Match length	145
% identity	82
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	175721
Seq. ID	jC-atXLIB327438P3e03a2
Method	BLASTX
NCBI GI	g1172872
BLAST score	166
E value	2.0e-11
Match length	151
% identity	26
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	175722
Seq. ID	jC-atXLIB327438P3f02a2
Method	BLASTX
NCBI GI	g131143
BLAST score	543
E value	1.0e-55
Match length	136
% identity	76
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]

Seq. No.	175723
Seq. ID	jC-atXLIB327438P3f03a2
Method	BLASTX
NCBI GI	g3913733
BLAST score	280
E value	8.0e-25
Match length	137
% identity	31
NCBI Description	HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME (GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana]

Seq. No.	175724
Seq. ID	jC-atXLIB327438P3f03b1
Method	BLASTN
NCBI GI	g2570341
BLAST score	33
E value	7.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana glyoxalase II cytoplasmic isozyme (Glx2-2) mRNA, complete cds

Seq. No.	175725
Seq. ID	jC-atXLIB327438P3f06a2
Method	BLASTN
NCBI GI	g4165340
BLAST score	110
E value	8.0e-55
Match length	246
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175726
Seq. ID	jC-atXLIB327438P3f09a2
Method	BLASTX
NCBI GI	g4455210
BLAST score	249
E value	3.0e-21
Match length	63
% identity	76
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	175727
Seq. ID	jC-atXLIB327438P3g07a2
Method	BLASTX
NCBI GI	g4206789
BLAST score	352
E value	3.0e-33
Match length	107
% identity	69
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	175728
Seq. ID	jC-atXLIB327438P3g08b1
Method	BLASTN
NCBI GI	g2980787
BLAST score	40
E value	4.0e-13
Match length	132
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	175729
Seq. ID	jC-atXLIB327438P3h02a2

Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	5.0e-19
Match length	54
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175730
Seq. ID	jC-atXLIB327438P3h03a2
Method	BLASTX
NCBI GI	g2507455
BLAST score	271
E value	1.0e-23
Match length	91
% identity	55
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	175731
Seq. ID	jC-atXLIB327438P3h04b1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	8.0e-18
Match length	67
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175732
Seq. ID	jC-atXLIB327438P3h06b1
Method	BLASTX
NCBI GI	g4406816
BLAST score	508
E value	2.0e-51
Match length	139
% identity	80
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	175733
Seq. ID	jC-atXLIB327438P3h12a2
Method	BLASTX
NCBI GI	g2104536
BLAST score	241
E value	3.0e-20
Match length	47
% identity	85
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	175734
Seq. ID	jC-atXLIB327438P4a06a2
Method	BLASTN

NCBI GI	g2924653
BLAST score	109
E value	3.0e-54
Match length	285
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	175735
Seq. ID	jC-atXLIB327438P4a08a2
Method	BLASTX
NCBI GI	g4572672
BLAST score	185
E value	2.0e-33
Match length	135
% identity	62
NCBI Description	(AC006954) hypothetical protein [Arabidopsis thaliana]

Seq. No.	175736
Seq. ID	jC-atXLIB327438P4a10a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	34
E value	2.0e-09
Match length	49
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175737
Seq. ID	jC-atXLIB327438P4a12a2
Method	BLASTX
NCBI GI	g2078298
BLAST score	246
E value	7.0e-21
Match length	127
% identity	47
NCBI Description	(U97257) glyceraldehyde 3-phosphate dehydrogenase [Lycopersicon esculentum]

Seq. No.	175738
Seq. ID	jC-atXLIB327438P4b02a2
Method	BLASTX
NCBI GI	g2352492
BLAST score	579
E value	6.0e-76
Match length	149
% identity	95
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	175739
Seq. ID	jC-atXLIB327438P4b07a2
Method	BLASTN
NCBI GI	g3335331
BLAST score	80

E value	7.0e-37
Match length	128
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175740
Seq. ID	jC-atXLIB327438P4b08a2
Method	BLASTN
NCBI GI	g4006815
BLAST score	103
E value	1.0e-50
Match length	417
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175741
Seq. ID	jC-atXLIB327438P4b12a2
Method	BLASTX
NCBI GI	g2194138
BLAST score	73
E value	8.0e-12
Match length	141
% identity	33
NCBI Description	(AC002062) Similar to Arabidopsis receptor-like protein kinase precursor (gb_M84659). [Arabidopsis thaliana]

Seq. No.	175742
Seq. ID	jC-atXLIB327438P4c02a2
Method	BLASTN
NCBI GI	g3869070
BLAST score	175
E value	1.0e-93
Match length	258
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No.	175743
Seq. ID	jC-atXLIB327438P4c05a2
Method	BLASTN
NCBI GI	g3510343
BLAST score	21
E value	1.1e-01
Match length	188
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	175744
Seq. ID	jC-atXLIB327438P4c06a2
Method	BLASTX
NCBI GI	g3819710
BLAST score	139
E value	5.0e-23
Match length	83

% identity	58
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	175745
Seq. ID	jC-atXLIB327438P4c09b2
Method	BLASTX
NCBI GI	g2739046
BLAST score	184
E value	1.0e-13
Match length	69
% identity	51
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	175746
Seq. ID	jC-atXLIB327438P4d03a2
Method	BLASTX
NCBI GI	g1705794
BLAST score	164
E value	3.0e-11
Match length	80
% identity	53
NCBI Description	HEAT SHOCK PROTEIN 60 PRECURSOR (ANTIGEN HIS-62)

Seq. No.	175747
Seq. ID	jC-atXLIB327438P4e02a2
Method	BLASTN
NCBI GI	g2832689
BLAST score	330
E value	0.0e+00
Match length	439
% identity	43
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	175748
Seq. ID	jC-atXLIB327438P4e07a2
Method	BLASTX
NCBI GI	g1771160
BLAST score	168
E value	8.0e-12
Match length	112
% identity	40
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	175749
Seq. ID	jC-atXLIB327438P4e10a2
Method	BLASTX
NCBI GI	g3288821
BLAST score	206
E value	4.0e-16
Match length	104
% identity	48
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	175750
Seq. ID	jC-atXLIB327438P4e12a2
Method	BLASTX
NCBI GI	g1352463
BLAST score	734
E value	5.0e-78
Match length	142
% identity	100
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	175751
Seq. ID	jC-atXLIB327438P4f03a2
Method	BLASTN
NCBI GI	g3687221
BLAST score	57
E value	4.0e-23
Match length	383
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175752
Seq. ID	jC-atXLIB327438P4f06a2
Method	BLASTN
NCBI GI	g2924734
BLAST score	61
E value	2.0e-25
Match length	177
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	175753
Seq. ID	jC-atXLIB327438P4f07a2
Method	BLASTX
NCBI GI	g208092
BLAST score	228
E value	1.0e-18
Match length	128
% identity	38
NCBI Description	(M11334) synthetic calmodulin [Artificial gene] >gi_208412 (M26151) camodulin [Artificial sequence]

Seq. No.	175754
Seq. ID	jC-atXLIB327438P4f08a2
Method	BLASTX
NCBI GI	g4455169
BLAST score	338
E value	1.0e-31
Match length	154
% identity	50

NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	175755
Seq. ID	jC-atXLIB327438P4f09a2
Method	BLASTN
NCBI GI	g4159706
BLAST score	36
E value	9.0e-11
Match length	132
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	175756
Seq. ID	jC-atXLIB327438P4g04a2
Method	BLASTN
NCBI GI	g3859658
BLAST score	48
E value	8.0e-18
Match length	80
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	175757
Seq. ID	jC-atXLIB327438P4g06a2
Method	BLASTN
NCBI GI	g2351069
BLAST score	54
E value	2.0e-21
Match length	120
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	175758
Seq. ID	jC-atXLIB327438P4g08a2
Method	BLASTX
NCBI GI	g1169598
BLAST score	268
E value	2.0e-23
Match length	94
% identity	60
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	175759
Seq. ID	jC-atXLIB327438P4g10a2
Method	BLASTX
NCBI GI	g3288821
BLAST score	79
E value	3.0e-10
Match length	68
% identity	54
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]
>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	175760
Seq. ID	jC-atXLIB327438P4g12a2
Method	BLASTX
NCBI GI	g2160175
BLAST score	473
E value	2.0e-47
Match length	126
% identity	75
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	175761
Seq. ID	jC-atXLIB327438P4h06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	3.0e-17
Match length	79
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175762
Seq. ID	jC-atXLIB327438P4h11a2
Method	BLASTN
NCBI GI	g3386593
BLAST score	53
E value	8.0e-21
Match length	222
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175763
Seq. ID	jC-atXLIB327439P1a06a1
Method	BLASTN
NCBI GI	g693691
BLAST score	53
E value	9.0e-21
Match length	105
% identity	89
NCBI Description	Arabidopsis thaliana aspartate aminotransferase (Asp3) mRNA, complete cds

Seq. No.	175764
Seq. ID	jC-atXLIB327439P1b03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175765
Seq. ID	jC-atXLIB327439P1b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175766
Seq. ID	jC-atXLIB327439P1b06a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	9.0e-21
Match length	61
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175767
Seq. ID	jC-atXLIB327439P1b06a2
Method	BLASTX
NCBI GI	g1703478
BLAST score	274
E value	4.0e-24
Match length	132
% identity	50
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	175768
Seq. ID	jC-atXLIB327439P1b07a1
Method	BLASTX
NCBI GI	g3123271
BLAST score	193
E value	1.0e-14
Match length	84
% identity	56
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	175769
Seq. ID	jC-atXLIB327439P1b07a2
Method	BLASTX
NCBI GI	g3123271
BLAST score	324
E value	6.0e-30
Match length	89
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	175770
Seq. ID	jC-atXLIB327439P1c03a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175771
Seq. ID	jC-atXLIB327439P1c07b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	72
E value	4.0e-32
Match length	264
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175772
Seq. ID	jC-atXLIB327439P1c12a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	81
E value	2.0e-37
Match length	156
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	175773
Seq. ID	jC-atXLIB327439P1c12a2
Method	BLASTN
NCBI GI	g4587641
BLAST score	286
E value	1.0e-160
Match length	384
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	175774
Seq. ID	jC-atXLIB327439P1d04a1
Method	BLASTN
NCBI GI	g4567259
BLAST score	293
E value	1.0e-164
Match length	440
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	175775
Seq. ID	jC-atXLIB327439P1d04a2
Method	BLASTN
NCBI GI	g4567259
BLAST score	143

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E value	2.0e-74
Match length	293
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	175776
Seq. ID	jC-atXLIB327439P1d05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175777
Seq. ID	jC-atXLIB327439P1d05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175778
Seq. ID	jC-atXLIB327439P1d07a2
Method	BLASTN
NCBI GI	g2281081
BLAST score	82
E value	3.0e-38
Match length	257
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175779
Seq. ID	jC-atXLIB327439P1d07b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	230
E value	1.0e-126
Match length	306
% identity	73
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175780
Seq. ID	jC-atXLIB327439P1d10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	59
% identity	97

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175781
Seq. ID	jC-atXLIB327439P1d10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	5.0e-28
Match length	72
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175782
Seq. ID	jC-atXLIB327439P1d12a1
Method	BLASTN
NCBI GI	g4584531
BLAST score	69
E value	2.0e-30
Match length	261
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	175783
Seq. ID	jC-atXLIB327439P1d12a2
Method	BLASTN
NCBI GI	g4584531
BLAST score	83
E value	1.0e-38
Match length	339
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	175784
Seq. ID	jC-atXLIB327439P1d12b1
Method	BLASTN
NCBI GI	g4584531
BLAST score	63
E value	6.0e-27
Match length	121
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	175785
Seq. ID	jC-atXLIB327439P1e02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	7.0e-15
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175786

Seq. ID	jC-atXLIB327439P1e03a1
Method	BLASTN
NCBI GI	g3785968
BLAST score	60
E value	6.0e-25
Match length	177
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175787
Seq. ID	jC-atXLIB327439P1e08a2
Method	BLASTN
NCBI GI	g4454447
BLAST score	363
E value	0.0e+00
Match length	429
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175788
Seq. ID	jC-atXLIB327439P1e09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175789
Seq. ID	jC-atXLIB327439P1f01a2
Method	BLASTN
NCBI GI	g454358
BLAST score	144
E value	3.0e-75
Match length	315
% identity	91
NCBI Description	Arabidopsis thaliana Columbia glutamyl-tRNA reductase (hemA) gene

Seq. No.	175790
Seq. ID	jC-atXLIB327439P1f03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	6.0e-22
Match length	55
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175791
Seq. ID	jC-atXLIB327439P1f03a2
Method	BLASTN
NCBI GI	g3766106
BLAST score	45

E value	6.0e-16
Match length	93
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175792
Seq. ID	jC-atXLIB327439P1f04a2
Method	BLASTX
NCBI GI	g2244835
BLAST score	310
E value	2.0e-28
Match length	92
% identity	66
NCBI Description	(Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	175793
Seq. ID	jC-atXLIB327439P1f05b1
Method	BLASTN
NCBI GI	g4756963
BLAST score	126
E value	3.0e-64
Match length	267
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	175794
Seq. ID	jC-atXLIB327439P1f07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	8.0e-12
Match length	54
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175795
Seq. ID	jC-atXLIB327439P1f07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175796
Seq. ID	jC-atXLIB327439P1f10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	9.0e-12
Match length	54
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175797
Seq. ID	jC-atXLIB327439P1f12a2
Method	BLASTX
NCBI GI	g2695641
BLAST score	168
E value	1.0e-11
Match length	66
% identity	53
NCBI Description	(U94174) mammary tumor-associated protein INT6 [Homo sapiens]

Seq. No.	175798
Seq. ID	jC-atXLIB327439P1g01a2
Method	BLASTX
NCBI GI	g1170505
BLAST score	275
E value	3.0e-24
Match length	64
% identity	86
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	175799
Seq. ID	jC-atXLIB327439P1g02a1
Method	BLASTN
NCBI GI	g4455321
BLAST score	43
E value	1.0e-14
Match length	131
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	175800
Seq. ID	jC-atXLIB327439P1g05a2
Method	BLASTX
NCBI GI	g1707955
BLAST score	226
E value	2.0e-18
Match length	59
% identity	78
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No.	175801
Seq. ID	jC-atXLIB327439P1g09a1
Method	BLASTN
NCBI GI	g2262155
BLAST score	99
E value	3.0e-48
Match length	160

% identity	96
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	175802
Seq. ID	jC-atXLIB327439P1g11a1
Method	BLASTN
NCBI GI	g3451055
BLAST score	33
E value	8.0e-09
Match length	61
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	175803
Seq. ID	jC-atXLIB327439P1g11b2
Method	BLASTX
NCBI GI	g3451068
BLAST score	93
E value	3.0e-53
Match length	146
% identity	86
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	175804
Seq. ID	jC-atXLIB327439P1h01a2
Method	BLASTN
NCBI GI	g3046853
BLAST score	56
E value	1.0e-22
Match length	112
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	175805
Seq. ID	jC-atXLIB327439P1h01b2
Method	BLASTX
NCBI GI	g1170203
BLAST score	235
E value	2.0e-19
Match length	128
% identity	45
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	175806
Seq. ID	jC-atXLIB327439P1h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	56
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175807
Seq. ID	jC-atXLIB327439P1h04a2
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	3.0e-14
Match length	46
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175808
Seq. ID	jC-atXLIB327439P1h05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175809
Seq. ID	jC-atXLIB327439P1h08a1
Method	BLASTX
NCBI GI	g1785681
BLAST score	291
E value	4.0e-26
Match length	120
% identity	55
NCBI Description	(Y08501) ribosomal protein S3 [Arabidopsis thaliana]

Seq. No.	175810
Seq. ID	jC-atXLIB327439P1h08a2
Method	BLASTX
NCBI GI	g1785681
BLAST score	239
E value	7.0e-43
Match length	134
% identity	65
NCBI Description	(Y08501) ribosomal protein S3 [Arabidopsis thaliana]

Seq. No.	175811
Seq. ID	jC-atXLIB327439P1h10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175812
Seq. ID	jC-atXLIB327439P1h10a2
Method	BLASTN
NCBI GI	g4589438
BLAST score	195
E value	1.0e-105
Match length	361

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	175813
Seq. ID	jC-atXLIB327439P1h12a1
Method	BLASTN
NCBI GI	g2182286
BLAST score	51
E value	1.0e-19
Match length	81
% identity	93
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	175814
Seq. ID	jC-atXLIB327439P1h12a2
Method	BLASTX
NCBI GI	g1912286
BLAST score	60
E value	3.0e-16
Match length	76
% identity	59
NCBI Description	(U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No.	175815
Seq. ID	jC-atXLIB327439P2a04b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	36
E value	1.0e-10
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	175816
Seq. ID	jC-atXLIB327439P2a08b2
Method	BLASTN
NCBI GI	g3785968
BLAST score	47
E value	3.0e-17
Match length	304
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175817
Seq. ID	jC-atXLIB327439P2b04a2
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	71

% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175818
Seq. ID	jC-atXLIB327439P2b07a2
Method	BLASTN
NCBI GI	g4115930
BLAST score	59
E value	2.0e-24
Match length	267
% identity	89
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	175819
Seq. ID	jC-atXLIB327439P2c10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175820
Seq. ID	jC-atXLIB327439P2d08a2
Method	BLASTN
NCBI GI	g3228516
BLAST score	106
E value	2.0e-52
Match length	294
% identity	84
NCBI Description	Arabidopsis thaliana ETTIN gene, complete cds

Seq. No.	175821
Seq. ID	jC-atXLIB327439P2d12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	5.0e-13
Match length	52
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175822
Seq. ID	jC-atXLIB327439P2e02a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	41
E value	1.0e-13
Match length	45
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175823
Seq. ID	jC-atXLIB327439P2e11a2

Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175824
Seq. ID	jC-atXLIB327439P2f02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175825
Seq. ID	jC-atXLIB327439P2f05a2
Method	BLASTX
NCBI GI	g4220462
BLAST score	233
E value	3.0e-19
Match length	74
% identity	59
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	175826
Seq. ID	jC-atXLIB327439P2f06b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	62
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175827
Seq. ID	jC-atXLIB327439P2g05a2
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	7.0e-12
Match length	66
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175828
Seq. ID	jC-atXLIB327439P2g08a2
Method	BLASTN
NCBI GI	g4678705

BLAST score 123
E value 1.0e-62
Match length 271
% identity 86
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No. 175829
Seq. ID jC-atXLIB327439P2g08b2
Method BLASTN
NCBI GI g4678705
BLAST score 73
E value 8.0e-33
Match length 115
% identity 96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No. 175830
Seq. ID jC-atXLIB327439P2h03a2
Method BLASTN
NCBI GI g4678705
BLAST score 165
E value 1.0e-87
Match length 284
% identity 90
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No. 175831
Seq. ID jC-atXLIB327439P2h12b2
Method BLASTX
NCBI GI g2924781
BLAST score 645
E value 1.0e-67
Match length 145
% identity 80
NCBI Description (AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No. 175832
Seq. ID jC-atXLIB327439P3a05a2
Method BLASTN
NCBI GI g2462264
BLAST score 47
E value 3.0e-17
Match length 47
% identity 100
NCBI Description Cucumis sativus mRNA for patatin-like protein, partial

Seq. No. 175833
Seq. ID jC-atXLIB327439P3a08a2
Method BLASTN
NCBI GI g2462264
BLAST score 47
E value 2.0e-17
Match length 59

% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175834
Seq. ID	jC-atXLIB327439P3a08b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	9.0e-21
Match length	72
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175835
Seq. ID	jC-atXLIB327439P3a09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175836
Seq. ID	jC-atXLIB327439P3b01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	60
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175837
Seq. ID	jC-atXLIB327439P3b02a2
Method	BLASTN
NCBI GI	g2815404
BLAST score	46
E value	1.0e-16
Match length	78
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	175838
Seq. ID	jC-atXLIB327439P3b10a2
Method	BLASTN
NCBI GI	g531832
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175839

Seq. ID	jC-atXLIB327439P3c03b2
Method	BLASTN
NCBI GI	g13192
BLAST score	64
E value	1.0e-27
Match length	143
% identity	89
NCBI Description	Oenothera berteriana mitDNA with part of plastid rRNA operon

Seq. No.	175840
Seq. ID	jC-atXLIB327439P3c06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	57
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175841
Seq. ID	jC-atXLIB327439P3d03a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	6.0e-15
Match length	59
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175842
Seq. ID	jC-atXLIB327439P3d05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175843
Seq. ID	jC-atXLIB327439P3d06b2
Method	BLASTX
NCBI GI	g3834312
BLAST score	516
E value	2.0e-52
Match length	108
% identity	89
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an

Seq. No.	175844
Seq. ID	jC-atXLIB327439P3d10b2

Method	BLASTX
NCBI GI	g4468979
BLAST score	176
E value	1.0e-12
Match length	44
% identity	73
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	175845
Seq. ID	jC-atXLIB327439P3e10a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175846
Seq. ID	jC-atXLIB327439P3f05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	53
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175847
Seq. ID	jC-atXLIB327439P3h01b2
Method	BLASTN
NCBI GI	g531832
BLAST score	43
E value	7.0e-15
Match length	67
% identity	91
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	175848
Seq. ID	jC-atXLIB327439P3h03a2
Method	BLASTN
NCBI GI	g4185120
BLAST score	34
E value	2.0e-09
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175849
Seq. ID	jC-atXLIB327439P3h04a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	35
E value	6.0e-10
Match length	63
% identity	92

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	175850
Seq. ID	jC-atXLIB327439P3h06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	46
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	175851
Seq. ID	jC-atXLIB327440P1a02a1
Method	BLASTN
NCBI GI	g1707006
BLAST score	271
E value	1.0e-151
Match length	358
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	175852
Seq. ID	jC-atXLIB327440P1a02b1
Method	BLASTN
NCBI GI	g1707006
BLAST score	64
E value	2.0e-27
Match length	107
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	175853
Seq. ID	jC-atXLIB327440P1a03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	175854
Seq. ID	jC-atXLIB327440P1a04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	6.0e-21
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	175855
Seq. ID	jC-atXLIB327440P1f03a1

Method	BLASTN
NCBI GI	g4589437
BLAST score	79
E value	1.0e-36
Match length	181
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	175856
Seq. ID	jC-atXLIB327440P1f12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	3.0e-14
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175857
Seq. ID	jC-atXLIB327440P1g05a1
Method	BLASTX
NCBI GI	g2181180
BLAST score	199
E value	2.0e-15
Match length	118
% identity	36
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	175858
Seq. ID	jC-atXLIB327440P1g08a1
Method	BLASTX
NCBI GI	g480907
BLAST score	753
E value	3.0e-80
Match length	152
% identity	95
NCBI Description	peroxidase (EC 1.11.1.7) - Arabidopsis thaliana >gi_405611_emb_CAA50677_ (X71794) peroxidase [Arabidopsis thaliana]

Seq. No.	175859
Seq. ID	jC-atXLIB327440P1h06a1
Method	BLASTN
NCBI GI	g16519
BLAST score	55
E value	6.0e-22
Match length	110
% identity	90
NCBI Description	A.thaliana STP1 mRNA for glucose transporter

Seq. No.	175860
Seq. ID	jC-atXLIB327440P2b07a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	34
E value	2.0e-09

Match length	54
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	175861
Seq. ID	jC-atXLIB327440P2b12a1
Method	BLASTN
NCBI GI	g2262097
BLAST score	101
E value	2.0e-49
Match length	155
% identity	95
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	175862
Seq. ID	jC-atXLIB327440P2d02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	7.0e-17
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175863
Seq. ID	jC-atXLIB327440P2e06a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	41
E value	1.0e-13
Match length	52
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	175864
Seq. ID	jC-atXLIB327440P2g04a1
Method	BLASTX
NCBI GI	g4104224
BLAST score	182
E value	2.0e-13
Match length	78
% identity	49
NCBI Description	(AF033540) caffeic acid O-methyltransferase; LPOMT3 [Lolium perenne]

Seq. No.	175865
Seq. ID	jC-atXLIB327440P2g08a1
Method	BLASTN
NCBI GI	g1769904
BLAST score	45
E value	4.0e-16
Match length	92
% identity	87
NCBI Description	A.thaliana psbP gene

Seq. No.	175866
Seq. ID	jC-atXLIB327440P2g11a1
Method	BLASTN
NCBI GI	g4803835
BLAST score	261
E value	1.0e-145
Match length	319
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No.	175867
Seq. ID	jC-atXLIB327440P3b10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175868
Seq. ID	jC-atXLIB327440P3c03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	64
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175869
Seq. ID	jC-atXLIB327440P3c06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	38
E value	8.0e-12
Match length	42
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175870
Seq. ID	jC-atXLIB327440P3c07a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175871
Seq. ID	jC-atXLIB327440P3c10a1
Method	BLASTN
NCBI GI	g3738313
BLAST score	169

E value	4.0e-90
Match length	266
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175872
Seq. ID	jC-atXLIB327440P3d07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175873
Seq. ID	jC-atXLIB327440P3d10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	175874
Seq. ID	jC-atXLIB327440P3d11a1
Method	BLASTX
NCBI GI	g1669387
BLAST score	355
E value	1.0e-33
Match length	76
% identity	91
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	175875
Seq. ID	jC-atXLIB327440P3e04a1
Method	BLASTN
NCBI GI	g1523799
BLAST score	76
E value	6.0e-35
Match length	100
% identity	95
NCBI Description	A.thaliana mRNA for MAP kinase kinase alpha

Seq. No.	175876
Seq. ID	jC-atXLIB327440P3f06a1
Method	BLASTN
NCBI GI	g4490701
BLAST score	74
E value	3.0e-33
Match length	90
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	175877
Seq. ID	jC-atXLIB327440P3f07a1
Method	BLASTN
NCBI GI	g2252823
BLAST score	53
E value	9.0e-21
Match length	93
% identity	87
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	175878
Seq. ID	jC-atXLIB327440P3f09a1
Method	BLASTN
NCBI GI	g4757392
BLAST score	122
E value	6.0e-62
Match length	227
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	175879
Seq. ID	jC-atXLIB327440P3f10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	8.0e-15
Match length	67
% identity	91
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175880
Seq. ID	jC-atXLIB327440P4c02b2
Method	BLASTN
NCBI GI	g3132469
BLAST score	176
E value	4.0e-94
Match length	265
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175881
Seq. ID	jC-atXLIB327440P4c09b2
Method	BLASTN
NCBI GI	g3282170
BLAST score	85
E value	7.0e-40
Match length	128
% identity	33
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175882
Seq. ID	jC-atXLIB327440P4d07b2
Method	BLASTN
NCBI GI	g2582640

BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	175883
Seq. ID	jC-atXLIB327440P4d12b2
Method	BLASTN
NCBI GI	g3335331
BLAST score	82
E value	5.0e-38
Match length	150
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175884
Seq. ID	jC-atXLIB327440P4e05a1
Method	BLASTN
NCBI GI	g4539331
BLAST score	40
E value	5.0e-13
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	175885
Seq. ID	jC-atXLIB327440P4e06a1
Method	BLASTN
NCBI GI	g217870
BLAST score	34
E value	2.0e-09
Match length	82
% identity	85
NCBI Description	A. thaliana mRNA for t-complex polypeptide 1 homologue, complete cds

Seq. No.	175886
Seq. ID	jC-atXLIB327440P4e07a1
Method	BLASTX
NCBI GI	g4769004
BLAST score	189
E value	4.0e-14
Match length	77
% identity	55
NCBI Description	(AF140598) ring-box protein 1 [Homo sapiens] >gi_4769006_gb_AAD29716.1_AF140599_1 (AF140599) ring-box protein 1 [Mus musculus]

Seq. No.	175887
Seq. ID	jC-atXLIB327440P4e10a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	49

E value	2.0e-18
Match length	65
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175888
Seq. ID	jC-atXLIB327440P4e11a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	175889
Seq. ID	jC-atXLIB327440P4f12a1
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	5.0e-13
Match length	64
% identity	91
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	175890
Seq. ID	jC-atXLIB327440P4g06a1
Method	BLASTX
NCBI GI	g3169171
BLAST score	337
E value	2.0e-31
Match length	134
% identity	53
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445213 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	175891
Seq. ID	jC-atXLIB327440P4g09b2
Method	BLASTN
NCBI GI	g2894591
BLAST score	98
E value	1.0e-47
Match length	304
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	175892
Seq. ID	jC-atXLIB327440P4g12a1
Method	BLASTN
NCBI GI	g4191771
BLAST score	73
E value	1.0e-32
Match length	326

% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175893
Seq. ID	jC-atXN10515r1
Method	BLASTX
NCBI GI	g1619602
BLAST score	467
E value	2.0e-46
Match length	160
% identity	56
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	175894
Seq. ID	jC-atXN209221a1
Method	BLASTX
NCBI GI	g3881189
BLAST score	323
E value	1.0e-29
Match length	114
% identity	59
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No.	175895
Seq. ID	jC-atXN23643a2
Method	BLASTN
NCBI GI	g4585620
BLAST score	284
E value	1.0e-158
Match length	337
% identity	97
NCBI Description	Zea mays hmgi/y gene, exons 1-2

Seq. No.	175896
Seq. ID	jC-atXN23846f2
Method	BLASTN
NCBI GI	g165316
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	O.cunniculus germline IgH heavy chain V-H pseudogene, allotype VHa2

Seq. No.	175897
Seq. ID	jC-atXN23948f2
Method	BLASTX
NCBI GI	g3056586
BLAST score	132
E value	2.0e-19
Match length	129
% identity	39
NCBI Description	(AC004255) T1F9.7 [Arabidopsis thaliana]

Seq. No.	175898
Seq. ID	jC-atXN272114a1
Method	BLASTX
NCBI GI	g1167955
BLAST score	144
E value	1.0e-08
Match length	57
% identity	47
NCBI Description	(U43497) putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare]

Seq. No.	175899
Seq. ID	jC-atXN27742a1
Method	BLASTX
NCBI GI	g2586083
BLAST score	112
E value	7.0e-05
Match length	218
% identity	11
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	175900
Seq. ID	jC-atXN28474a1
Method	BLASTN
NCBI GI	g415413
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	{multiple cloning sites, vector} [bacteriophage M13, M13mp29/pUC29, Genomic, 157 nt]

Seq. No.	175901
Seq. ID	jC-atXN28593f1
Method	BLASTN
NCBI GI	g310778
BLAST score	37
E value	5.0e-11
Match length	37
% identity	100
NCBI Description	pIBI25 cloning vector

Seq. No.	175902
Seq. ID	jC-atXN28761f1
Method	BLASTN
NCBI GI	g619522
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	Synechococcus PCC 6301 genomic DNA (clone PJRSY01)

Seq. No.	175903
Seq. ID	jC-atXN288113a1

Method	BLASTN
NCBI GI	g485852
BLAST score	33
E value	9.0e-09
Match length	33
% identity	100
NCBI Description	H.sapiens EWS gene, exon

Seq. No.	175904
Seq. ID	jC-atXN30618a1
Method	BLASTX
NCBI GI	g2558654
BLAST score	151
E value	2.0e-09
Match length	132
% identity	33
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	175905
Seq. ID	jC-atXN38694a1
Method	BLASTX
NCBI GI	g1497987
BLAST score	154
E value	6.0e-10
Match length	100
% identity	36
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	175906
Seq. ID	jC-atXN392166f1
Method	BLASTX
NCBI GI	g4741187
BLAST score	391
E value	1.0e-37
Match length	186
% identity	45
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	175907
Seq. ID	jC-atXN40083d1
Method	BLASTN
NCBI GI	g3819625
BLAST score	65
E value	8.0e-28
Match length	73
% identity	97
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG2217

Seq. No.	175908
Seq. ID	jC-atXN40292d1
Method	BLASTN
NCBI GI	g209100
BLAST score	43
E value	1.0e-14
Match length	43
% identity	100
NCBI Description	Shuttle vector consisting of DNA from E.coli and yeast.

>gi_1250056_gb_I15148_I15148 Sequence 19 from patent US

Seq. No.	175909
Seq. ID	jC-atXN40990f2
Method	BLASTN
NCBI GI	g209614
BLAST score	35
E value	7.0e-10
Match length	35
% identity	100
NCBI Description	Cloning vector pEZZ18 fusion gene, partial cds

Seq. No.	175910
Seq. ID	jC-atXN414104f2
Method	BLASTX
NCBI GI	g3420052
BLAST score	361
E value	4.0e-34
Match length	141
% identity	56
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	175911
Seq. ID	jC-atXN421120a2
Method	BLASTX
NCBI GI	g4417289
BLAST score	157
E value	4.0e-10
Match length	75
% identity	47
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	175912
Seq. ID	jC-atXN458168r2
Method	BLASTX
NCBI GI	g2160144
BLAST score	89
E value	1.0e-20
Match length	126
% identity	43
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	175913
Seq. ID	jC-atXN563193a2
Method	BLASTX
NCBI GI	g3941500
BLAST score	184
E value	3.0e-13
Match length	64
% identity	61
NCBI Description	(AF062904) putative transcription factor [Arabidopsis thaliana]

Seq. No.	175914
Seq. ID	jC-atXN593177r1

Method	BLASTX
NCBI GI	g2738996
BLAST score	231
E value	9.0e-19
Match length	107
% identity	74
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	175915
Seq. ID	jC-atXN605212a2
Method	BLASTX
NCBI GI	g3551954
BLAST score	384
E value	1.0e-36
Match length	144
% identity	48
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	175916
Seq. ID	jC-atXP100C251L20T7b1
Method	BLASTX
NCBI GI	g1408471
BLAST score	508
E value	2.0e-51
Match length	112
% identity	88
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	175917
Seq. ID	jC-atXP100C251L20T7d1
Method	BLASTX
NCBI GI	g4584533
BLAST score	481
E value	2.0e-48
Match length	134
% identity	73
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	175918
Seq. ID	jC-atXP100C251M21T7b1
Method	BLASTX
NCBI GI	g2104536
BLAST score	391
E value	1.0e-37
Match length	142
% identity	58
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	175919
Seq. ID	jC-atXP100C251M5T7b1
Method	BLASTX
NCBI GI	g2464879
BLAST score	846

E value	6.0e-91
Match length	167
% identity	99
NCBI Description	(Z99707) caltractin-like protein [Arabidopsis thaliana]

Seq. No.	175920
Seq. ID	jC-atXP100C251N12T7b1
Method	BLASTN
NCBI GI	g3702315
BLAST score	99
E value	7.0e-48
Match length	352
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175921
Seq. ID	jC-atXP100C251N14T7b1
Method	BLASTN
NCBI GI	g2632075
BLAST score	52
E value	7.0e-20
Match length	56
% identity	98
NCBI Description	X.laevis mRNA for cortical granule lectin

Seq. No.	175922
Seq. ID	jC-atXP100C251N21T7b1
Method	BLASTN
NCBI GI	g3641835
BLAST score	309
E value	1.0e-173
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	175923
Seq. ID	jC-atXP100C251N4T7b1
Method	BLASTX
NCBI GI	g2281631
BLAST score	54
E value	4.0e-63
Match length	167
% identity	76
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	175924
Seq. ID	jC-atXP100C251P17T7b1
Method	BLASTX
NCBI GI	g1345594
BLAST score	591
E value	4.0e-61
Match length	148
% identity	86
NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14

Kappa isoform [Arabidopsis thaliana]

Seq. No.	175925
Seq. ID	jC-atXP100C269A7T7b1
Method	BLASTN
NCBI GI	g4159706
BLAST score	302
E value	1.0e-169
Match length	380
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	175926
Seq. ID	jC-atXP100C269F10T7b1
Method	BLASTX
NCBI GI	g2982463
BLAST score	376
E value	9.0e-36
Match length	138
% identity	57
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	175927
Seq. ID	jC-atXP100C269F10T7d1
Method	BLASTN
NCBI GI	g3395757
BLAST score	275
E value	1.0e-153
Match length	283
% identity	99
NCBI Description	Arabidopsis thaliana unknown mRNA

Seq. No.	175928
Seq. ID	jC-atXP100C269G1T7b1
Method	BLASTX
NCBI GI	g320563
BLAST score	399
E value	2.0e-38
Match length	81
% identity	99
NCBI Description	transcription factor tga1 - Arabidopsis thaliana >gi_16550_emb_CAA48189_ (X68053) transcription factor [Arabidopsis thaliana]

Seq. No.	175929
Seq. ID	jC-atXP100C269H7T7b1
Method	BLASTN
NCBI GI	g3702737
BLAST score	186
E value	1.0e-100
Match length	300
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No. 175930

Seq. ID	jC-atXP100CE1B1T7b1
Method	BLASTX
NCBI GI	g4539405
BLAST score	383
E value	1.0e-36
Match length	86
% identity	90
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	175931
Seq. ID	jC-atXP100CE1C8T7b1
Method	BLASTN
NCBI GI	g2804255
BLAST score	49
E value	3.0e-18
Match length	69
% identity	93
NCBI Description	Oryctolagus cuniculus mRNA for interferon gamma, complete cds

Seq. No.	175932
Seq. ID	jC-atXP100CE3E6T7b1
Method	BLASTX
NCBI GI	g464985
BLAST score	234
E value	2.0e-22
Match length	123
% identity	53
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	175933
Seq. ID	jC-atXP100CE3G4T7b1
Method	BLASTX
NCBI GI	g3914442
BLAST score	158
E value	2.0e-10
Match length	51
% identity	67
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	175934
Seq. ID	jC-atXP101CE1D11T7089b1
Method	BLASTN
NCBI GI	g516042
BLAST score	60
E value	6.0e-25
Match length	241
% identity	87
NCBI Description	Arabidopsis thaliana Columbia Dwarf1 (DWF1) mRNA, complete cds

Seq. No.	175935
Seq. ID	jC-atXP101CE1E10T7058b1
Method	BLASTX
NCBI GI	g3790593
BLAST score	460
E value	6.0e-46
Match length	87
% identity	94
NCBI Description	(AF079185) RING-H2 finger protein RHY1a [Arabidopsis thaliana]

Seq. No.	175936
Seq. ID	jC-atXP101CE1E10T7058d1
Method	BLASTN
NCBI GI	g3790592
BLAST score	287
E value	1.0e-160
Match length	448
% identity	92
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHY1a mRNA, partial cds

Seq. No.	175937
Seq. ID	jC-atXP101CE1E11T7066d1
Method	BLASTX
NCBI GI	g4156243
BLAST score	729
E value	2.0e-77
Match length	150
% identity	95
NCBI Description	(AB012569) ATHP2 [Arabidopsis thaliana]

Seq. No.	175938
Seq. ID	jC-atXP101CE1E1T7010b1
Method	BLASTN
NCBI GI	g4741939
BLAST score	83
E value	1.0e-38
Match length	107
% identity	94
NCBI Description	Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds

Seq. No.	175939
Seq. ID	jC-atXP101CE1E1T7010d1
Method	BLASTX
NCBI GI	g1399450
BLAST score	433
E value	9.0e-43
Match length	135
% identity	64
NCBI Description	(U47660) beta-tubulin 2 [Lupinus albus]

Seq. No.	175940
Seq. ID	jC-atXP101CE1E5T7026d1
Method	BLASTX
NCBI GI	g2493896

BLAST score 345
E value 2.0e-32
Match length 159
% identity 52
NCBI Description CYSTEINE SYNTHASE MITOCHONDRIAL PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1488519_emb_CAA57498_ (X81973) cysteine synthase [Arabidopsis thaliana]

Seq. No. 175941
Seq. ID jC-atXP101CE1F11T7043b1
Method BLASTX
NCBI GI g730450
BLAST score 80
E value 2.0e-09
Match length 89
% identity 55
NCBI Description 60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) >gi_480649_pir__S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein (BnC24B) [Brassica napus]

Seq. No. 175942
Seq. ID jC-atXP101CE1F11T7043d1
Method BLASTX
NCBI GI g730526
BLAST score 226
E value 2.0e-18
Match length 97
% identity 56
NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No. 175943
Seq. ID jC-atXP101CE1F3T7090d1
Method BLASTX
NCBI GI g2499327
BLAST score 392
E value 6.0e-38
Match length 84
% identity 87
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No. 175944
Seq. ID jC-atXP101CE1F5T7011d1
Method BLASTN
NCBI GI g3510347
BLAST score 40
E value 3.0e-13
Match length 166
% identity 91

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	175945
Seq. ID	jC-atXP101CE1G10T7091b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	44
E value	2.0e-15
Match length	68
% identity	91
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	175946
Seq. ID	jC-atXP101CE1G10T7091d1
Method	BLASTX
NCBI GI	g4455295
BLAST score	220
E value	4.0e-21
Match length	90
% identity	60
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	175947
Seq. ID	jC-atXP101CE1G12T7012b1
Method	BLASTN
NCBI GI	g488614
BLAST score	43
E value	8.0e-15
Match length	119
% identity	87
NCBI Description	A.thaliana Chloroplast gsh1 mRNA for glutamate-cysteine ligase

Seq. No.	175948
Seq. ID	jC-atXP101CE1G4T7059d1
Method	BLASTX
NCBI GI	g4454036
BLAST score	743
E value	5.0e-79
Match length	136
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	175949
Seq. ID	jC-atXP101CE1G7T7067d1
Method	BLASTN
NCBI GI	g4538990
BLAST score	56
E value	9.0e-23
Match length	148
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	175950
Seq. ID	jC-atXP101CE1H10T7068d1
Method	BLASTX
NCBI GI	g99749
BLAST score	192
E value	2.0e-14
Match length	83
% identity	48
NCBI Description	probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana >gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana]

Seq. No.	175951
Seq. ID	jC-atXP101CE1H11T7076b1
Method	BLASTX
NCBI GI	g786117
BLAST score	112
E value	5.0e-05
Match length	183
% identity	4
NCBI Description	(L41834) nuclear protein [Ensis minor]

Seq. No.	175952
Seq. ID	jC-atXP101CE1H12T7084d1
Method	BLASTN
NCBI GI	g2924257
BLAST score	54
E value	2.0e-21
Match length	159
% identity	92
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	175953
Seq. ID	jC-atXP101CE1H1T7020d1
Method	BLASTX
NCBI GI	g2072628
BLAST score	619
E value	2.0e-64
Match length	154
% identity	79
NCBI Description	(Y12641) superoxide dismutase [Arabidopsis thaliana]

Seq. No.	175954
Seq. ID	jC-atXP101CE1H9T7060d1
Method	BLASTX
NCBI GI	g4454036
BLAST score	177
E value	8.0e-13
Match length	135
% identity	23
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	175955
Seq. ID	jC-atXP101CE2A1T7092b1
Method	BLASTN

NCBI GI	g3892595
BLAST score	47
E value	3.0e-17
Match length	71
% identity	92
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	175956
Seq. ID	jC-atXP101CE2A2T7005b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	34
E value	2.0e-09
Match length	69
% identity	89
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	175957
Seq. ID	jC-atXP101CE2A4T7021d1
Method	BLASTN
NCBI GI	g4056476
BLAST score	46
E value	4.0e-17
Match length	50
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	175958
Seq. ID	jC-atXP101CE2A8T7045b1
Method	BLASTN
NCBI GI	g4090883
BLAST score	54
E value	2.0e-21
Match length	120
% identity	94
NCBI Description	Arabidopsis thaliana vesicle-associated membrane protein 7B (At VAMP7B) mRNA, complete cds

Seq. No.	175959
Seq. ID	jC-atXP101CE2A8T7045d1
Method	BLASTX
NCBI GI	g2494115
BLAST score	235
E value	2.0e-19
Match length	77
% identity	69
NCBI Description	(AC002376) Strong similarity to Arabidopsis ATHSAR1 (gb_M90418). ESTs gb_T44122,gb_N65276,gb_AA041135 come from this gene. [Arabidopsis thaliana]

Seq. No.	175960
Seq. ID	jC-atXP101CE2C1T7054b1
Method	BLASTX
NCBI GI	g4371284
BLAST score	507
E value	2.0e-51

Match length	110
% identity	89
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	175961
Seq. ID	jC-atXP101CE2C1T7054d1
Method	BLASTX
NCBI GI	g1175013
BLAST score	143
E value	9.0e-13
Match length	75
% identity	60
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	175962
Seq. ID	jC-atXP101CE2C7T7086d1
Method	BLASTX
NCBI GI	g4417280
BLAST score	186
E value	2.0e-36
Match length	135
% identity	66
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	175963
Seq. ID	jC-atXP101CE2C9T7007b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	38
E value	7.0e-12
Match length	82
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	175964
Seq. ID	jC-atXP101CE2C9T7007d1
Method	BLASTN
NCBI GI	g4510338
BLAST score	133
E value	1.0e-68
Match length	153
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	175965
Seq. ID	jC-atXP101CE2D4T7055b1
Method	BLASTN
NCBI GI	g2264305
BLAST score	63
E value	1.0e-26
Match length	145

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	175966
Seq. ID	jC-atXP101CE2E11T7088d1
Method	BLASTX
NCBI GI	g926931
BLAST score	412
E value	3.0e-40
Match length	117
% identity	77
NCBI Description	(L44582) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	175967
Seq. ID	jC-atXP101CE2E12T7096b1
Method	BLASTX
NCBI GI	g3193289
BLAST score	145
E value	5.0e-09
Match length	138
% identity	36
NCBI Description	(AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

Seq. No.	175968
Seq. ID	jC-atXP101CE2E4T7048b1
Method	BLASTX
NCBI GI	g2829899
BLAST score	49
E value	1.0e-32
Match length	140
% identity	51
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	175969
Seq. ID	jC-atXP101CE3G9T7033d1
Method	BLASTN
NCBI GI	g16311
BLAST score	66
E value	1.0e-28
Match length	102
% identity	93
NCBI Description	A.thaliana gene for tonoplast intrinsic protein gamma-TIP(Ara) >gi_166731_gb_M84344_ATHGTIP Arabidopsis thaliana tonoplast intrinsic protein (gamma-TIP) gene, complete cds

Seq. No.	175970
Seq. ID	jC-atXP102CE2F10T7b1
Method	BLASTX
NCBI GI	g2143767

BLAST score	123
E value	4.0e-06
Match length	169
% identity	8
NCBI Description	glycoprotein - rat >gi_986943 (L08134) glycoprotein [Rattus norvegicus] >gi_1094950_prf__2107200A glycoprotein [Rattus norvegicus]

Seq. No.	175971
Seq. ID	jC-atXP102CE2F12T7049d1
Method	BLASTX
NCBI GI	g1755164
BLAST score	148
E value	1.0e-09
Match length	72
% identity	47
NCBI Description	(U75193) germin-like protein [Arabidopsis thaliana] >gi_1755168 (U75195) germin-like protein [Arabidopsis thaliana] >gi_2239042_emb_CAA73213_ (Y12673) GLP3 protein [Arabidopsis thaliana] >gi_4666250_dbj_BAA77208.1_ (D89374) germin-like protein 2 precursor [Arabidopsis thaliana]

Seq. No.	175972
Seq. ID	jC-atXP102CE2G5T7b1
Method	BLASTX
NCBI GI	g2143767
BLAST score	155
E value	9.0e-10
Match length	205
% identity	16
NCBI Description	glycoprotein - rat >gi_986943 (L08134) glycoprotein [Rattus norvegicus] >gi_1094950_prf__2107200A glycoprotein [Rattus norvegicus]

Seq. No.	175973
Seq. ID	jC-atXP102CE2H2T7050d1
Method	BLASTN
NCBI GI	g4049332
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	175974
Seq. ID	jC-atXP102CE2H4T7066d1
Method	BLASTX
NCBI GI	g1170091
BLAST score	195
E value	3.0e-15
Match length	63
% identity	67
NCBI Description	GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis

thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana]

Seq. No.	175975
Seq. ID	jC-atXP102CE2H8T7003d1
Method	BLASTX
NCBI GI	g2618723
BLAST score	275
E value	7.0e-25
Match length	72
% identity	75
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	175976
Seq. ID	jC-atXP102CE3H6T7b1
Method	BLASTX
NCBI GI	g2618723
BLAST score	186
E value	1.0e-13
Match length	90
% identity	56
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	175977
Seq. ID	jC-atXP102CE4B5T7052d1
Method	BLASTN
NCBI GI	g2864607
BLAST score	235
E value	1.0e-129
Match length	243
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	175978
Seq. ID	jC-atXP102CE4C11T7068d1
Method	BLASTX
NCBI GI	g4510345
BLAST score	293
E value	1.0e-26
Match length	53
% identity	98
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	175979
Seq. ID	jC-atXP102CE4D12T7092d1
Method	BLASTX
NCBI GI	g3212879
BLAST score	277
E value	9.0e-25
Match length	78
% identity	74
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	175980
Seq. ID	jC-atXP102CE4E6T7029d1
Method	BLASTN
NCBI GI	g3449320
BLAST score	91
E value	1.0e-43
Match length	147
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	175981
Seq. ID	jC-atXP102CE4F3T7085d1
Method	BLASTX
NCBI GI	g1944575
BLAST score	404
E value	1.0e-39
Match length	86
% identity	86
NCBI Description	(Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No.	175982
Seq. ID	jC-atXP102CE4F4T7093d1
Method	BLASTX
NCBI GI	g3334150
BLAST score	317
E value	2.0e-29
Match length	85
% identity	78
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	175983
Seq. ID	jC-atXP102CE4F5T7b1
Method	BLASTX
NCBI GI	g2654122
BLAST score	152
E value	1.0e-09
Match length	33
% identity	82
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	175984

Seq. ID	jC-atXP102CE4F6T7b1
Method	BLASTX
NCBI GI	g786117
BLAST score	127
E value	1.0e-06
Match length	231
% identity	5
NCBI Description	(L41834) nuclear protein [Ensis minor]

Seq. No.	175985
Seq. ID	jC-atXP102CE5A5T7b1
Method	BLASTX
NCBI GI	g4138137
BLAST score	283
E value	5.0e-25
Match length	77
% identity	65
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	175986
Seq. ID	jC-atXP102CE5D12T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	49
E value	3.0e-18
Match length	57
% identity	96
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	175987
Seq. ID	jC-atXP102CE5D7T7094d1
Method	BLASTX
NCBI GI	g3334149
BLAST score	191
E value	9.0e-15
Match length	68
% identity	59
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2323329 (AF014053) Mg protoporphyrin chelatase subunit [Nicotiana tabacum]

Seq. No.	175988
Seq. ID	jC-atXP102CE5E1T7b1
Method	BLASTN
NCBI GI	g560553
BLAST score	43
E value	7.0e-15
Match length	55
% identity	95
NCBI Description	truncated protein {frame 1, multiple cloning site} [Saccharomyces cerevisiae=yeast, cloning vector YCpIF1-12, Other Plasmid Synthetic Partial, 99 nt]

Seq. No.	175989
Seq. ID	jC-atXP102CE5F5T7040d1
Method	BLASTN
NCBI GI	g166935

BLAST score	105
E value	5.0e-52
Match length	232
% identity	86
NCBI Description	A.thaliana ubiquitin extension protein (UBQ6) gene, complete cds

Seq. No.	175990
Seq. ID	jC-atXP102CE6A5T7051d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	175991
Seq. ID	jC-atXP104CE10D4T7b1
Method	BLASTN
NCBI GI	g1765898
BLAST score	178
E value	5.0e-95
Match length	298
% identity	91
NCBI Description	A.thaliana mRNA for Spot 3 protein

Seq. No.	175992
Seq. ID	jC-atXP104CE10E8T7b1
Method	BLASTN
NCBI GI	g710625
BLAST score	410
E value	0.0e+00
Match length	489
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	175993
Seq. ID	jC-atXP104CE7A12T7b1
Method	BLASTN
NCBI GI	g2598931
BLAST score	40
E value	9.0e-13
Match length	118
% identity	93
NCBI Description	Arabidopsis thaliana auxin-responsive protein IAA2 gene, complete cds

Seq. No.	175994
Seq. ID	jC-atXP104CE7C1T7b1
Method	BLASTN
NCBI GI	g984755
BLAST score	55
E value	7.0e-22
Match length	55
% identity	100
NCBI Description	O.sativa mRNA for chilling-inducible protein

Seq. No.	175995
Seq. ID	jC-atXP107C105A22T7d1
Method	BLASTN
NCBI GI	g2289094
BLAST score	39
E value	4.0e-13
Match length	59
% identity	92
NCBI Description	Arabidopsis thaliana WD-40 repeat protein (AtArcA) mRNA, complete cds

Seq. No.	175996
Seq. ID	jC-atXP107C111I9T7s1
Method	BLASTN
NCBI GI	g166709
BLAST score	82
E value	8.0e-39
Match length	106
% identity	94
NCBI Description	Arabidopsis thaliana cytosolic glyceraldehyde-3-phosphate dehydrogenase (GapC) gene, exons 1-9, complete cds

Seq. No.	175997
Seq. ID	jC-atXP107C123C17T7s1
Method	BLASTX
NCBI GI	g3874563
BLAST score	237
E value	9.0e-20
Match length	106
% identity	47
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	175998
Seq. ID	jC-atXP107C23E4T7s1
Method	BLASTX
NCBI GI	g4455349
BLAST score	424
E value	1.0e-41
Match length	84
% identity	100
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	175999
Seq. ID	jC-atXP107C39G2T7s1
Method	BLASTX
NCBI GI	g3236242
BLAST score	161
E value	3.0e-11

Match length	59
% identity	63
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	176000
Seq. ID	jC-atXP108C144D14T7065d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	3.0e-13
Match length	41
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176001
Seq. ID	jC-atXP108C144I3T7089d1
Method	BLASTN
NCBI GI	g2828184
BLAST score	131
E value	3.0e-67
Match length	443
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	176002
Seq. ID	jC-atXP108C147F19T7010d1
Method	BLASTN
NCBI GI	g2828184
BLAST score	59
E value	5.0e-24
Match length	250
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	176003
Seq. ID	jC-atXP108C147K15T7026d1
Method	BLASTX
NCBI GI	g135406
BLAST score	337
E value	3.0e-31
Match length	114
% identity	61
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	176004
Seq. ID	jC-atXP108C151H20T7082d1
Method	BLASTX
NCBI GI	g4115916
BLAST score	111
E value	3.0e-15

Match length	136
% identity	49
NCBI Description	(AF118222) F3H7.9 gene product [Arabidopsis thaliana] >gi_4539441_emb_CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	176005
Seq. ID	jC-atXP108C153H24T7090d1
Method	BLASTX
NCBI GI	g584741
BLAST score	172
E value	5.0e-12
Match length	86
% identity	43
NCBI Description	ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis thaliana]

Seq. No.	176006
Seq. ID	jC-atXP108C157G10T7027d1
Method	BLASTX
NCBI GI	g135406
BLAST score	762
E value	4.0e-81
Match length	174
% identity	86
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	176007
Seq. ID	jC-atXP108C157G23T7s1
Method	BLASTN
NCBI GI	g4510360
BLAST score	369
E value	0.0e+00
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	176008
Seq. ID	jC-atXP108C160M18T7067d1
Method	BLASTX
NCBI GI	g543841
BLAST score	750
E value	1.0e-79
Match length	151
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	176009
Seq. ID	jC-atXP108C161I22T7083d1
Method	BLASTN
NCBI GI	g2337888
BLAST score	42
E value	5.0e-14
Match length	334
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	176010
Seq. ID	jC-atXP108C166H5T7028d1
Method	BLASTX
NCBI GI	g1935914
BLAST score	281
E value	1.0e-67
Match length	186
% identity	73
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	176011
Seq. ID	jC-atXP108C169D18T7060d1
Method	BLASTN
NCBI GI	g1935913
BLAST score	178
E value	3.0e-95
Match length	434
% identity	86
NCBI Description	Arabidopsis thaliana lethal leaf-spot 1 homolog (Lls1) mRNA, partial cds

Seq. No.	176012
Seq. ID	jC-atXP108C173N16T7053d1
Method	BLASTX
NCBI GI	g461899
BLAST score	198
E value	3.0e-45
Match length	152
% identity	66
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	176013
Seq. ID	jC-atXP108C174D10T7s1
Method	BLASTX
NCBI GI	g404688
BLAST score	225
E value	8.0e-19
Match length	71
% identity	51
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	176014
Seq. ID	jC-atXP108C174G13T7069d1
Method	BLASTX
NCBI GI	g461812
BLAST score	424
E value	2.0e-41
Match length	187
% identity	48
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	176015
Seq. ID	jC-atXP108C175O12T7093d1
Method	BLASTX
NCBI GI	g584741
BLAST score	226
E value	3.0e-18
Match length	104
% identity	20
NCBI Description	ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis thaliana]

Seq. No.	176016
Seq. ID	jC-atXP108C181H5T7070d1
Method	BLASTX
NCBI GI	g1572721
BLAST score	145
E value	1.0e-08
Match length	248
% identity	7
NCBI Description	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]

Seq. No.	176017
Seq. ID	jC-atXP108C184O24T7047d1
Method	BLASTN
NCBI GI	g4835223
BLAST score	52
E value	9.0e-20
Match length	80
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	176018
Seq. ID	jC-atXP108C185N19T7063d1
Method	BLASTX
NCBI GI	g2829899
BLAST score	457
E value	2.0e-45
Match length	142

% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	176019
Seq. ID	jC-atXP108C186B9T7055d1
Method	BLASTX
NCBI GI	g2497886
BLAST score	282
E value	5.0e-25
Match length	54
% identity	93
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	176020
Seq. ID	jC-atXP108C190P4T7056d1
Method	BLASTN
NCBI GI	g1086462
BLAST score	80
E value	1.0e-36
Match length	175
% identity	93
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT2b) gene, complete cds

Seq. No.	176021
Seq. ID	jC-atXP108C191A15T7024d1
Method	BLASTX
NCBI GI	g4206763
BLAST score	488
E value	7.0e-49
Match length	92
% identity	99
NCBI Description	(AF104328) cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana]

Seq. No.	176022
Seq. ID	jC-atXP108C191E5T7032d1
Method	BLASTX
NCBI GI	g4531443
BLAST score	66
E value	4.0e-20
Match length	131
% identity	53
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	176023
Seq. ID	jC-atXP108C192G21T7096d1
Method	BLASTX
NCBI GI	g1071912
BLAST score	708
E value	2.0e-90

Match length	199
% identity	89
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	176024
Seq. ID	jC-atXP108C192P19T7s1
Method	BLASTN
NCBI GI	g4757405
BLAST score	155
E value	7.0e-82
Match length	313
% identity	75
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	176025
Seq. ID	jC-atXP108C63E2T7s1
Method	BLASTN
NCBI GI	g3582315
BLAST score	86
E value	4.0e-41
Match length	102
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176026
Seq. ID	jC-atXP109C201O14T7s1
Method	BLASTX
NCBI GI	g2501669
BLAST score	154
E value	4.0e-10
Match length	114
% identity	34
NCBI Description	HYPOTHETICAL 48.1 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION >gi_1787241 (AE000202) putative transport protein [Escherichia coli]

Seq. No.	176027
Seq. ID	jC-atXP109C202I14T7s1
Method	BLASTX
NCBI GI	g3128176
BLAST score	86
E value	7.0e-09
Match length	108
% identity	32
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	176028
Seq. ID	jC-atXP109C205I7T7s1
Method	BLASTX
NCBI GI	g3695017
BLAST score	209
E value	1.0e-16
Match length	41

% identity	100
NCBI Description	(AF055847) similar to the C-terminus of putative plasma membrane-cell wall linker proteins [Arabidopsis thaliana]

Seq. No.	176029
Seq. ID	jC-atXP109C208I9T7s1
Method	BLASTN
NCBI GI	g2264309
BLAST score	55
E value	4.0e-22
Match length	115
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	176030
Seq. ID	jC-atXP109C73E12T7s1
Method	BLASTX
NCBI GI	g2245076
BLAST score	253
E value	1.0e-21
Match length	51
% identity	100
NCBI Description	(Z97343) GTP-binding RAB2A protein [Arabidopsis thaliana]

Seq. No.	176031
Seq. ID	jC-atXP109C93F8T7s1
Method	BLASTN
NCBI GI	g3046850
BLAST score	200
E value	1.0e-108
Match length	409
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	176032
Seq. ID	jC-atXP109C95E3T7s1
Method	BLASTN
NCBI GI	g3046851
BLAST score	62
E value	3.0e-26
Match length	323
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	176033
Seq. ID	jC-atXP109C97B4T7s1
Method	BLASTX
NCBI GI	g2982331
BLAST score	270
E value	5.0e-24
Match length	55
% identity	96
NCBI Description	(AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No.	176034
Seq. ID	jC-atXP109C98H23T7s1
Method	BLASTN
NCBI GI	g3426063
BLAST score	94
E value	9.0e-46
Match length	146
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for monooxygenase

Seq. No.	176035
Seq. ID	jC-atXP109C98O17T7s1
Method	BLASTN
NCBI GI	g634002
BLAST score	193
E value	1.0e-104
Match length	230
% identity	95
NCBI Description	A.thaliana mRNA for acyl-(acyl carrier protein) thioesterase

Seq. No.	176036
Seq. ID	jC-atXP109C99M15T7s1
Method	BLASTN
NCBI GI	g3941465
BLAST score	37
E value	1.0e-11
Match length	121
% identity	89
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB51) mRNA, complete cds

Seq. No.	176037
Seq. ID	jC-atXP10C94M1T7s2
Method	BLASTX
NCBI GI	g3269291
BLAST score	330
E value	7.0e-31
Match length	69
% identity	94
NCBI Description	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	176038
Seq. ID	jC-atXP10C95K24T7s2
Method	BLASTN
NCBI GI	g2656029
BLAST score	68
E value	6.0e-30
Match length	302
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	176039
Seq. ID	jC-atXP10C95M21T7s1
Method	BLASTN

NCBI GI	g4580522
BLAST score	117
E value	3.0e-59
Match length	228
% identity	91
NCBI Description	Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial cds

Seq. No.	176040
Seq. ID	jC-atXP10C95O20T7s1
Method	BLASTN
NCBI GI	g4454022
BLAST score	42
E value	8.0e-15
Match length	134
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	176041
Seq. ID	jC-atXP10C97A16T7s2
Method	BLASTN
NCBI GI	g4521999
BLAST score	36
E value	8.0e-11
Match length	144
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	176042
Seq. ID	jC-atXP10C97A3T7s1
Method	BLASTN
NCBI GI	g2760169
BLAST score	208
E value	1.0e-113
Match length	303
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	176043
Seq. ID	jC-atXP10C97B17T7d1
Method	BLASTN
NCBI GI	g3859658
BLAST score	309
E value	1.0e-173
Match length	342
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	176044
Seq. ID	jC-atXP10C97B17T7s1
Method	BLASTN
NCBI GI	g3859658
BLAST score	252

E value	1.0e-139
Match length	304
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	176045
Seq. ID	jC-atXP10C97D16T7s2
Method	BLASTX
NCBI GI	g3540185
BLAST score	415
E value	1.0e-40
Match length	86
% identity	98
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	176046
Seq. ID	jC-atXP110C119E3T7041a1
Method	BLASTX
NCBI GI	g1076413
BLAST score	999
E value	1.0e-109
Match length	191
% identity	100
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_2146776_pir__S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_608577 (L34076) serine acetyltransferase [Arabidopsis thaliana] >gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase [Arabidopsis thaliana] >gi_1093493_prf__2104212A Ser acetyltransferase [Arabidopsis thaliana]

Seq. No.	176047
Seq. ID	jC-atXP110C95J23T7016a1
Method	BLASTX
NCBI GI	g3341680
BLAST score	265
E value	8.0e-23
Match length	85
% identity	67
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	176048
Seq. ID	jC-atXP110CG3H3T7022a1
Method	BLASTX
NCBI GI	g464727
BLAST score	52
E value	4.0e-23
Match length	113
% identity	72
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_481451_pir__S38642 chaperonin-60 alpha chain - rape >gi_415925_emb_CAA81736_ (Z27222) chaperonin-60 alpha subunit [Brassica napus]

Seq. No.	176049
Seq. ID	jC-atXP110CG4A4T7015a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176050
Seq. ID	jC-atXP110CG4A5T7023a1
Method	BLASTX
NCBI GI	g2979552
BLAST score	43
E value	1.0e-83
Match length	151
% identity	98
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	176051
Seq. ID	jC-atXP111C106O4T7s1
Method	BLASTN
NCBI GI	g3335331
BLAST score	45
E value	1.0e-16
Match length	65
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176052
Seq. ID	jC-atXP111C106P13T7d1
Method	BLASTX
NCBI GI	g3894171
BLAST score	300
E value	4.0e-53
Match length	112
% identity	98
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	176053
Seq. ID	jC-atXP111C116O18T7s1
Method	BLASTN
NCBI GI	g3080352
BLAST score	271
E value	1.0e-151
Match length	359
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	176054
Seq. ID	jC-atXP111C122I17T7s1
Method	BLASTN
NCBI GI	g3228389

BLAST score	368
E value	0.0e+00
Match length	380
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	176055
Seq. ID	jC-atXP111C122M19T7s1
Method	BLASTN
NCBI GI	g4733953
BLAST score	477
E value	0.0e+00
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	176056
Seq. ID	jC-atXP111C123I6T7s1
Method	BLASTX
NCBI GI	g4314366
BLAST score	467
E value	6.0e-47
Match length	85
% identity	100
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176057
Seq. ID	jC-atXP111C124J7T7s1
Method	BLASTX
NCBI GI	g2190558
BLAST score	281
E value	4.0e-25
Match length	56
% identity	98
NCBI Description	(AC001229) F5I14.14 [Arabidopsis thaliana]

Seq. No.	176058
Seq. ID	jC-atXP111C125L24T7s1
Method	BLASTN
NCBI GI	g2618600
BLAST score	105
E value	4.0e-52
Match length	234
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	176059
Seq. ID	jC-atXP111C126G8T7s1
Method	BLASTX
NCBI GI	g4417286
BLAST score	227
E value	1.0e-18
Match length	66
% identity	73

NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]
Seq. No.	176060
Seq. ID	jC-atXP111C126M8T7s1
Method	BLASTX
NCBI GI	g67243
BLAST score	362
E value	2.0e-34
Match length	126
% identity	56
NCBI Description	fructose-bisphosphatase (EC 3.1.3.11), chloroplast - spinach >gi_999621_pdb_1SPI_A Spinacia oleracea >gi_999622_pdb_1SPI_B Spinacia oleracea >gi_999623_pdb_1SPI_C Spinacia oleracea >gi_999624_pdb_1SPI_D Spinacia oleracea
Seq. No.	176061
Seq. ID	jC-atXP112C124O17T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	6.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176062
Seq. ID	jC-atXP112C124P16T7d2
Method	BLASTX
NCBI GI	g4220481
BLAST score	292
E value	5.0e-26
Match length	117
% identity	55
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	176063
Seq. ID	jC-atXP112C125P10T7d2
Method	BLASTN
NCBI GI	g4757394
BLAST score	364
E value	0.0e+00
Match length	422
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence
Seq. No.	176064
Seq. ID	jC-atXP112C125P3T7d2
Method	BLASTN
NCBI GI	g2832639
BLAST score	483
E value	0.0e+00
Match length	507
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	176065
Seq. ID	jC-atXP112C126N4T4d2
Method	BLASTX
NCBI GI	g1170373
BLAST score	323
E value	2.0e-67
Match length	160
% identity	85
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	176066
Seq. ID	jC-atXP112C126O20T7a1
Method	BLASTX
NCBI GI	g3021274
BLAST score	411
E value	7.0e-40
Match length	162
% identity	58
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	176067
Seq. ID	jC-atXP112C126O22T7d2
Method	BLASTX
NCBI GI	g4056506
BLAST score	304
E value	6.0e-33
Match length	152
% identity	47
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	176068
Seq. ID	jC-atXP112C127B8T7a1
Method	BLASTN
NCBI GI	g3150395
BLAST score	359
E value	0.0e+00
Match length	552
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T9D9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176069
Seq. ID	jC-atXP112C127K6T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176070

Seq. ID	jC-atXP112C127K6T7d2
Method	BLASTX
NCBI GI	g4218122
BLAST score	183
E value	2.0e-13
Match length	69
% identity	55
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	176071
Seq. ID	jC-atXP112C127L23T7a1
Method	BLASTX
NCBI GI	g134940
BLAST score	223
E value	7.0e-18
Match length	70
% identity	63
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME (STRESS-INDUCIBLE PROTEIN STI35) >gi_102018_pir__A37767 stress-inducible protein sti35 - fungus (Fusarium solani) >gi_168162 (M33642) STI35 protein [Fusarium solani]

Seq. No.	176072
Seq. ID	jC-atXP112C127L23T7d2
Method	BLASTX
NCBI GI	g1351122
BLAST score	912
E value	1.0e-98
Match length	216
% identity	82
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME (STRESS-INDUCIBLE PROTEIN STI35) >gi_280494_pir__B37767 stress-inducible protein sti35 - fungus (Fusarium oxysporum) >gi_168164 (M33643) STI35 protein [Fusarium oxysporum]

Seq. No.	176073
Seq. ID	jC-atXP112C127M17T7a1
Method	BLASTX
NCBI GI	g4006943
BLAST score	782
E value	2.0e-83
Match length	159
% identity	93
NCBI Description	(AJ131392) alternative oxidase [Arabidopsis thaliana]

Seq. No.	176074
Seq. ID	jC-atXP112C127M17T7d2
Method	BLASTX
NCBI GI	g3915639
BLAST score	771
E value	7.0e-96
Match length	209
% identity	85
NCBI Description	ALTERNATIVE OXIDASE 1A PRECURSOR >gi_2506083_dbj_BAA22625_ (D89875) alternative oxidase [Arabidopsis thaliana]

Seq. No.	176075

Seq. ID	jC-atXP112C127N18T7a1
Method	BLASTX
NCBI GI	g3451068
BLAST score	406
E value	3.0e-39
Match length	164
% identity	59
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	176076
Seq. ID	jC-atXP112C127N23T7d2
Method	BLASTX
NCBI GI	g3914425
BLAST score	482
E value	3.0e-48
Match length	96
% identity	95
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No.	176077
Seq. ID	jC-atXP112C127P3T7a1
Method	BLASTN
NCBI GI	g2739359
BLAST score	395
E value	0.0e+00
Match length	556
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176078
Seq. ID	jC-atXP112C128E16T7a1
Method	BLASTX
NCBI GI	g4468218
BLAST score	245
E value	2.0e-20
Match length	93
% identity	51
NCBI Description	(AJ010025) unr-interacting protein [Homo sapiens]

Seq. No.	176079
Seq. ID	jC-atXP112C129A4T7d2
Method	BLASTX
NCBI GI	g4585872
BLAST score	250
E value	5.0e-21
Match length	118
% identity	48
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	176080
Seq. ID	jC-atXP112C129C11T7d2

Method	BLASTX
NCBI GI	g3915842
BLAST score	708
E value	9.0e-75
Match length	143
% identity	97
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_2598229_emb_CAA70112_ (Y08904) Rab11 protein [Arabidopsis thaliana]

Seq. No.	176081
Seq. ID	jC-atXP112C129D6T7a1
Method	BLASTX
NCBI GI	g3643607
BLAST score	227
E value	2.0e-18
Match length	85
% identity	56
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	176082
Seq. ID	jC-atXP112C129D6T7d2
Method	BLASTX
NCBI GI	g3643607
BLAST score	162
E value	1.0e-10
Match length	83
% identity	45
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	176083
Seq. ID	jC-atXP112C129F5T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176084
Seq. ID	jC-atXP112C129G10T7a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	63
E value	2.0e-26
Match length	95
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176085
Seq. ID	jC-atXP112C129G21T7d2
Method	BLASTN
NCBI GI	g2689438
BLAST score	528
E value	0.0e+00
Match length	613

% identity	96
NCBI Description	Arabidopsis thaliana BAC F24O1 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176086
Seq. ID	jC-atXP112C129H11T7d2
Method	BLASTX
NCBI GI	g3929364
BLAST score	1039
E value	1.0e-113
Match length	216
% identity	94
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	176087
Seq. ID	jC-atXP112C129N2T7d2
Method	BLASTN
NCBI GI	g1785673
BLAST score	268
E value	1.0e-149
Match length	428
% identity	91
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	176088
Seq. ID	jC-atXP112C129P12T7a1
Method	BLASTN
NCBI GI	g2245031
BLAST score	513
E value	0.0e+00
Match length	537
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176089
Seq. ID	jC-atXP112C129P9T7a1
Method	BLASTX
NCBI GI	g99735
BLAST score	448
E value	3.0e-44
Match length	158
% identity	68
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	176090
Seq. ID	jC-atXP112C130B1T7a1
Method	BLASTX
NCBI GI	g322618

BLAST score	203
E value	2.0e-15
Match length	38
% identity	92
NCBI Description	U1 snRNP 70K protein - Arabidopsis thaliana (fragment)

Seq. No.	176091
Seq. ID	jC-atXP112C130B1T7d2
Method	BLASTX
NCBI GI	g2129740
BLAST score	321
E value	3.0e-29
Match length	61
% identity	98
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	176092
Seq. ID	jC-atXP112C130O14T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176093
Seq. ID	jC-atXP112C131B9T7d2
Method	BLASTX
NCBI GI	g115385
BLAST score	813
E value	6.0e-87
Match length	215
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	176094
Seq. ID	jC-atXP112C131G18T7d2
Method	BLASTN
NCBI GI	g3335356
BLAST score	131
E value	4.0e-67
Match length	444
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176095
Seq. ID	jC-atXP112C131I4T7a1
Method	BLASTN
NCBI GI	g3212846

BLAST score	241
E value	1.0e-133
Match length	545
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176096
Seq. ID	jC-atXP112C131I4T7d2
Method	BLASTN
NCBI GI	g3212846
BLAST score	263
E value	1.0e-146
Match length	593
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176097
Seq. ID	jC-atXP112C132D16T7a1
Method	BLASTX
NCBI GI	g1710424
BLAST score	605
E value	1.0e-62
Match length	135
% identity	90
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	176098
Seq. ID	jC-atXP112C132D16T7d2
Method	BLASTX
NCBI GI	g1710424
BLAST score	807
E value	2.0e-86
Match length	193
% identity	85
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	176099
Seq. ID	jC-atXP112C132E21T7a1
Method	BLASTN
NCBI GI	g3335356
BLAST score	60
E value	9.0e-25
Match length	152
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176100
Seq. ID	jC-atXP112C132G2T7a1

Method	BLASTX
NCBI GI	g2655008
BLAST score	251
E value	4.0e-21
Match length	130
% identity	44
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	176101
Seq. ID	jC-atXP113C105L6T7013a1
Method	BLASTN
NCBI GI	g4589440
BLAST score	70
E value	6.0e-31
Match length	110
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	176102
Seq. ID	jC-atXP113C125C9T7021a2
Method	BLASTN
NCBI GI	g4115370
BLAST score	178
E value	3.0e-95
Match length	422
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176103
Seq. ID	jC-atXP113C132J10T7009a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	8.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176104
Seq. ID	jC-atXP113C132J12T7017a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176105
Seq. ID	jC-atXP113C132J6T7001a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	4.0e-13

Match length	52
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176106
Seq. ID	jC-atXP113C132J6T7001a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176107
Seq. ID	jC-atXP113C132L18T7041a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176108
Seq. ID	jC-atXP113C132M14T7049a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	2.0e-17
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176109
Seq. ID	jC-atXP113C132M21T7057a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176110
Seq. ID	jC-atXP113C132M21T7057a2
Method	BLASTX
NCBI GI	g4758340
BLAST score	213
E value	8.0e-17
Match length	88
% identity	48
NCBI Description	phenylalanine-tRNA synthetase-like >gi_2102679 (U07424) putative tRNA synthetase-like protein [Homo sapiens] >gi_4104935_gb_AAD02221_ (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo sapiens]

Seq. No.	176111
Seq. ID	jC-atXP113C132O13T7073a1
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	9.0e-14
Match length	41
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176112
Seq. ID	jC-atXP113C132O7T7065a1
Method	BLASTN
NCBI GI	g1732518
BLAST score	48
E value	7.0e-18
Match length	160
% identity	84
NCBI Description	Arabidopsis thaliana Rho1Ps homolog mRNA, complete cds

Seq. No.	176113
Seq. ID	jC-atXP113C132P9T7081a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176114
Seq. ID	jC-atXP113C132P9T7081a2
Method	BLASTN
NCBI GI	g598848
BLAST score	47
E value	5.0e-17
Match length	55
% identity	96
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176115
Seq. ID	jC-atXP113C133J2T7050a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176116
Seq. ID	jC-atXP113C133L7T7019a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	56

E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176117
Seq. ID	jC-atXP113C133M13T7035a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	40
E value	1.0e-12
Match length	44
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176118
Seq. ID	jC-atXP113C133M14T7043a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176119
Seq. ID	jC-atXP113C133M20T7051a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176120
Seq. ID	jC-atXP113C133M6T7027a2
Method	BLASTX
NCBI GI	g2961357
BLAST score	145
E value	8.0e-09
Match length	117
% identity	32
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	176121
Seq. ID	jC-atXP113C133N11T7059a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	1.0e-21
Match length	55
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176122
Seq. ID	jC-atXP113C133N20T7d1

Method	BLASTN
NCBI GI	g4589437
BLAST score	206
E value	1.0e-112
Match length	342
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	176123
Seq. ID	jC-atXP113C133O15T7091a2
Method	BLASTN
NCBI GI	g598848
BLAST score	55
E value	7.0e-22
Match length	63
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176124
Seq. ID	jC-atXP113C133O4T7083a1
Method	BLASTN
NCBI GI	g2264318
BLAST score	37
E value	2.0e-11
Match length	77
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	176125
Seq. ID	jC-atXP113C133O4T7083a2
Method	BLASTN
NCBI GI	g598848
BLAST score	34
E value	2.0e-09
Match length	42
% identity	95
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176126
Seq. ID	jC-atXP113C133P12T7012a2
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176127
Seq. ID	jC-atXP113C134H20T7058a2
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	1.0e-17
Match length	48

% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176128
Seq. ID	jC-atXP113C134I5T7066a2
Method	BLASTN
NCBI GI	g4589437
BLAST score	278
E value	1.0e-155
Match length	484
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	176129
Seq. ID	jC-atXP113C134L6T7082a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176130
Seq. ID	jC-atXP113C134M18T7020a1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	1.0e-12
Match length	54
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176131
Seq. ID	jC-atXP113C134M21T7028a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176132
Seq. ID	jC-atXP113C134M21T7028a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176133
Seq. ID	jC-atXP113C134N12T7036a2
Method	BLASTN

NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176134
Seq. ID	jC-atXP113C134O13T7052a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	9.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176135
Seq. ID	jC-atXP113C134O9T7044a1
Method	BLASTN
NCBI GI	g2252823
BLAST score	87
E value	4.0e-41
Match length	268
% identity	89
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	176136
Seq. ID	jC-atXP113C134O9T7044a2
Method	BLASTX
NCBI GI	g2252840
BLAST score	423
E value	2.0e-41
Match length	124
% identity	72
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	176137
Seq. ID	jC-atXP113C135C12T7084a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	1.0e-15
Match length	45
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176138
Seq. ID	jC-atXP113C135C14T7092a2
Method	BLASTN
NCBI GI	g598848
BLAST score	44
E value	4.0e-15
Match length	52
% identity	96
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176139
Seq. ID	jC-atXP113C217O6T7d1
Method	BLASTN
NCBI GI	g2980757
BLAST score	95
E value	6.0e-46
Match length	305
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	176140
Seq. ID	jC-atXP113C220J17T7053a1
Method	BLASTN
NCBI GI	g4159708
BLAST score	71
E value	1.0e-31
Match length	129
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	176141
Seq. ID	jC-atXP113C221P16T7022a2
Method	BLASTN
NCBI GI	g3337347
BLAST score	493
E value	0.0e+00
Match length	513
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176142
Seq. ID	jC-atXP113C221P7T7014a1
Method	BLASTN
NCBI GI	g1655481
BLAST score	100
E value	8.0e-49
Match length	174
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for delta subunit of mitochondrial F1-ATPase, complete cds

Seq. No.	176143
Seq. ID	jC-atXP113C221P7T7014a2
Method	BLASTX
NCBI GI	g3334124
BLAST score	90
E value	3.0e-30
Match length	94
% identity	83
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	176144
Seq. ID	jC-atXP113C222P9T7085a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	101
E value	2.0e-49
Match length	353
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176145
Seq. ID	jC-atXP113C228B18T7086a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176146
Seq. ID	jC-atXP113C228F24T7094a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	8.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176147
Seq. ID	jC-atXP113C228L18T7047a1
Method	BLASTX
NCBI GI	g3953473
BLAST score	604
E value	9.0e-63
Match length	120
% identity	99
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	176148
Seq. ID	jC-atXP113C228M2T7015a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	3.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176149
Seq. ID	jC-atXP113C228M9T7023a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51

E value	1.0e-19
Match length	58
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176150
Seq. ID	jC-atXP113C228M9T7023a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	63
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176151
Seq. ID	jC-atXP113C229A8T7063a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	8.0e-20
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176152
Seq. ID	jC-atXP113C229B3T7048a1
Method	BLASTX
NCBI GI	g2924784
BLAST score	172
E value	4.0e-12
Match length	63
% identity	51
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	176153
Seq. ID	jC-atXP113C229B3T7048a2
Method	BLASTN
NCBI GI	g2924768
BLAST score	94
E value	4.0e-45
Match length	226
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176154
Seq. ID	jC-atXP113C229C8T7056a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	3.0e-16
Match length	50
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176155
Seq. ID	jC-atXP113C229D9T7072a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	45
E value	5.0e-16
Match length	257
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	176156
Seq. ID	jC-atXP113C229D9T7072a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176157
Seq. ID	jC-atXP113C229E14T7080a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	7.0e-12
Match length	54
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176158
Seq. ID	jC-atXP113C229E14T7080a2
Method	BLASTN
NCBI GI	g540252
BLAST score	42
E value	2.0e-14
Match length	50
% identity	96
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.	176159
Seq. ID	jC-atXP113C229E21T7096a1
Method	BLASTX
NCBI GI	g2924784
BLAST score	398
E value	1.0e-38
Match length	94
% identity	79
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]
Seq. No.	176160
Seq. ID	jC-atXP113C229E21T7d1
Method	BLASTX

NCBI GI	g2117612
BLAST score	266
E value	7.0e-24
Match length	64
% identity	78
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	176161
Seq. ID	jC-atXP113C230A10T7079a2
Method	BLASTN
NCBI GI	g2924768
BLAST score	72
E value	9.0e-32
Match length	193
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176162
Seq. ID	jC-atXP113C230D16T7087a1
Method	BLASTN
NCBI GI	g2924733
BLAST score	72
E value	4.0e-32
Match length	228
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	176163
Seq. ID	jC-atXP113C230D16T7087a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176164
Seq. ID	jC-atXP113C230D23T7095a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	5.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176165
Seq. ID	jC-atXP113C230I4T7008a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56

% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176166
Seq. ID	jC-atXP113C230J24T7016a1
Method	BLASTX
NCBI GI	g2924784
BLAST score	324
E value	5.0e-30
Match length	82
% identity	73
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]
Seq. No.	176167
Seq. ID	jC-atXP113C230K22T7024a1
Method	BLASTN
NCBI GI	g540252
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds
Seq. No.	176168
Seq. ID	jC-atXP113C230K22T7024a2
Method	BLASTX
NCBI GI	g2924784
BLAST score	307
E value	1.0e-27
Match length	111
% identity	62
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]
Seq. No.	176169
Seq. ID	jC-atXP114C230O23T7s1
Method	BLASTX
NCBI GI	g3982576
BLAST score	280
E value	5.0e-25
Match length	67
% identity	85
NCBI Description	(AF023140) imidazoleglycerol phosphate dehydratase [Thlaspi goesingense]
Seq. No.	176170
Seq. ID	jC-atXP114C231L24T7s1
Method	BLASTN
NCBI GI	g2760170
BLAST score	248
E value	1.0e-137
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	176171
Seq. ID	jC-atXP114C231M17T7s1
Method	BLASTN
NCBI GI	g4467094
BLAST score	78
E value	3.0e-36
Match length	114
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	176172
Seq. ID	jC-atXP114C232A14T7s1
Method	BLASTN
NCBI GI	g3193311
BLAST score	434
E value	0.0e+00
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	176173
Seq. ID	jC-atXP115C116J22T7079d1
Method	BLASTN
NCBI GI	g2656031
BLAST score	392
E value	0.0e+00
Match length	655
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	176174
Seq. ID	jC-atXP115C117L10T7095d1
Method	BLASTX
NCBI GI	g166834
BLAST score	813
E value	5.0e-87
Match length	158
% identity	99
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	176175
Seq. ID	jC-atXP115C119L5T7071d1
Method	BLASTX
NCBI GI	g585536
BLAST score	1124
E value	1.0e-123
Match length	221
% identity	95
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	176176
Seq. ID	jC-atXP115C244I24T7025d1
Method	BLASTN
NCBI GI	g2343110
BLAST score	35
E value	1.0e-09
Match length	35
% identity	100
NCBI Description	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds

Seq. No.	176177
Seq. ID	jC-atXP115C246O13T7042d1
Method	BLASTX
NCBI GI	g2661422
BLAST score	566
E value	4.0e-58
Match length	214
% identity	58
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	176178
Seq. ID	jC-atXP115C247H12T7057d1
Method	BLASTN
NCBI GI	g2342673
BLAST score	127
E value	1.0e-64
Match length	633
% identity	91
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176179
Seq. ID	jC-atXP115C247L4T7081d1
Method	BLASTX
NCBI GI	g2795806
BLAST score	448
E value	6.0e-56
Match length	160
% identity	73
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	176180
Seq. ID	jC-atXP115C247M1T7s1
Method	BLASTN
NCBI GI	g634002
BLAST score	44
E value	4.0e-16
Match length	56
% identity	95
NCBI Description	A.thaliana mRNA for acyl-(acyl carrier protein) thioesterase

Seq. No.	176181
Seq. ID	jC-atXP115C248I23T7028d1
Method	BLASTN
NCBI GI	g4678371
BLAST score	89
E value	5.0e-42
Match length	433
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	176182
Seq. ID	jC-atXP115C248I6T7s1
Method	BLASTN
NCBI GI	g2459406
BLAST score	114
E value	2.0e-57
Match length	210
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176183
Seq. ID	jC-atXP115C248O19T7s1
Method	BLASTX
NCBI GI	g3834314
BLAST score	486
E value	3.0e-49
Match length	94
% identity	100
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	176184
Seq. ID	jC-atXP115C248O20T7s1
Method	BLASTX
NCBI GI	g4587535
BLAST score	110
E value	6.0e-05
Match length	111
% identity	27
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. EST gb_R29935 comes from this gene. [Arabidopsis thaliana]

Seq. No.	176185
Seq. ID	jC-atXP115C248O2T7s1
Method	BLASTN
NCBI GI	g3269280
BLAST score	161
E value	1.0e-85
Match length	221
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	176186
Seq. ID	jC-atXP115C249C20T7058d1
Method	BLASTX
NCBI GI	g2117937
BLAST score	45
E value	7.0e-14
Match length	210
% identity	28
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	176187
Seq. ID	jC-atXP115C249G23T7066d1
Method	BLASTX
NCBI GI	g3256075
BLAST score	181
E value	4.0e-32
Match length	137
% identity	64
NCBI Description	(Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]

Seq. No.	176188
Seq. ID	jC-atXP115C249N15T7030d1
Method	BLASTX
NCBI GI	g4587542
BLAST score	188
E value	9.0e-14
Match length	178
% identity	23
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	176189
Seq. ID	jC-atXP115C249O15T7s1
Method	BLASTN
NCBI GI	g3985934
BLAST score	95
E value	2.0e-46
Match length	147
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	176190
Seq. ID	jC-atXP115C250F5T7d1
Method	BLASTX
NCBI GI	g2911040
BLAST score	62
E value	2.0e-69
Match length	148
% identity	93
NCBI Description	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	176191
Seq. ID	jC-atXP115C250H2T7d1
Method	BLASTX
NCBI GI	g3377817
BLAST score	216
E value	1.0e-29
Match length	78
% identity	80
NCBI Description	(AF076275) contains similarity to C3HC4-type zinc fingers (Pfam: zf-C3HC4.hmm, score: 29.48) [Arabidopsis thaliana]

Seq. No.	176192
Seq. ID	jC-atXP115C251A11T7062d1
Method	BLASTX
NCBI GI	g4490750
BLAST score	859
E value	1.0e-103
Match length	207
% identity	97
NCBI Description	(AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]

Seq. No.	176193
Seq. ID	jC-atXP115C251B22T7070d1
Method	BLASTX
NCBI GI	g585536
BLAST score	113
E value	1.0e-32
Match length	165
% identity	53
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	176194
Seq. ID	jC-atXP115C251B22T7s1
Method	BLASTX
NCBI GI	g4154352
BLAST score	184
E value	1.0e-13
Match length	105
% identity	38
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	176195
Seq. ID	jC-atXP115C251M20T7d1
Method	BLASTN
NCBI GI	g3193282
BLAST score	234
E value	1.0e-129
Match length	262
% identity	97
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	176196
Seq. ID	jC-atXP116C126N11T7s1

Method	BLASTX
NCBI GI	g3193316
BLAST score	261
E value	1.0e-22
Match length	71
% identity	77
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	176197
Seq. ID	jC-atXP116C135F22T7s1
Method	BLASTN
NCBI GI	g4063706
BLAST score	124
E value	2.0e-63
Match length	228
% identity	89
NCBI Description	Arabidopsis thaliana extensin-like protein (ELP) mRNA, complete cds

Seq. No.	176198
Seq. ID	jC-atXP116C136H5T7s1
Method	BLASTX
NCBI GI	g4678384
BLAST score	435
E value	4.0e-43
Match length	100
% identity	86
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	176199
Seq. ID	jC-atXP116C139F17T7s1
Method	BLASTN
NCBI GI	g4587677
BLAST score	93
E value	1.0e-44
Match length	169
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T22C12 genomic sequence, complete sequence

Seq. No.	176200
Seq. ID	jC-atXP116C139J5T7s1
Method	BLASTN
NCBI GI	g2660661
BLAST score	48
E value	2.0e-18
Match length	88
% identity	72
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176201
Seq. ID	jC-atXP117C139P15T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53

E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176202
Seq. ID	jC-atXP117C140D2T7a1
Method	BLASTN
NCBI GI	g4678371
BLAST score	166
E value	5.0e-88
Match length	477
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	176203
Seq. ID	jC-atXP117C140E24T7a1
Method	BLASTX
NCBI GI	g3046700
BLAST score	66
E value	5.0e-76
Match length	161
% identity	85
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	176204
Seq. ID	jC-atXP117C140F17T7a1
Method	BLASTN
NCBI GI	g391602
BLAST score	68
E value	2.0e-29
Match length	351
% identity	84
NCBI Description	Arabidopsis thaliana ATPK12D mRNA for casein kinase II catalytic subunit, complete cds

Seq. No.	176205
Seq. ID	jC-atXP117C140F6T7a1
Method	BLASTX
NCBI GI	g3269301
BLAST score	269
E value	2.0e-23
Match length	98
% identity	59
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	176206
Seq. ID	jC-atXP117C140I17T7a1
Method	BLASTX
NCBI GI	g2739375
BLAST score	51
E value	3.0e-18
Match length	89

% identity	63
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	176207
Seq. ID	jC-atXP117C140K11T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	48
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176208
Seq. ID	jC-atXP117C140L8T7a1
Method	BLASTN
NCBI GI	g2924652
BLAST score	51
E value	2.0e-19
Match length	167
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	176209
Seq. ID	jC-atXP117C140L8T7d1
Method	BLASTN
NCBI GI	g2924652
BLAST score	55
E value	2.0e-22
Match length	114
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	176210
Seq. ID	jC-atXP117C140M22T7a1
Method	BLASTN
NCBI GI	g540252
BLAST score	39
E value	3.0e-12
Match length	51
% identity	94
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	176211
Seq. ID	jC-atXP117C140M22T7d1
Method	BLASTN
NCBI GI	g4589428
BLAST score	52
E value	9.0e-21
Match length	117
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	176212

Seq. ID	jC-atXP117C141C4T7a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176213
Seq. ID	jC-atXP117C141E21T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176214
Seq. ID	jC-atXP117C141E22T7a1
Method	BLASTN
NCBI GI	g4490291
BLAST score	150
E value	2.0e-78
Match length	463
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	176215
Seq. ID	jC-atXP117C141F24T7d1
Method	BLASTN
NCBI GI	g2244901
BLAST score	107
E value	2.0e-53
Match length	148
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176216
Seq. ID	jC-atXP117C141H11T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	55
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176217
Seq. ID	jC-atXP117C141H17T7a1
Method	BLASTX
NCBI GI	g4006934
BLAST score	389

E value	3.0e-37
Match length	99
% identity	77
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	176218
Seq. ID	jC-atXP117C141H3T7a1
Method	BLASTX
NCBI GI	g1709535
BLAST score	199
E value	4.0e-44
Match length	104
% identity	88
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	176219
Seq. ID	jC-atXP117C141I10T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	6.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176220
Seq. ID	jC-atXP117C141I22T7a1
Method	BLASTX
NCBI GI	g1730512
BLAST score	431
E value	2.0e-42
Match length	153
% identity	64
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805 (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	176221
Seq. ID	jC-atXP117C141K5T7d1
Method	BLASTN
NCBI GI	g4371278
BLAST score	97
E value	3.0e-47
Match length	238
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176222

Seq. ID	jC-atXP117C141L4T7d1
Method	BLASTN
NCBI GI	g3985949
BLAST score	149
E value	2.0e-78
Match length	170
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	176223
Seq. ID	jC-atXP117C141M13T7a1
Method	BLASTX
NCBI GI	g4539343
BLAST score	198
E value	6.0e-15
Match length	108
% identity	46
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	176224
Seq. ID	jC-atXP117C142B9T7a1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	1.0e-15
Match length	53
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176225
Seq. ID	jC-atXP117C142F15T7a1
Method	BLASTX
NCBI GI	g629592
BLAST score	249
E value	6.0e-21
Match length	114
% identity	46
NCBI Description	hypothetical protein - rape

Seq. No.	176226
Seq. ID	jC-atXP117C142F2T7a1
Method	BLASTX
NCBI GI	g4539459
BLAST score	270
E value	2.0e-23
Match length	111
% identity	47
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	176227
Seq. ID	jC-atXP117C143A21T7a1
Method	BLASTX
NCBI GI	g3510254
BLAST score	502
E value	2.0e-54
Match length	154

% identity	82
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	176228
Seq. ID	jC-atXP117C143A6T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	54
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176229
Seq. ID	jC-atXP118C142N22T7035a1
Method	BLASTN
NCBI GI	g3927822
BLAST score	667
E value	0.0e+00
Match length	675
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176230
Seq. ID	jC-atXP118C143C23T7033a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	2.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176231
Seq. ID	jC-atXP118C143D19T7057a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176232
Seq. ID	jC-atXP118C143D3T7041a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	3.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176233
Seq. ID	jC-atXP118C143E9T7081d2
Method	BLASTX

NCBI GI	g1542941
BLAST score	352
E value	5.0e-33
Match length	81
% identity	79
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	176234
Seq. ID	jC-atXP118C143N16T7019d2
Method	BLASTX
NCBI GI	g3005587
BLAST score	99
E value	4.0e-03
Match length	349
% identity	5
NCBI Description	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]

Seq. No.	176235
Seq. ID	jC-atXP118C144B4T7083a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	2.0e-19
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176236
Seq. ID	jC-atXP118C144B4T7083d2
Method	BLASTX
NCBI GI	g1542941
BLAST score	352
E value	5.0e-33
Match length	81
% identity	79
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	176237
Seq. ID	jC-atXP118C144G12T7045a1
Method	BLASTX
NCBI GI	g2245125
BLAST score	144
E value	1.0e-08
Match length	62
% identity	50
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176238
Seq. ID	jC-atXP118C144J15T7093d2
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	9.0e-13
Match length	40
% identity	100

NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	176239
Seq. ID	jC-atXP118C145G4T7068d2
Method	BLASTX
NCBI GI	g132090
BLAST score	83
E value	1.0e-36
Match length	180
% identity	50
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	176240
Seq. ID	jC-atXP118C146A8T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	6.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176241
Seq. ID	jC-atXP118C146A8T7043d2
Method	BLASTN
NCBI GI	g1848276
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Human telomerase-associated protein TP-1 mRNA, complete cds

Seq. No.	176242
Seq. ID	jC-atXP118C146D3T7059d2
Method	BLASTN
NCBI GI	g2264320
BLAST score	30
E value	1.0e-06
Match length	100
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	176243
Seq. ID	jC-atXP118C155D24T7023a1
Method	BLASTN
NCBI GI	g3399678
BLAST score	116
E value	4.0e-58
Match length	371
% identity	81

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	176244
Seq. ID	jC-atXP118C155H23T7048a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	6.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176245
Seq. ID	jC-atXP118C155H23T7048d2
Method	BLASTX
NCBI GI	g2385344
BLAST score	1101
E value	1.0e-121
Match length	223
% identity	97
NCBI Description	(Y14567) sigma factorB [Arabidopsis thaliana]
Seq. No.	176246
Seq. ID	jC-atXP119C155P20T7033a1
Method	BLASTN
NCBI GI	g2979540
BLAST score	348
E value	0.0e+00
Match length	496
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	176247
Seq. ID	jC-atXP119C156D23T7002a1
Method	BLASTX
NCBI GI	g346312
BLAST score	76
E value	1.8e+00
Match length	304
% identity	18
NCBI Description	profilaggrin - human (fragment) >gi_553621 (L01089) profilaggrin [Homo sapiens]
Seq. No.	176248
Seq. ID	jC-atXP119C156E12T7018a1
Method	BLASTX
NCBI GI	g2454184
BLAST score	207
E value	7.0e-16
Match length	91
% identity	53
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]
Seq. No.	176249

Seq. ID	jC-atXP119C156E20T7034a1
Method	BLASTN
NCBI GI	g4263694
BLAST score	50
E value	1.0e-18
Match length	105
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176250
Seq. ID	jC-atXP119C156I9T7065a1
Method	BLASTX
NCBI GI	g3033385
BLAST score	263
E value	1.0e-22
Match length	111
% identity	57
NCBI Description	(AC004238) similar to Human XE169 protein (escapes X-chromosome inactivation) [Arabidopsis thaliana]

Seq. No.	176251
Seq. ID	jC-atXP119C166E1T7035a1
Method	BLASTN
NCBI GI	g16192
BLAST score	42
E value	8.0e-14
Match length	74
% identity	91
NCBI Description	A.thaliana ats1B, ats2B and ats3B gene for ribulose-1,5-biphosphate carboxylase small subunit (rbcS) (EC 4.1.1.39)

Seq. No.	176252
Seq. ID	jC-atXP119C166H22T7040a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	1.0e-13
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176253
Seq. ID	jC-atXP119C166H2T7067a1
Method	BLASTX
NCBI GI	g629562
BLAST score	771
E value	4.0e-82
Match length	147
% identity	99
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana]

	>gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]
Seq. No.	176254
Seq. ID	jC-atXP119C166I6T7048a1
Method	BLASTN
NCBI GI	g4519194
BLAST score	35
E value	6.0e-10
Match length	90
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence
Seq. No.	176255
Seq. ID	jC-atXP119C166K17T7080a1
Method	BLASTX
NCBI GI	g2347098
BLAST score	276
E value	5.0e-24
Match length	105
% identity	63
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]
Seq. No.	176256
Seq. ID	jC-atXP119C166L18T7088a1
Method	BLASTX
NCBI GI	g4558664
BLAST score	197
E value	9.0e-15
Match length	104
% identity	38
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]
Seq. No.	176257
Seq. ID	jC-atXP119C193G18T7012a1
Method	BLASTX
NCBI GI	g2961352
BLAST score	510
E value	1.0e-51
Match length	147
% identity	75
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]
Seq. No.	176258
Seq. ID	jC-atXP119C194G20T7091a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176259
Seq. ID	jC-atXP119C194O15T7020a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176260
Seq. ID	jC-atXP119C196K11T7029a1
Method	BLASTN
NCBI GI	g3128136
BLAST score	140
E value	1.0e-72
Match length	216
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	176261
Seq. ID	jC-atXP119C196M16T7069a1
Method	BLASTN
NCBI GI	g642161
BLAST score	53
E value	1.0e-20
Match length	64
% identity	97
NCBI Description	A.thaliana gene for chloroplast ribosomal protein S13

Seq. No.	176262
Seq. ID	jC-atXP119C196M8T7061a1
Method	BLASTX
NCBI GI	g3236242
BLAST score	251
E value	2.0e-21
Match length	99
% identity	58
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	176263
Seq. ID	jC-atXP119C196O5T7085a1
Method	BLASTN
NCBI GI	g3168839
BLAST score	113
E value	2.0e-56
Match length	351
% identity	84
NCBI Description	Arabidopsis thaliana copper homeostasis factor (CCH) mRNA, complete cds

Seq. No.	176264
Seq. ID	jC-atXP119C201D8T7d1
Method	BLASTN

NCBI GI	g4263694
BLAST score	164
E value	3.0e-87
Match length	201
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176265
Seq. ID	jC-atXP119C206D21T7007a1
Method	BLASTX
NCBI GI	g4454467
BLAST score	499
E value	3.0e-50
Match length	186
% identity	53
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	176266
Seq. ID	jC-atXP119C211O14T7095a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	49
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176267
Seq. ID	jC-atXP11C97E11T7s1
Method	BLASTN
NCBI GI	g2827698
BLAST score	287
E value	1.0e-160
Match length	417
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)

Seq. No.	176268
Seq. ID	jC-atXP11C97E18T7005d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176269
Seq. ID	jC-atXP11C97E4T7s1
Method	BLASTN
NCBI GI	g3868858
BLAST score	65
E value	2.0e-28
Match length	108

% identity	95
NCBI Description	Arabidopsis thaliana mRNA for RAV2, complete cds

Seq. No.	176270
Seq. ID	jC-atXP11C97N9T7s1
Method	BLASTN
NCBI GI	g2262135
BLAST score	84
E value	8.0e-40
Match length	152
% identity	89
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	176271
Seq. ID	jC-atXP11C97O20T7027d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	36
E value	1.0e-10
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	176272
Seq. ID	jC-atXP11C97P15T7033d1
Method	BLASTX
NCBI GI	g3738291
BLAST score	519
E value	8.0e-53
Match length	143
% identity	72
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	176273
Seq. ID	jC-atXP11C97P18T7036d1
Method	BLASTN
NCBI GI	g3128135
BLAST score	212
E value	1.0e-115
Match length	471
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	176274
Seq. ID	jC-atXP11C97P9T7031d1
Method	BLASTX
NCBI GI	g1695717
BLAST score	218
E value	2.0e-48
Match length	154
% identity	71
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	176275

Seq. ID	jC-atXP11C98B4T7039d1
Method	BLASTX
NCBI GI	g2623304
BLAST score	619
E value	1.0e-64
Match length	152
% identity	84
NCBI Description	(AC002409) similar to Medicago nodulin N21 [Arabidopsis thaliana]

Seq. No.	176276
Seq. ID	jC-atXP11C98B4T7s1
Method	BLASTN
NCBI GI	g4249393
BLAST score	368
E value	0.0e+00
Match length	413
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176277
Seq. ID	jC-atXP11C98D23T7047d1
Method	BLASTN
NCBI GI	g2342673
BLAST score	275
E value	1.0e-153
Match length	325
% identity	97
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176278
Seq. ID	jC-atXP11C98E12T7s1
Method	BLASTN
NCBI GI	g2341023
BLAST score	126
E value	8.0e-65
Match length	166
% identity	94
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176279
Seq. ID	jC-atXP11C98F1T7051d1
Method	BLASTX
NCBI GI	g3024434
BLAST score	209
E value	1.0e-16
Match length	125
% identity	45
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	176280
Seq. ID	jC-atXP11C98G7T7057d1

Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	47
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176281
Seq. ID	jC-atXP11C98H7T7059d1
Method	BLASTX
NCBI GI	g4581162
BLAST score	361
E value	3.0e-34
Match length	92
% identity	74
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	176282
Seq. ID	jC-atXP11C98J21T7s1
Method	BLASTN
NCBI GI	g2656028
BLAST score	439
E value	0.0e+00
Match length	479
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	176283
Seq. ID	jC-atXP11C98L24T7071d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	54
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176284
Seq. ID	jC-atXP11C99A2T7085d1
Method	BLASTN
NCBI GI	g2262155
BLAST score	39
E value	2.0e-12
Match length	253
% identity	87
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	176285
Seq. ID	jC-atXP11C99B10T7090d1
Method	BLASTX
NCBI GI	g4455256

BLAST score	53
E value	8.0e-10
Match length	87
% identity	48
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	176286
Seq. ID	jC-atXP121C116F4T7051d1
Method	BLASTX
NCBI GI	g3834310
BLAST score	318
E value	1.0e-41
Match length	135
% identity	73
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	176287
Seq. ID	jC-atXP121C117G5T7056d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	2.0e-10
Match length	44
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176288
Seq. ID	jC-atXP121C118A13T7014d1
Method	BLASTX
NCBI GI	g123178
BLAST score	64
E value	6.0e-57
Match length	202
% identity	60
NCBI Description	HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir__A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi_167142 (M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No.	176289
Seq. ID	jC-atXP121C118B12T7054d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	176290
Seq. ID	jC-atXP121C118B15T7062d1

Method	BLASTN
NCBI GI	g3941523
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	176291
Seq. ID	jC-atXP121C118B8T7046d1
Method	BLASTX
NCBI GI	g2062158
BLAST score	768
E value	7.0e-82
Match length	190
% identity	41
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	176292
Seq. ID	jC-atXP121C118D4T7023d1
Method	BLASTX
NCBI GI	g2494175
BLAST score	143
E value	2.0e-17
Match length	135
% identity	44
NCBI Description	GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665) glutamate decarboxylase 2 [Arabidopsis thaliana] >gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	176293
Seq. ID	jC-atXP121C120C10T7055d1
Method	BLASTN
NCBI GI	g3600045
BLAST score	129
E value	6.0e-66
Match length	185
% identity	94
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	176294
Seq. ID	jC-atXP121C120E3T7024d1
Method	BLASTX
NCBI GI	g544255
BLAST score	215
E value	3.0e-17
Match length	135
% identity	44
NCBI Description	ESTERASE E4 PRECURSOR (CARBOXYLIC-ESTER HYDROLASE) >gi_480385_pir__S36786 carboxylesterase (EC 3.1.1.1) E4 - green peach aphid >gi_397511_emb_CAA52648_ (X74554) esterase E4 [Myzus persicae]

Seq. No.	176295

Seq. ID	jC-atXP121C120E8T7040d1
Method	BLASTX
NCBI GI	g4581856
BLAST score	258
E value	7.0e-36
Match length	196
% identity	54
NCBI Description	(AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita]

Seq. No.	176296
Seq. ID	jC-atXP121C125A5T7067d1
Method	BLASTX
NCBI GI	g4454025
BLAST score	250
E value	4.0e-21
Match length	105
% identity	51
NCBI Description	(AL035394) putative cellulase [Arabidopsis thaliana]

Seq. No.	176297
Seq. ID	jC-atXP121C131P20T7061d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176298
Seq. ID	jC-atXP121C131P21T7069d1
Method	BLASTN
NCBI GI	g881474
BLAST score	34
E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds

Seq. No.	176299
Seq. ID	jC-atXP121C133A23T7034d1
Method	BLASTN
NCBI GI	g3281847
BLAST score	39
E value	2.0e-12
Match length	111
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	176300
Seq. ID	jC-atXP121C134D21T7066d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38

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E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176301
Seq. ID	jC-atXP121C134D9T7058d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176302
Seq. ID	jC-atXP121C134G3T7011d1
Method	BLASTN
NCBI GI	g3243255
BLAST score	34
E value	3.0e-09
Match length	38
% identity	97
NCBI Description	Vigna unguiculata phosphoribosylpyrophosphate amidotransferase (pur1) mRNA, complete cds

Seq. No.	176303
Seq. ID	jC-atXP121C135A2T7077d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176304
Seq. ID	jC-atXP121C88F8T7020d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	35
E value	6.0e-10
Match length	35
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176305
Seq. ID	jC-atXP121C94N21T7052d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	1.0e-11
Match length	38

% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176306
Seq. ID	jC-atXP121C96C14T7013d1
Method	BLASTN
NCBI GI	g3449330
BLAST score	462
E value	0.0e+00
Match length	589
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	176307
Seq. ID	jC-atXP121CH2D1T7081d1
Method	BLASTX
NCBI GI	g4454025
BLAST score	318
E value	3.0e-29
Match length	104
% identity	63
NCBI Description	(AL035394) putative cellulase [Arabidopsis thaliana]

Seq. No.	176308
Seq. ID	jC-atXP122C118E4T7042a1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	8.0e-17
Match length	50
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176309
Seq. ID	jC-atXP122C118G10T7050a1
Method	BLASTX
NCBI GI	g4545231
BLAST score	531
E value	6.0e-54
Match length	131
% identity	79
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	176310
Seq. ID	jC-atXP122C120H10T7005a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176311

Seq. ID	jC-atXP122C120H21T7037a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176312
Seq. ID	jC-atXP122C120H2T7084a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176313
Seq. ID	jC-atXP122C156J20T7085a1
Method	BLASTX
NCBI GI	g2129740
BLAST score	399
E value	2.0e-38
Match length	123
% identity	65
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	176314
Seq. ID	jC-atXP122C156M8T7038a1
Method	BLASTN
NCBI GI	g2564050
BLAST score	180
E value	2.0e-96
Match length	487
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	176315
Seq. ID	jC-atXP122C156P4T7086a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176316
Seq. ID	jC-atXP122C158F1T7071a1
Method	BLASTN

NCBI GI	g2275194
BLAST score	118
E value	2.0e-59
Match length	277
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176317
Seq. ID	jC-atXP122C159E19T7087a1
Method	BLASTX
NCBI GI	g4538926
BLAST score	508
E value	2.0e-51
Match length	111
% identity	91
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]

Seq. No.	176318
Seq. ID	jC-atXP122C159H19T7024a1
Method	BLASTN
NCBI GI	g3540210
BLAST score	519
E value	0.0e+00
Match length	543
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176319
Seq. ID	jC-atXP122C159H24T7d1
Method	BLASTN
NCBI GI	g1353764
BLAST score	119
E value	1.0e-60
Match length	151
% identity	95
NCBI Description	Arabidopsis thaliana profilin 2 and profilin 3 genes, complete cds

Seq. No.	176320
Seq. ID	jC-atXP123C117C21T7083a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176321
Seq. ID	jC-atXP123C117C5T7005a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20

Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176322
Seq. ID	jC-atXP123C117C5T7005d1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176323
Seq. ID	jC-atXP123C117D14T7020a1
Method	BLASTX
NCBI GI	g4512698
BLAST score	710
E value	5.0e-75
Match length	140
% identity	97
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176324
Seq. ID	jC-atXP123C117D21T7028a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176325
Seq. ID	jC-atXP123C117D2T7004a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176326
Seq. ID	jC-atXP123C117N23T7055a1
Method	BLASTN
NCBI GI	g928937
BLAST score	235
E value	1.0e-129
Match length	400
% identity	91
NCBI Description	A.thaliana mRNA for ketoconazole resistent protein

Seq. No.	176327
Seq. ID	jC-atXP123C117O24T7008d1
Method	BLASTN

NCBI GI	g4376087
BLAST score	192
E value	1.0e-103
Match length	385
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	176328
Seq. ID	jC-atXP123C117P11T7032a1
Method	BLASTN
NCBI GI	g3766106
BLAST score	234
E value	1.0e-128
Match length	394
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176329
Seq. ID	jC-atXP123C117P13T7040a1
Method	BLASTN
NCBI GI	g2924733
BLAST score	309
E value	1.0e-173
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	176330
Seq. ID	jC-atXP123C117P14T7048a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176331
Seq. ID	jC-atXP123C117P14T7048d1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	3.0e-12
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176332
Seq. ID	jC-atXP123C117P18T7064a1
Method	BLASTX
NCBI GI	g3164140
BLAST score	636
E value	3.0e-66
Match length	151

% identity	82
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	176333
Seq. ID	jC-atXP123C117P5T7016a1
Method	BLASTN
NCBI GI	g3868856
BLAST score	231
E value	1.0e-126
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for RAV1, complete cds

Seq. No.	176334
Seq. ID	jC-atXP123C117P5T7016d1
Method	BLASTX
NCBI GI	g3377808
BLAST score	460
E value	1.0e-45
Match length	106
% identity	84
NCBI Description	(AF075597) contains similarity to Nicotiana alata pistil extensin-like protein (GB:U45958) [Arabidopsis thaliana]

Seq. No.	176335
Seq. ID	jC-atXP123C117P7T7024a1
Method	BLASTN
NCBI GI	g2832667
BLAST score	104
E value	6.0e-51
Match length	273
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	176336
Seq. ID	jC-atXP123C118K22T7030d1
Method	BLASTX
NCBI GI	g4505725
BLAST score	156
E value	9.0e-22
Match length	136
% identity	49
NCBI Description	peroxisome biogenesis factor 1 >gi_2655141 (AF026086) peroxisome biogenesis disorder protein 1 [Homo sapiens] >gi_2827156 (AF030356) peroxisome biogenesis gene 1 [Homo sapiens]

Seq. No.	176337
Seq. ID	jC-atXP123C118L9T7046d1
Method	BLASTX
NCBI GI	g1208497
BLAST score	47
E value	5.0e-13
Match length	141
% identity	37

NCBI Description	(D38125) EREBP-4 [Nicotiana tabacum]

Seq. No.	176338
Seq. ID	jC-atXP123C118M10T7023a1
Method	BLASTX
NCBI GI	g3201632
BLAST score	452
E value	1.0e-44
Match length	102
% identity	87
NCBI Description	(AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	176339
Seq. ID	jC-atXP123C118M10T7023d1
Method	BLASTX
NCBI GI	g2997593
BLAST score	297
E value	1.0e-26
Match length	106
% identity	55
NCBI Description	(AF020816) glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum]

Seq. No.	176340
Seq. ID	jC-atXP123C118M3T7086d1
Method	BLASTN
NCBI GI	g4585890
BLAST score	132
E value	1.0e-67
Match length	413
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	176341
Seq. ID	jC-atXP123C118M9T7015d1
Method	BLASTX
NCBI GI	g4678338
BLAST score	43
E value	4.0e-34
Match length	121
% identity	62
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	176342
Seq. ID	jC-atXP123C119M11T7066a1
Method	BLASTN
NCBI GI	g4539309
BLAST score	182
E value	1.0e-97
Match length	388
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	176343
Seq. ID	jC-atXP123C119M19T7018d1

Method	BLASTN
NCBI GI	g2828183
BLAST score	354
E value	0.0e+00
Match length	519
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	176344
Seq. ID	jC-atXP123C119O23T7082a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	7.0e-19
Match length	62
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176345
Seq. ID	jC-atXP123C119P10T7027a1
Method	BLASTN
NCBI GI	g2398530
BLAST score	211
E value	1.0e-115
Match length	476
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for Hap5a transcription factor

Seq. No.	176346
Seq. ID	jC-atXP123C119P17T7035a1
Method	BLASTN
NCBI GI	g4006815
BLAST score	264
E value	1.0e-146
Match length	541
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176347
Seq. ID	jC-atXP123C121A4T7080a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	6.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176348
Seq. ID	jC-atXP124C118O7T7d1
Method	BLASTX
NCBI GI	g3738289
BLAST score	698
E value	7.0e-74

Match length	145
% identity	90
NCBI Description	(AC005309) Not56-like protein [Arabidopsis thaliana]

Seq. No.	176349
Seq. ID	jC-atXP124C118P17T7d1
Method	BLASTX
NCBI GI	g1652057
BLAST score	220
E value	1.0e-17
Match length	88
% identity	47
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	176350
Seq. ID	jC-atXP124C121B16T7d1
Method	BLASTN
NCBI GI	g3695372
BLAST score	170
E value	7.0e-91
Match length	255
% identity	90
NCBI Description	Arabidopsis thaliana BAC F1104

Seq. No.	176351
Seq. ID	jC-atXP124C121D1T7d1
Method	BLASTX
NCBI GI	g2244827
BLAST score	194
E value	2.0e-15
Match length	49
% identity	47
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176352
Seq. ID	jC-atXP124C125H21T7d1
Method	BLASTX
NCBI GI	g2464881
BLAST score	385
E value	3.0e-37
Match length	73
% identity	100
NCBI Description	(Z99707) heat shock transcription factor HSF4 [Arabidopsis thaliana] >gi_3256070_emb_CAA74398_ (Y14069) Heat Shock Factor 4 [Arabidopsis thaliana]

Seq. No.	176353
Seq. ID	jC-atXP125C133F12T7025a1
Method	BLASTN
NCBI GI	g2339977
BLAST score	153
E value	1.0e-80
Match length	169
% identity	98
NCBI Description	A.thaliana mRNA for RGA1 gene

Seq. No.	176354

Seq. ID	jC-atXP125C133G10T7033a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176355
Seq. ID	jC-atXP125C133H9T7020a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176356
Seq. ID	jC-atXP125C134L19T7052a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176357
Seq. ID	jC-atXP125C136P7T7077a1
Method	BLASTX
NCBI GI	g4741940
BLAST score	188
E value	9.0e-14
Match length	84
% identity	55
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	176358
Seq. ID	jC-atXP125C155I23T7018a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176359
Seq. ID	jC-atXP125C177I16T7082a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	41
E value	1.0e-13
Match length	69
% identity	93

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	176360
Seq. ID	jC-atXP125C223L18T7076a1
Method	BLASTX
NCBI GI	g4581123
BLAST score	395
E value	5.0e-38
Match length	128
% identity	68
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]
Seq. No.	176361
Seq. ID	jC-atXP125C230P20T7005a1
Method	BLASTX
NCBI GI	g4204285
BLAST score	312
E value	2.0e-28
Match length	97
% identity	60
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	176362
Seq. ID	jC-atXP125C240K9T7013a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176363
Seq. ID	jC-atXP125C241J19T7029a1
Method	BLASTN
NCBI GI	g3367500
BLAST score	446
E value	0.0e+00
Match length	606
% identity	99
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.	176364
Seq. ID	jC-atXP125CF10078a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176365
Seq. ID	jC-atXP125CF3022a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176366
Seq. ID	jC-atXP125CF3E10T7027a1
Method	BLASTN
NCBI GI	g4678258
BLAST score	38
E value	1.0e-11
Match length	66
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	176367
Seq. ID	jC-atXP125CF7054a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	6.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176368
Seq. ID	jC-atXP125CF9070a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	3.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176369
Seq. ID	jC-atXP125CG10079a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	1.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176370
Seq. ID	jC-atXP125CG5039a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176371
Seq. ID	jC-atXP125CG6047a1
Method	BLASTX
NCBI GI	g134104
BLAST score	280
E value	1.0e-24
Match length	139
% identity	45
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_99800_pir__PW0007 chaperonin 62.5K beta chain - rape plastid >gi_167117 (M35600) 60-kDa beta-polypeptide of plastid chaperonin-60 precursor [Brassica napus]

Seq. No.	176372
Seq. ID	jC-atXP125CG7055a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176373
Seq. ID	jC-atXP125CH2016a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	43
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176374
Seq. ID	jC-atXP125CH3024a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176375
Seq. ID	jC-atXP125CH7056a1
Method	BLASTN
NCBI GI	g4376087
BLAST score	324
E value	0.0e+00
Match length	461
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	176376
Seq. ID	jC-atXP125CH8064a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176377
Seq. ID	jC-atXP12C103C24T7055a1
Method	BLASTX
NCBI GI	g3164136
BLAST score	661
E value	3.0e-69
Match length	158
% identity	84
NCBI Description	(D78603) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	176378
Seq. ID	jC-atXP12C103D18T7056a1
Method	BLASTX
NCBI GI	g1402902
BLAST score	224
E value	4.0e-18
Match length	127
% identity	46
NCBI Description	(X98323) peroxidase [Arabidopsis thaliana] >gi_1419386_emb_CAA67428_ (X98928) peroxidase ATP10a [Arabidopsis thaliana]

Seq. No.	176379
Seq. ID	jC-atXP12C103F4T7064a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176380
Seq. ID	jC-atXP12C103G6T7070a1
Method	BLASTN
NCBI GI	g4490291
BLAST score	96
E value	3.0e-46
Match length	337
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	176381
Seq. ID	jC-atXP12C103K9T7082a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	33
E value	6.0e-09
Match length	44
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176382
Seq. ID	jC-atXP12C103L20T7088a1
Method	BLASTX
NCBI GI	g4204300
BLAST score	419
E value	6.0e-41
Match length	158
% identity	57
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	176383
Seq. ID	jC-atXP12C103L24T7091a1
Method	BLASTN
NCBI GI	g598848
BLAST score	41
E value	1.0e-13
Match length	41
% identity	100
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176384
Seq. ID	jC-atXP12C103M11T7d2
Method	BLASTN
NCBI GI	g3402695
BLAST score	273
E value	1.0e-152
Match length	301
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176385
Seq. ID	jC-atXP12C103N4T7095a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176386
Seq. ID	jC-atXP12C99H9T7d2
Method	BLASTX
NCBI GI	g2618689
BLAST score	145
E value	1.0e-09
Match length	50
% identity	52
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	176387
Seq. ID	jC-atXP12C99K24T7017a1
Method	BLASTN
NCBI GI	g598848
BLAST score	36
E value	7.0e-11
Match length	40
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176388
Seq. ID	jC-atXP12C99N9T7028a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176389
Seq. ID	jC-atXP12C99P18T7038a1
Method	BLASTX
NCBI GI	g4835234
BLAST score	108
E value	2.0e-04
Match length	87
% identity	69
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]

Seq. No.	176390
Seq. ID	jC-atXP13C103O2T7003a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	86
E value	3.0e-40
Match length	319
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176391
Seq. ID	jC-atXP13C103O3T7004a1
Method	BLASTX
NCBI GI	g2344889
BLAST score	211
E value	2.0e-16
Match length	67
% identity	52
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	176392
Seq. ID	jC-atXP13C103P4T7008a1
Method	BLASTN
NCBI GI	g2462264

BLAST score	35
E value	7.0e-10
Match length	43
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176393
Seq. ID	jC-atXP13C104A2T7032a1
Method	BLASTN
NCBI GI	g2264321
BLAST score	72
E value	5.0e-32
Match length	228
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	176394
Seq. ID	jC-atXP13C104A5T7033a1
Method	BLASTX
NCBI GI	g3861117
BLAST score	192
E value	3.0e-14
Match length	139
% identity	37
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	176395
Seq. ID	jC-atXP13C104C17T7044a1
Method	BLASTN
NCBI GI	g598848
BLAST score	45
E value	8.0e-16
Match length	45
% identity	100
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176396
Seq. ID	jC-atXP13C104D20T7047a1
Method	BLASTN
NCBI GI	g3298610
BLAST score	66
E value	3.0e-28
Match length	190
% identity	85
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	176397
Seq. ID	jC-atXP13C104E6T7053a1
Method	BLASTN
NCBI GI	g2358139
BLAST score	198
E value	1.0e-107
Match length	491
% identity	85
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	176398
Seq. ID	jC-atXP13C104G4T7d2
Method	BLASTX
NCBI GI	g1107501
BLAST score	454
E value	3.0e-45
Match length	137
% identity	67
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	176399
Seq. ID	jC-atXP13C104G9T7024a1
Method	BLASTX
NCBI GI	g1710124
BLAST score	189
E value	6.0e-14
Match length	153
% identity	37
NCBI Description	(U62279) leucine-rich repeat-containing extracellular glycoprotein; contains six N-glycosylation sites [NX(S/T)] [Sorghum bicolor]

Seq. No.	176400
Seq. ID	jC-atXP13C104H9T7056a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	3.0e-15
Match length	64
% identity	92
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176401
Seq. ID	jC-atXP13C104K13T7068a1
Method	BLASTX
NCBI GI	g3413705
BLAST score	457
E value	2.0e-45
Match length	116
% identity	78
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	176402
Seq. ID	jC-atXP13C104M14T7081a1
Method	BLASTN
NCBI GI	g4519188
BLAST score	37
E value	4.0e-11
Match length	122
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21L19, complete sequence

Seq. No.	176403
Seq. ID	jC-atXP13C104N23T7089a1
Method	BLASTX
NCBI GI	g1170373
BLAST score	231
E value	8.0e-19
Match length	96
% identity	56
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	176404
Seq. ID	jC-atXP13C104O12T7093a1
Method	BLASTN
NCBI GI	g3798730
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Arabidopsis thaliana transgenic line C DNA

Seq. No.	176405
Seq. ID	jC-atXP13C104O14T7094a1
Method	BLASTN
NCBI GI	g2262135
BLAST score	31
E value	2.0e-07
Match length	126
% identity	90
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	176406
Seq. ID	jC-atXP13C104O1T7090a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176407
Seq. ID	jC-atXP13C104O9T7092a1
Method	BLASTN
NCBI GI	g4757390
BLAST score	152
E value	1.0e-79
Match length	398
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	176408
Seq. ID	jC-atXP14C105A14T7s1
Method	BLASTN
NCBI GI	g2264314
BLAST score	235
E value	1.0e-129
Match length	299
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	176409
Seq. ID	jC-atXP14C105E20T7s1
Method	BLASTX
NCBI GI	g2688822
BLAST score	316
E value	5.0e-29
Match length	79
% identity	76
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	176410
Seq. ID	jC-atXP14C105K17T7d1
Method	BLASTN
NCBI GI	g4589419
BLAST score	35
E value	1.0e-10
Match length	43
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	176411
Seq. ID	jC-atXP14C105L12T7d1
Method	BLASTX
NCBI GI	g1946371
BLAST score	715
E value	6.0e-76
Match length	141
% identity	97
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	176412
Seq. ID	jC-atXP14C105P10T7d1
Method	BLASTN
NCBI GI	g4585891
BLAST score	48
E value	2.0e-18
Match length	118
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T1O3 genomic sequence, complete sequence

Seq. No.	176413
Seq. ID	jC-atXP14C105P24T7s1

Method	BLASTX
NCBI GI	g1162986
BLAST score	436
E value	5.0e-43
Match length	83
% identity	99
NCBI Description	(M32430) beta-2 tubulin [Lytechinus pictus]

Seq. No.	176414
Seq. ID	jC-atXP14C106A14T7d1
Method	BLASTN
NCBI GI	g4262221
BLAST score	70
E value	2.0e-31
Match length	138
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176415
Seq. ID	jC-atXP15C106F16T7018a1
Method	BLASTX
NCBI GI	g4335764
BLAST score	393
E value	8.0e-38
Match length	89
% identity	49
NCBI Description	(AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No.	176416
Seq. ID	jC-atXP15C106F5T7d1
Method	BLASTX
NCBI GI	g4335764
BLAST score	160
E value	2.0e-11
Match length	49
% identity	63
NCBI Description	(AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No.	176417
Seq. ID	jC-atXP15C106K8T7d1
Method	BLASTX
NCBI GI	g3201633
BLAST score	416
E value	7.0e-41
Match length	131
% identity	68
NCBI Description	(AC004669) putative cell division protein [Arabidopsis thaliana]

Seq. No.	176418
Seq. ID	jC-atXP15C106P17T7033a1
Method	BLASTX
NCBI GI	g4646203
BLAST score	291

E value	7.0e-26
Match length	118
% identity	47
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	176419
Seq. ID	jC-atXP15C106P8T7032a1
Method	BLASTX
NCBI GI	g4678923
BLAST score	295
E value	2.0e-26
Match length	111
% identity	53
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	176420
Seq. ID	jC-atXP15C107C5T7037a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	6.0e-10
Match length	51
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176421
Seq. ID	jC-atXP15C107E10T7040a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176422
Seq. ID	jC-atXP15C107F19T7046a1
Method	BLASTX
NCBI GI	g541858
BLAST score	891
E value	3.0e-96
Match length	158
% identity	99
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	176423
Seq. ID	jC-atXP15C107G2T7048a1
Method	BLASTX
NCBI GI	g3212869
BLAST score	402
E value	7.0e-39
Match length	142
% identity	54

NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	176424
Seq. ID	jC-atXP16C110A12T7s1
Method	BLASTN
NCBI GI	g3420043
BLAST score	94
E value	1.0e-45
Match length	204
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	176425
Seq. ID	jC-atXP16C110B15T7s1
Method	BLASTN
NCBI GI	g4079614
BLAST score	126
E value	8.0e-65
Match length	162
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	176426
Seq. ID	jC-atXP17C110F21T7s3
Method	BLASTN
NCBI GI	g1644426
BLAST score	38
E value	2.0e-12
Match length	139
% identity	81
NCBI Description	Arabidopsis thaliana putative glyoxalase II mRNA, complete cds
Seq. No.	176427
Seq. ID	jC-atXP17C110G3T7s3
Method	BLASTN
NCBI GI	g4406776
BLAST score	97
E value	3.0e-47
Match length	274
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	176428
Seq. ID	jC-atXP17C110L7T7s3
Method	BLASTN
NCBI GI	g4519192
BLAST score	315
E value	1.0e-177
Match length	372
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	176429
Seq. ID	jC-atXP17C110M12T7s3
Method	BLASTX
NCBI GI	g3171731
BLAST score	244
E value	2.0e-20
Match length	127
% identity	28
NCBI Description	(AJ006406) AgPET8 [Eremothecium gossypii]

Seq. No.	176430
Seq. ID	jC-atXP17C110O2T7s3
Method	BLASTN
NCBI GI	g3702736
BLAST score	112
E value	3.0e-56
Match length	227
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	176431
Seq. ID	jC-atXP17C113E20T7s3
Method	BLASTX
NCBI GI	g4531437
BLAST score	175
E value	9.0e-13
Match length	67
% identity	60
NCBI Description	(AC006224) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	176432
Seq. ID	jC-atXP18C108N11T7061a1
Method	BLASTN
NCBI GI	g2275194
BLAST score	72
E value	2.0e-32
Match length	112
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176433
Seq. ID	jC-atXP18C108N12T7069a1
Method	BLASTN
NCBI GI	g2275194
BLAST score	92
E value	2.0e-44
Match length	120
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176434
Seq. ID	jC-atXP18C108N16T7085a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176435
Seq. ID	jC-atXP18C108N1T7037a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	1.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176436
Seq. ID	jC-atXP18C108N23T7093a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176437
Seq. ID	jC-atXP18C108N4T7053a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176438
Seq. ID	jC-atXP18C108O13T7014a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176439
Seq. ID	jC-atXP18C108O17T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176440
Seq. ID	jC-atXP18C108O19T7030a1
Method	BLASTN
NCBI GI	g3256065
BLAST score	108
E value	5.0e-54
Match length	123
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for chloroplast NAD-dependent malate dehydrogenase

Seq. No.	176441
Seq. ID	jC-atXP18C108O23T7038a1
Method	BLASTN
NCBI GI	g3805839
BLAST score	119
E value	1.0e-60
Match length	119
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	176442
Seq. ID	jC-atXP18C108O9T7006a1
Method	BLASTN
NCBI GI	g3717945
BLAST score	109
E value	1.0e-54
Match length	136
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for V-ATPase subunit G (vag1 gene)

Seq. No.	176443
Seq. ID	jC-atXP18C108P20T7062a1
Method	BLASTN
NCBI GI	g2696018
BLAST score	84
E value	1.0e-39
Match length	120
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	176444
Seq. ID	jC-atXP18C108P23T7070a1
Method	BLASTN
NCBI GI	g4733953
BLAST score	75
E value	3.0e-34
Match length	95
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	176445
Seq. ID	jC-atXP18C108P24T7078a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176446
Seq. ID	jC-atXP18C108P8T7054a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176447
Seq. ID	jC-atXP18C111A12T7094a1
Method	BLASTN
NCBI GI	g3348076
BLAST score	113
E value	5.0e-57
Match length	116
% identity	99
NCBI Description	Arabidopsis thaliana isochorismate synthase mRNA, complete cds

Seq. No.	176448
Seq. ID	jC-atXP18C111A21T7015a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	8.0e-16
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176449
Seq. ID	jC-atXP18C111A23T7023a1
Method	BLASTN
NCBI GI	g2252471
BLAST score	131
E value	1.0e-67
Match length	131
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for argininosuccinate lyase

Seq. No.	176450
Seq. ID	jC-atXP18C111B21T7047a1
Method	BLASTN
NCBI GI	g3249094
BLAST score	124
E value	1.0e-63
Match length	128
% identity	99

NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176451
Seq. ID	jC-atXP18C111B23T7055a1
Method	BLASTN
NCBI GI	g3449315
BLAST score	60
E value	2.0e-25
Match length	80
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	176452
Seq. ID	jC-atXP18C111C13T7071a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	6.0e-23
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176453
Seq. ID	jC-atXP18C111C22T7087a1
Method	BLASTN
NCBI GI	g3885325
BLAST score	117
E value	2.0e-59
Match length	124
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176454
Seq. ID	jC-atXP18C111C4T7063a1
Method	BLASTN
NCBI GI	g2341023
BLAST score	96
E value	7.0e-47
Match length	117
% identity	94
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176455
Seq. ID	jC-atXP18C111D16T7024a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	5.0e-17
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176456

Seq. ID	jC-atXP18C111D20T7032a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176457
Seq. ID	jC-atXP18C111D24T7040a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176458
Seq. ID	jC-atXP18C111D4T7095a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	2.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176459
Seq. ID	jC-atXP18C111E10T7064a1
Method	BLASTN
NCBI GI	g598848
BLAST score	40
E value	2.0e-13
Match length	44
% identity	98
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176460
Seq. ID	jC-atXP18C111E1T7048a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176461
Seq. ID	jC-atXP18C111E2T7056a1
Method	BLASTN
NCBI GI	g2832689
BLAST score	97
E value	2.0e-47
Match length	105
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	176462
Seq. ID	jC-atXP18C113J10T7001a1
Method	BLASTN
NCBI GI	g3449326
BLAST score	92
E value	2.0e-44
Match length	132
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	176463
Seq. ID	jC-atXP18C113J12T7009a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176464
Seq. ID	jC-atXP18C113J16T7025a1
Method	BLASTN
NCBI GI	g4371278
BLAST score	92
E value	2.0e-44
Match length	92
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176465
Seq. ID	jC-atXP18C113J17T7033a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	3.0e-12
Match length	42
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176466
Seq. ID	jC-atXP18C113J22T7041a1
Method	BLASTN
NCBI GI	g2815404
BLAST score	135
E value	4.0e-70
Match length	135
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No. 176467

Seq. ID	jC-atXP18C113K14T7057a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	1.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176468
Seq. ID	jC-atXP18C113K16T7073a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	5.0e-23
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176469
Seq. ID	jC-atXP18C113K17T7081a1
Method	BLASTN
NCBI GI	g4584841
BLAST score	112
E value	2.0e-56
Match length	124
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	176470
Seq. ID	jC-atXP18C113K9T7049a1
Method	BLASTN
NCBI GI	g4741961
BLAST score	92
E value	2.0e-44
Match length	92
% identity	100
NCBI Description	Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No.	176471
Seq. ID	jC-atXP18C113L20T7002a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176472
Seq. ID	jC-atXP18C113L3T7089a1
Method	BLASTN
NCBI GI	g598848
BLAST score	48
E value	3.0e-18
Match length	56

% identity	98
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176473
Seq. ID	jC-atXP18C113M1T7010a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	125
E value	4.0e-64
Match length	125
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176474
Seq. ID	jC-atXP18C113M4T7018a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	99
E value	1.0e-48
Match length	115
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AF2 contig fragment No

Seq. No.	176475
Seq. ID	jC-atXP18C113M5T7026a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176476
Seq. ID	jC-atXP18C113M6T7034a1
Method	BLASTN
NCBI GI	g3608126
BLAST score	134
E value	2.0e-69
Match length	134
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176477
Seq. ID	jC-atXP18C113N14T7074a1
Method	BLASTN
NCBI GI	g4589438
BLAST score	71
E value	6.0e-32
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	176478
Seq. ID	jC-atXP18C113N16T7090a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	102
E value	2.0e-50
Match length	110
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	176479
Seq. ID	jC-atXP18C113O10T7019a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176480
Seq. ID	jC-atXP18C113O13T7027a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176481
Seq. ID	jC-atXP18C113O14T7035a1
Method	BLASTN
NCBI GI	g2921828
BLAST score	126
E value	9.0e-65
Match length	126
% identity	100
NCBI Description	Arabidopsis thaliana IAA-amino acid hydrolase (ILL1 and ILL2) genes, complete cds

Seq. No.	176482
Seq. ID	jC-atXP18C113O17T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176483
Seq. ID	jC-atXP18C113O6T7011a1
Method	BLASTN
NCBI GI	g3241920
BLAST score	133

E value	6.0e-69
Match length	133
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	176484
Seq. ID	jC-atXP18C113P10T7075a1
Method	BLASTN
NCBI GI	g16192
BLAST score	124
E value	1.0e-63
Match length	124
% identity	100
NCBI Description	A.thaliana ats1B, ats2B and ats3B gene for ribulose-1,5-biphosphate carboxylase small subunit (rbcS) (EC 4.1.1.39)

Seq. No.	176485
Seq. ID	jC-atXP18C113P12T7083a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	9.0e-25
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176486
Seq. ID	jC-atXP18C113P13T7091a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	2.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176487
Seq. ID	jC-atXP18C113P14T7004a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	119
E value	1.0e-60
Match length	119
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176488
Seq. ID	jC-atXP18C113P21T7020a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176489
Seq. ID	jC-atXP18C113P5T7067a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	1.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176490
Seq. ID	jC-atXP18C115A12T7036a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176491
Seq. ID	jC-atXP18C115A20T7044a1
Method	BLASTN
NCBI GI	g4371278
BLAST score	131
E value	9.0e-68
Match length	131
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176492
Seq. ID	jC-atXP18C115A22T7052a1
Method	BLASTN
NCBI GI	g3264804
BLAST score	106
E value	8.0e-53
Match length	110
% identity	99
NCBI Description	Arabidopsis thaliana phosphoenolpyruvate carboxylase (PPC) mRNA, complete cds

Seq. No.	176493
Seq. ID	jC-atXP18C115A9T7028a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	5.0e-20
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176494
Seq. ID	jC-atXP18C115B13T7084a1
Method	BLASTN

NCBI GI	g4519187
BLAST score	101
E value	8.0e-50
Match length	124
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No.	176495
Seq. ID	jC-atXP18C115B4T7060a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	2.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176496
Seq. ID	jC-atXP18C115B7T7068a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	1.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176497
Seq. ID	jC-atXP18C115B8T7076a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	5.0e-23
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176498
Seq. ID	jC-atXP18C115C18T7013a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	1.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176499
Seq. ID	jC-atXP18C115C18T7d2
Method	BLASTX
NCBI GI	g2980783
BLAST score	143
E value	7.0e-09
Match length	94
% identity	35
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	176500
Seq. ID	jC-atXP18C115C4T7005a1
Method	BLASTN
NCBI GI	g3449326
BLAST score	133
E value	6.0e-69
Match length	133
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	176501
Seq. ID	jC-atXP18C115D11T7021a1
Method	BLASTN
NCBI GI	g4490717
BLAST score	135
E value	4.0e-70
Match length	135
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	176502
Seq. ID	jC-atXP18C115D23T7029a1
Method	BLASTN
NCBI GI	g2760316
BLAST score	132
E value	2.0e-68
Match length	132
% identity	100
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176503
Seq. ID	jC-atXP19C109J15T7045a1
Method	BLASTX
NCBI GI	g2347098
BLAST score	63
E value	1.0e-28
Match length	109
% identity	66
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	176504
Seq. ID	jC-atXP19C109K13T7006a1
Method	BLASTN
NCBI GI	g1732514
BLAST score	105
E value	1.0e-51
Match length	354
% identity	87
NCBI Description	Arabidopsis thaliana myosin heavy chain-like protein mRNA, complete cds

Seq. No.	176505
Seq. ID	jC-atXP19C109L6T7038a1
Method	BLASTX
NCBI GI	g3421072
BLAST score	515
E value	4.0e-52
Match length	107
% identity	94
NCBI Description	(AF043519) 20S proteasome subunit PAA2 [Arabidopsis thaliana] >gi_4006819 (AC005970) 20S proteasome subunit PAA2 [Arabidopsis thaliana]

Seq. No.	176506
Seq. ID	jC-atXP19C109M22T7094a1
Method	BLASTN
NCBI GI	g2245073
BLAST score	143
E value	1.0e-74
Match length	282
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176507
Seq. ID	jC-atXP19C109N11T7031a1
Method	BLASTX
NCBI GI	g1912286
BLAST score	731
E value	2.0e-77
Match length	133
% identity	99
NCBI Description	(U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No.	176508
Seq. ID	jC-atXP19C109P22T7016a1
Method	BLASTN
NCBI GI	g2191126
BLAST score	179
E value	8.0e-96
Match length	354
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	176509
Seq. ID	jC-atXP19C111H8T7081a1
Method	BLASTX
NCBI GI	g1825727
BLAST score	224
E value	5.0e-18
Match length	83
% identity	53
NCBI Description	(U88308) C32E8.5 gene product [Caenorhabditis elegans]

Seq. No. 176510

Seq. ID	jC-atXP19C111L20T7d2
Method	BLASTN
NCBI GI	g3341671
BLAST score	384
E value	0.0e+00
Match length	636
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176511
Seq. ID	jC-atXP19C111N21T7004a1
Method	BLASTX
NCBI GI	g4589980
BLAST score	167
E value	3.0e-11
Match length	79
% identity	51
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	176512
Seq. ID	jC-atXP19C111N23T7012a1
Method	BLASTX
NCBI GI	g2341034
BLAST score	577
E value	2.0e-59
Match length	126
% identity	88
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	176513
Seq. ID	jC-atXP19C111O19T7044a1
Method	BLASTX
NCBI GI	g4827253
BLAST score	108
E value	2.0e-04
Match length	155
% identity	24
NCBI Description	(AB027002) plastidic aldolase [Nicotiana paniculata]

Seq. No.	176514
Seq. ID	jC-atXP19C113A22T7040a1
Method	BLASTX
NCBI GI	g3123712
BLAST score	262
E value	2.0e-22
Match length	129
% identity	41
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	176515
Seq. ID	jC-atXP19C113B2T7056a1
Method	BLASTN
NCBI GI	g2739021
BLAST score	37
E value	5.0e-11
Match length	89

% identity	92
NCBI Description	Rhododendron metternichii var. hondoense CT repeats, genomic sequence

Seq. No.	176516
Seq. ID	jC-atXP1C64A5T7s2
Method	BLASTN
NCBI GI	g3985958
BLAST score	321
E value	0.0e+00
Match length	476
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	176517
Seq. ID	jC-atXP1C64B5T7s2
Method	BLASTN
NCBI GI	g4733953
BLAST score	59
E value	9.0e-25
Match length	163
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	176518
Seq. ID	jC-atXP1C66F12T7s2
Method	BLASTN
NCBI GI	g3128136
BLAST score	198
E value	1.0e-107
Match length	314
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	176519
Seq. ID	jC-atXP1C67A8T7s2
Method	BLASTX
NCBI GI	g4512651
BLAST score	210
E value	8.0e-17
Match length	67
% identity	55
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	176520
Seq. ID	jC-atXP1C67F2T7s2
Method	BLASTN
NCBI GI	g3075383
BLAST score	336
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic

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sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176521
Seq. ID	jC-atXP1C69H6T7s2
Method	BLASTN
NCBI GI	g4757390
BLAST score	170
E value	1.0e-90
Match length	398
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	176522
Seq. ID	jC-atXP1C70G7T7s2
Method	BLASTX
NCBI GI	g2369714
BLAST score	174
E value	1.0e-12
Match length	50
% identity	68
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	176523
Seq. ID	jC-atXP1C72D2T7s2
Method	BLASTX
NCBI GI	g3128201
BLAST score	192
E value	1.0e-14
Match length	47
% identity	79
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	176524
Seq. ID	jC-atXP20075f2
Method	BLASTX
NCBI GI	g2982285
BLAST score	327
E value	4.0e-30
Match length	63
% identity	78
NCBI Description	(AF051227) GASA5-like protein [Picea mariana]

Seq. No.	176525
Seq. ID	jC-atXP20725a2
Method	BLASTN
NCBI GI	g4416300
BLAST score	377
E value	0.0e+00
Match length	713
% identity	96
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No.	176526
Seq. ID	jC-atXP20725f2
Method	BLASTX

NCBI GI	g4416307
BLAST score	217
E value	4.0e-17
Match length	41
% identity	95
NCBI Description	(AF105716) hypothetical protein [Zea mays]

Seq. No.	176527
Seq. ID	jC-atXP20728f2
Method	BLASTX
NCBI GI	g4581109
BLAST score	54
E value	4.0e-50
Match length	146
% identity	66
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	176528
Seq. ID	jC-atXP20C113C23T7025a1
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	7.0e-13
Match length	72
% identity	92
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176529
Seq. ID	jC-atXP20C113D5T7033a1
Method	BLASTX
NCBI GI	g3434967
BLAST score	848
E value	4.0e-91
Match length	195
% identity	86
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	176530
Seq. ID	jC-atXP20C113G15T7d2
Method	BLASTX
NCBI GI	g4584343
BLAST score	375
E value	4.0e-36
Match length	92
% identity	84
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	176531
Seq. ID	jC-atXP20C113H16T7027a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	2.0e-19
Match length	66
% identity	94

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176532
Seq. ID	jC-atXP20C113H23T7043a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	42
E value	7.0e-14
Match length	50
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176533
Seq. ID	jC-atXP20C114B17T7036a1
Method	BLASTX
NCBI GI	g541858
BLAST score	350
E value	8.0e-33
Match length	123
% identity	66
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	176534
Seq. ID	jC-atXP20C114C19T7005a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176535
Seq. ID	jC-atXP20C114C21T7013a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	4.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176536
Seq. ID	jC-atXP20C114D18T7029a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	46
E value	2.0e-16
Match length	117
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176537
Seq. ID	jC-atXP20C114G3T7022a1
Method	BLASTN
NCBI GI	g531828
BLAST score	54
E value	4.0e-21
Match length	70
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176538
Seq. ID	jC-atXP20C115E7T7038a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	7.0e-10
Match length	67
% identity	88
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176539
Seq. ID	jC-atXP20C115I15T7024a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	40
E value	8.0e-13
Match length	56
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176540
Seq. ID	jC-atXP20C116A19T7d2
Method	BLASTX
NCBI GI	g3355476
BLAST score	489
E value	3.0e-69
Match length	131
% identity	100
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	176541
Seq. ID	jC-atXP21C115K16T7d2
Method	BLASTX
NCBI GI	g2129600
BLAST score	55
E value	4.0e-77
Match length	152
% identity	98
NCBI Description	glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A glutathione synthetase [Arabidopsis thaliana]

Seq. No.	176542
Seq. ID	jC-atXP21C115L5T7s2

Method	BLASTN
NCBI GI	g4415928
BLAST score	118
E value	5.0e-60
Match length	150
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176543
Seq. ID	jC-atXP21C116B11T7s2
Method	BLASTN
NCBI GI	g1616656
BLAST score	77
E value	8.0e-36
Match length	105
% identity	93
NCBI Description	Arabidopsis thaliana adenylosuccinate synthetase mRNA, complete cds

Seq. No.	176544
Seq. ID	jC-atXP21C116C12T7d2
Method	BLASTN
NCBI GI	g3985949
BLAST score	334
E value	0.0e+00
Match length	382
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	176545
Seq. ID	jC-atXP22C114L10T7073a1
Method	BLASTX
NCBI GI	g2511580
BLAST score	939
E value	1.0e-102
Match length	203
% identity	94
NCBI Description	(Y13179) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_2511582_emb_CAA73623.1_ (Y13180) multicatalytic endopeptidase [Arabidopsis thaliana]

Seq. No.	176546
Seq. ID	jC-atXP22C114N3T7042a1
Method	BLASTX
NCBI GI	g480725
BLAST score	607
E value	6.0e-63
Match length	134
% identity	93
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	176547
Seq. ID	jC-atXP22C114O16T7090a1
Method	BLASTN
NCBI GI	g4490734
BLAST score	177
E value	8.0e-95
Match length	210
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	176548
Seq. ID	jC-atXP22C115O3T7004a1
Method	BLASTN
NCBI GI	g3510336
BLAST score	203
E value	1.0e-110
Match length	473
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	176549
Seq. ID	jC-atXP22C119C18T7086a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	2.0e-14
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176550
Seq. ID	jC-atXP22C119L21T7021a1
Method	BLASTX
NCBI GI	g1399265
BLAST score	321
E value	2.0e-29
Match length	97
% identity	69
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	176551
Seq. ID	jC-atXP22C121K11T7056a1
Method	BLASTN
NCBI GI	g531832
BLAST score	36
E value	2.0e-10
Match length	216
% identity	80
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	176552
Seq. ID	jC-atXP22C121K12T7064a1
Method	BLASTN
NCBI GI	g4263762

BLAST score	186
E value	1.0e-100
Match length	458
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176553
Seq. ID	jC-atXP22C121K20T7072a1
Method	BLASTN
NCBI GI	g4519191
BLAST score	92
E value	7.0e-44
Match length	267
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	176554
Seq. ID	jC-atXP22C122D8T7071a1
Method	BLASTX
NCBI GI	g322596
BLAST score	290
E value	1.0e-25
Match length	108
% identity	64
NCBI Description	serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi_166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana] >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	176555
Seq. ID	jC-atXP22C122E7T7024a1
Method	BLASTX
NCBI GI	g322596
BLAST score	313
E value	2.0e-28
Match length	93
% identity	71
NCBI Description	serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi_166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana] >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	176556
Seq. ID	jC-atXP23C120K21T7d2
Method	BLASTN
NCBI GI	g4753195
BLAST score	365
E value	0.0e+00
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	176557
Seq. ID	jC-atXP23C120M13T7s2
Method	BLASTX
NCBI GI	g3355474
BLAST score	489
E value	2.0e-49
Match length	106
% identity	88
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	176558
Seq. ID	jC-atXP23C120N3T7s2
Method	BLASTX
NCBI GI	g4678322
BLAST score	459
E value	6.0e-46
Match length	88
% identity	99
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	176559
Seq. ID	jC-atXP23C121L17T7s2
Method	BLASTN
NCBI GI	g1931636
BLAST score	189
E value	1.0e-102
Match length	272
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	176560
Seq. ID	jC-atXP23C123A19T7d2
Method	BLASTN
NCBI GI	g3176693
BLAST score	112
E value	4.0e-56
Match length	354
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176561
Seq. ID	jC-atXP23C123A9T7s2
Method	BLASTX
NCBI GI	g3540181
BLAST score	151
E value	8.0e-10
Match length	60
% identity	53
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	176562
Seq. ID	jC-atXP24C120O21T7057d1
Method	BLASTX
NCBI GI	g2982458
BLAST score	203
E value	1.0e-15

Match length	130
% identity	42
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	176563
Seq. ID	jC-atXP24C122J19T7013d1
Method	BLASTX
NCBI GI	g1076414
BLAST score	191
E value	2.0e-14
Match length	65
% identity	52
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	176564
Seq. ID	jC-atXP24C123C16T7027a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176565
Seq. ID	jC-atXP24C123D10T7067d1
Method	BLASTX
NCBI GI	g3928079
BLAST score	278
E value	2.0e-24
Match length	165
% identity	38
NCBI Description	(AC005770) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176566
Seq. ID	jC-atXP24C123E11T7044a1
Method	BLASTX
NCBI GI	g2088658
BLAST score	349
E value	1.0e-32
Match length	70
% identity	99
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	176567
Seq. ID	jC-atXP24C123E4T7028a1
Method	BLASTN
NCBI GI	g2264312
BLAST score	550
E value	0.0e+00
Match length	590
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	176568
Seq. ID	jC-atXP24C123I15T7026d1
Method	BLASTX
NCBI GI	g4455314
BLAST score	565
E value	4.0e-58
Match length	150
% identity	76
NCBI Description	(AL035528) glycine-rich RNA-binding protein AtGRP2-like [Arabidopsis thaliana]

Seq. No.	176569
Seq. ID	jC-atXP24C123I16T7034d1
Method	BLASTX
NCBI GI	g3212880
BLAST score	173
E value	3.0e-36
Match length	124
% identity	66
NCBI Description	(AC004005) putative Mlo protein [Arabidopsis thaliana]

Seq. No.	176570
Seq. ID	jC-atXP24C123L10T7007a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176571
Seq. ID	jC-atXP24C123L18T7023d1
Method	BLASTX
NCBI GI	g3928543
BLAST score	881
E value	5.0e-95
Match length	179
% identity	95
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	176572
Seq. ID	jC-atXP24C123M2T7039d1
Method	BLASTX
NCBI GI	g2623304
BLAST score	951
E value	1.0e-103
Match length	216
% identity	90
NCBI Description	(AC002409) similar to Medicago nodulin N21 [Arabidopsis thaliana]

Seq. No.	176573
Seq. ID	jC-atXP24C123N12T7032a1
Method	BLASTX
NCBI GI	g1617274

BLAST score	292
E value	5.0e-26
Match length	105
% identity	57
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	176574
Seq. ID	jC-atXP24C123N13T7040a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176575
Seq. ID	jC-atXP24C123N20T7056a1
Method	BLASTX
NCBI GI	g4510373
BLAST score	423
E value	2.0e-41
Match length	142
% identity	58
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	176576
Seq. ID	jC-atXP24C123N8T7016a1
Method	BLASTX
NCBI GI	g2129770
BLAST score	470
E value	7.0e-47
Match length	104
% identity	88
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	176577
Seq. ID	jC-atXP25C122N15T7042a1
Method	BLASTX
NCBI GI	g125393
BLAST score	200
E value	3.0e-15
Match length	139
% identity	37
NCBI Description	HOMOSERINE KINASE (HK) >gi_79795_pir__S03743 homoserine kinase (EC 2.7.1.39) - Calothrix sp >gi_43396_emb_CAA68576_ (Y00522) homoserine kinase (AA 1-307) [Calothrix PCC7601]

Seq. No.	176578
Seq. ID	jC-atXP25C122P4T7011a1
Method	BLASTN
NCBI GI	g598848

BLAST score	55
E value	7.0e-22
Match length	63
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	176579
Seq. ID	jC-atXP25C123O18T7033a1
Method	BLASTN
NCBI GI	g2264311
BLAST score	281
E value	1.0e-157
Match length	499
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	176580
Seq. ID	jC-atXP25C124A21T7092a1
Method	BLASTX
NCBI GI	g2739373
BLAST score	47
E value	1.0e-26
Match length	113
% identity	53
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	176581
Seq. ID	jC-atXP25C124D22T7013a1
Method	BLASTX
NCBI GI	g4309738
BLAST score	383
E value	9.0e-37
Match length	100
% identity	72
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	176582
Seq. ID	jC-atXP25C124E1T7021a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176583
Seq. ID	jC-atXP25C125E23T7006a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	7.0e-22
Match length	55
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176584
Seq. ID	jC-atXP25C125H2T7031a1
Method	BLASTN
NCBI GI	g4519197
BLAST score	52
E value	4.0e-20
Match length	164
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MTC11, complete sequence

Seq. No.	176585
Seq. ID	jC-atXP25C125I6T7081a1
Method	BLASTX
NCBI GI	g1168729
BLAST score	517
E value	2.0e-52
Match length	123
% identity	86
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE ELI3-1 (CAD) >gi_282867_pir__S28044 ELI3-2 protein - Arabidopsis thaliana >gi_16267_emb_CAA48027_ (X67816) Eli3-1 [Arabidopsis thaliana]

Seq. No.	176586
Seq. ID	jC-atXP25C125K2T7018a1
Method	BLASTX
NCBI GI	g4689474
BLAST score	533
E value	2.0e-54
Match length	115
% identity	84
NCBI Description	(AC007213) unknown protein [Arabidopsis thaliana]

Seq. No.	176587
Seq. ID	jC-atXP25C125L3T7079a1
Method	BLASTX
NCBI GI	g730307
BLAST score	128
E value	2.0e-14
Match length	112
% identity	44
NCBI Description	PHOSPHOGLYCERATE KINASE >gi_3052_emb_CAA39865_ (X56512) phosphoglycerate kinase [Neurospora crassa]

Seq. No.	176588
Seq. ID	jC-atXP25C125N11T7056a1
Method	BLASTX
NCBI GI	g3914603
BLAST score	348
E value	1.0e-32
Match length	134
% identity	46
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Oryza sativa]

Seq. No.	176589
Seq. ID	jC-atXP26C124F13T7017a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176590
Seq. ID	jC-atXP26C124F5T7001a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176591
Seq. ID	jC-atXP26C124G21T7025a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	194
E value	2.0e-21
Match length	119
% identity	50
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176592
Seq. ID	jC-atXP26C124G24T7033a1
Method	BLASTX
NCBI GI	g1694976
BLAST score	148
E value	4.0e-09
Match length	77
% identity	49
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	176593
Seq. ID	jC-atXP26C124K13T7051a1
Method	BLASTX
NCBI GI	g1531672
BLAST score	49
E value	5.0e-20
Match length	75
% identity	83
NCBI Description	(U68461) actin [Striga asiatica]

Seq. No.	176594
Seq. ID	jC-atXP26C124N23T7004a1
Method	BLASTX

NCBI GI	g2832359
BLAST score	320
E value	4.0e-32
Match length	110
% identity	74
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176595
Seq. ID	jC-atXP26C124O14T7020a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	230
E value	1.0e-18
Match length	55
% identity	87
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176596
Seq. ID	jC-atXP26C124O4T7012a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	5.0e-23
Match length	61
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176597
Seq. ID	jC-atXP26C124P22T7052a1
Method	BLASTX
NCBI GI	g1352663
BLAST score	386
E value	5.0e-37
Match length	75
% identity	95
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana >gi_466441 (M96841) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4559341_gb_AAD23003.1_AC007087_22 (AC007087) serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] >gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956) serine/threonine protein phosphatase [Arabidopsis thaliana]

Seq. No.	176598
Seq. ID	jC-atXP26C126F19T7049a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	252
E value	3.0e-21
Match length	94
% identity	62
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176599
Seq. ID	jC-atXP26C126I18T7002a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176600
Seq. ID	jC-atXP26C126I20T7018a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	1.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176601
Seq. ID	jC-atXP26C126J2T7026a1
Method	BLASTX
NCBI GI	g2529665
BLAST score	283
E value	6.0e-25
Match length	105
% identity	61
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	176602
Seq. ID	jC-atXP26C126J3T7034a1
Method	BLASTX
NCBI GI	g4544443
BLAST score	197
E value	7.0e-15
Match length	98
% identity	52
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	176603
Seq. ID	jC-atXP26C126K21T7003a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	4.0e-09
Match length	46
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176604
Seq. ID	jC-atXP26C126L10T7027a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50

E value	8.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176605
Seq. ID	jC-atXP26C126L4T7011a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176606
Seq. ID	jC-atXP26C126L5T7019a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	5.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176607
Seq. ID	jC-atXP26C126N19T7021a1
Method	BLASTX
NCBI GI	g4586109
BLAST score	201
E value	2.0e-15
Match length	60
% identity	63
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	176608
Seq. ID	jC-atXP26C126O10T7045a1
Method	BLASTN
NCBI GI	g2252823
BLAST score	77
E value	6.0e-35
Match length	126
% identity	91
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	176609
Seq. ID	jC-atXP26C126O1T7029a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176610

Seq. ID	jC-atXP26C126P17T7d1
Method	BLASTN
NCBI GI	g2264304
BLAST score	62
E value	9.0e-27
Match length	138
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	176611
Seq. ID	jC-atXP26C127J20T7056a1
Method	BLASTN
NCBI GI	g3395421
BLAST score	117
E value	6.0e-59
Match length	387
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176612
Seq. ID	jC-atXP26C127M8T7096a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	177
E value	2.0e-12
Match length	110
% identity	45
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176613
Seq. ID	jC-atXP26C128A18T7046a1
Method	BLASTX
NCBI GI	g4325324
BLAST score	133
E value	3.0e-37
Match length	138
% identity	66
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	176614
Seq. ID	jC-atXP26C128I11T7015a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	3.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176615
Seq. ID	jC-atXP26C128I14T7023a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	90

E value	3.0e-19
Match length	124
% identity	44
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176616
Seq. ID	jC-atXP26C128I4T7007a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	259
E value	4.0e-22
Match length	71
% identity	77
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176617
Seq. ID	jC-atXP26C128L23T7016a1
Method	BLASTX
NCBI GI	g2832359
BLAST score	296
E value	2.0e-26
Match length	110
% identity	58
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	176618
Seq. ID	jC-atXP27C129B18T7d2
Method	BLASTX
NCBI GI	g3834325
BLAST score	171
E value	1.0e-12
Match length	39
% identity	82
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	176619
Seq. ID	jC-atXP27C129G19T7s2
Method	BLASTN
NCBI GI	g1359496
BLAST score	77
E value	2.0e-35
Match length	191
% identity	83
NCBI Description	A.thaliana mRNA for seryl-tRNA synthetase

Seq. No.	176620
Seq. ID	jC-atXP27C130E5T7d2
Method	BLASTN
NCBI GI	g4454587
BLAST score	33
E value	5.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61

cM, complete sequence [Arabidopsis thaliana]

Seq. No.	176621
Seq. ID	jC-atXP27C130L5T7s2
Method	BLASTX
NCBI GI	g1498120
BLAST score	342
E value	3.0e-32
Match length	93
% identity	77
NCBI Description	(D85416) sulfate transporter [Arabidopsis thaliana]

Seq. No.	176622
Seq. ID	jC-atXP27C131D1T7s2
Method	BLASTX
NCBI GI	g3236235
BLAST score	346
E value	2.0e-32
Match length	85
% identity	84
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	176623
Seq. ID	jC-atXP27C131H17T7d2
Method	BLASTX
NCBI GI	g4506225
BLAST score	256
E value	4.0e-22
Match length	142
% identity	44
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 >gi_3914474_sp_Q99460_PSD1_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S1 (P112) >gi_1808578_dbj_BAA07918_ (D44466) proteasome subunit p112 [Homo sapiens]

Seq. No.	176624
Seq. ID	jC-atXP27C131L1T7s2
Method	BLASTN
NCBI GI	g3449323
BLAST score	408
E value	0.0e+00
Match length	540
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	176625
Seq. ID	jC-atXP27C132O8T7s2
Method	BLASTX
NCBI GI	g3169173
BLAST score	148
E value	3.0e-09
Match length	70
% identity	44
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	176626
Seq. ID	jC-atXP27C134C20T7s2
Method	BLASTN
NCBI GI	g2266411
BLAST score	49
E value	1.0e-18
Match length	163
% identity	87
NCBI Description	Arabidopsis thaliana GST11 gene

Seq. No.	176627
Seq. ID	jC-atXP27C135A3T7s2
Method	BLASTX
NCBI GI	g2129517
BLAST score	729
E value	2.0e-77
Match length	138
% identity	100
NCBI Description	24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No.	176628
Seq. ID	jC-atXP28C134M11T7s1
Method	BLASTN
NCBI GI	g4589444
BLAST score	93
E value	4.0e-45
Match length	186
% identity	67
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	176629
Seq. ID	jC-atXP28C135H7T7s1
Method	BLASTN
NCBI GI	g2828185
BLAST score	98
E value	4.0e-48
Match length	122
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	176630
Seq. ID	jC-atXP28C136D2T7d1
Method	BLASTX
NCBI GI	g629561
BLAST score	144
E value	2.0e-09
Match length	43
% identity	58
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	176631
Seq. ID	jC-atXP28C136P5T7s1
Method	BLASTX
NCBI GI	g2961355
BLAST score	148
E value	9.0e-10
Match length	51
% identity	59
NCBI Description	(AL022140) glucosidase like protein [Arabidopsis thaliana]

Seq. No.	176632
Seq. ID	jC-atXP29C135J10T7041d1
Method	BLASTX
NCBI GI	g4678328
BLAST score	360
E value	3.0e-34
Match length	118
% identity	64
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	176633
Seq. ID	jC-atXP29C135K13T7089d1
Method	BLASTX
NCBI GI	g2623962
BLAST score	303
E value	3.0e-27
Match length	85
% identity	73
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	176634
Seq. ID	jC-atXP29C135N12T7045d1
Method	BLASTN
NCBI GI	g3928542
BLAST score	87
E value	7.0e-41
Match length	232
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for UDP-glucose glucosyltransferase, complete cds

Seq. No.	176635
Seq. ID	jC-atXP29C135N8T7029d1
Method	BLASTN
NCBI GI	g2341023
BLAST score	381
E value	0.0e+00
Match length	642
% identity	98
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176636
Seq. ID	jC-atXP29C137I15T7018d1

Method	BLASTN
NCBI GI	g3800746
BLAST score	34
E value	5.0e-09
Match length	42
% identity	95
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	176637
Seq. ID	jC-atXP29C137J1T7026d1
Method	BLASTX
NCBI GI	g2827704
BLAST score	392
E value	1.0e-37
Match length	128
% identity	64
NCBI Description	(AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No.	176638
Seq. ID	jC-atXP29C137J4T7034d1
Method	BLASTN
NCBI GI	g2760165
BLAST score	239
E value	1.0e-131
Match length	307
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	176639
Seq. ID	jC-atXP29C137M7T7s1
Method	BLASTN
NCBI GI	g4835223
BLAST score	84
E value	8.0e-40
Match length	113
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	176640
Seq. ID	jC-atXP29C138J22T7047d1
Method	BLASTX
NCBI GI	g3953601
BLAST score	798
E value	3.0e-85
Match length	175
% identity	91
NCBI Description	(AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No.	176641
Seq. ID	jC-atXP29C138K19T7s1
Method	BLASTN
NCBI GI	g4415928
BLAST score	99
E value	8.0e-49

Match length	139
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176642
Seq. ID	jC-atXP29C139G18T7022d1
Method	BLASTX
NCBI GI	g1888357
BLAST score	769
E value	6.0e-82
Match length	183
% identity	81
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	176643
Seq. ID	jC-atXP29C140A21T7006d1
Method	BLASTN
NCBI GI	g4691223
BLAST score	213
E value	1.0e-116
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	176644
Seq. ID	jC-atXP29C140A9T7d1
Method	BLASTN
NCBI GI	g3128166
BLAST score	416
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176645
Seq. ID	jC-atXP29C141G11T7088d1
Method	BLASTX
NCBI GI	g3288821
BLAST score	342
E value	6.0e-32
Match length	140
% identity	56
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	176646
Seq. ID	jC-atXP2C73D7T7001a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43

E value	1.0e-14
Match length	43
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176647
Seq. ID	jC-atXP2C73E8T7003a1
Method	BLASTX
NCBI GI	g1778141
BLAST score	202
E value	2.0e-15
Match length	115
% identity	45
NCBI Description	(U66321) phosphate/phosphoenolpyruvate translocator precursor; PPT [Arabidopsis thaliana]

Seq. No.	176648
Seq. ID	jC-atXP2C73F2T7005a1
Method	BLASTN
NCBI GI	g2564045
BLAST score	67
E value	4.0e-29
Match length	192
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	176649
Seq. ID	jC-atXP2C74F9T7019a1
Method	BLASTX
NCBI GI	g1362192
BLAST score	157
E value	3.0e-10
Match length	49
% identity	59
NCBI Description	ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable chain - maize

Seq. No.	176650
Seq. ID	jC-atXP2C75B3T7021a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176651
Seq. ID	jC-atXP2C75F5T7030a1
Method	BLASTX
NCBI GI	g119143
BLAST score	566
E value	4.0e-58
Match length	109
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	176652
Seq. ID	jC-atXP2C75G8T7032a1
Method	BLASTX
NCBI GI	g4185141
BLAST score	650
E value	5.0e-68
Match length	133
% identity	93
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	176653
Seq. ID	jC-atXP2C76C12T7040a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176654
Seq. ID	jC-atXP2C76D11T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	3.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176655
Seq. ID	jC-atXP2C77A2T7049a1
Method	BLASTX
NCBI GI	g2098778
BLAST score	681
E value	1.0e-71
Match length	134
% identity	99
NCBI Description	(U96045) APS reductase [Arabidopsis thaliana]

Seq. No.	176656
Seq. ID	jC-atXP2C78C9T7073a1
Method	BLASTX
NCBI GI	g2058456
BLAST score	773
E value	2.0e-82

Match length	151
% identity	97
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	176657
Seq. ID	jC-atXP2C79A3T7089a1
Method	BLASTN
NCBI GI	g3702315
BLAST score	224
E value	1.0e-122
Match length	544
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176658
Seq. ID	jC-atXP2C79F5T7094a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176659
Seq. ID	jC-atXP2C79G7T7096a1
Method	BLASTX
NCBI GI	g1710549
BLAST score	147
E value	5.0e-09
Match length	48
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L39

Seq. No.	176660
Seq. ID	jC-atXP30C142E13T7s2
Method	BLASTN
NCBI GI	g3766106
BLAST score	19
E value	7.9e-01
Match length	165
% identity	71
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176661
Seq. ID	jC-atXP30C142L2T7s2
Method	BLASTN
NCBI GI	g4732169
BLAST score	528
E value	0.0e+00
Match length	543
% identity	99
NCBI Description	Arabidopsis thaliana BAC T3E15

Seq. No.	176662
Seq. ID	jC-atXP30C142M7T7d2
Method	BLASTX
NCBI GI	g3236253
BLAST score	311
E value	2.0e-28
Match length	131
% identity	49
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	176663
Seq. ID	jC-atXP30C146A5T7s2
Method	BLASTX
NCBI GI	g461903
BLAST score	254
E value	6.0e-22
Match length	63
% identity	81
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_405129 (L14844) cyclophilin [Arabidopsis thaliana] >gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl isomerase ROC1 [Arabidopsis thaliana]

Seq. No.	176664
Seq. ID	jC-atXP31C144C19T7d2
Method	BLASTN
NCBI GI	g2828182
BLAST score	35
E value	6.0e-10
Match length	140
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	176665
Seq. ID	jC-atXP31C144I15T7d2
Method	BLASTN
NCBI GI	g4558586
BLAST score	126
E value	3.0e-64
Match length	411
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	176666
Seq. ID	jC-atXP31C144I7T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	121
E value	3.0e-11
Match length	89
% identity	54
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana]

	>gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]
Seq. No.	176667
Seq. ID	jC-atXP31C144J4T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	141
E value	1.0e-33
Match length	183
% identity	54
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]
Seq. No.	176668
Seq. ID	jC-atXP31C144K24T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	49
E value	1.0e-11
Match length	106
% identity	44
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]
Seq. No.	176669
Seq. ID	jC-atXP31C144L2T7d2
Method	BLASTX
NCBI GI	g4544399
BLAST score	174
E value	3.0e-12
Match length	146
% identity	34
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	176670
Seq. ID	jC-atXP31C145N10T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	237
E value	1.0e-19
Match length	117
% identity	54
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]
Seq. No.	176671
Seq. ID	jC-atXP31C145O5T7d2
Method	BLASTX

NCBI GI	g1046225
BLAST score	449
E value	1.0e-54
Match length	170
% identity	71
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	176672
Seq. ID	jC-atXP31C146C23T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	177
E value	3.0e-84
Match length	173
% identity	95
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	176673
Seq. ID	jC-atXP31C146E8T7d2
Method	BLASTX
NCBI GI	g1710424
BLAST score	411
E value	4.0e-40
Match length	94
% identity	89
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	176674
Seq. ID	jC-atXP31C146F10T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	332
E value	9.0e-31
Match length	155
% identity	31
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	176675
Seq. ID	jC-atXP31C146F3T7d2
Method	BLASTX
NCBI GI	g3702323
BLAST score	483
E value	2.0e-48
Match length	188
% identity	59

NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	176676
Seq. ID	jC-atXP31C146I10T7d2
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	176677
Seq. ID	jC-atXP31C146I19T7d2
Method	BLASTX
NCBI GI	g120675
BLAST score	275
E value	1.0e-82
Match length	166
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	176678
Seq. ID	jC-atXP31C146J24T7s1
Method	BLASTN
NCBI GI	g2264320
BLAST score	44
E value	7.0e-16
Match length	64
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	176679
Seq. ID	jC-atXP31C146J9T7d2
Method	BLASTX
NCBI GI	g2982455
BLAST score	205
E value	6.0e-63
Match length	175
% identity	74
NCBI Description	(AL022223) putative uracil phosphoribosyl transferase [Arabidopsis thaliana]

Seq. No.	176680
Seq. ID	jC-atXP31C147A15T7d2
Method	BLASTX
NCBI GI	g1174718
BLAST score	179
E value	1.0e-45
Match length	184
% identity	57

NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]
Seq. No.	176681
Seq. ID	jC-atXP31C147B12T7d2
Method	BLASTN
NCBI GI	g4519183
BLAST score	28
E value	7.0e-06
Match length	204
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence
Seq. No.	176682
Seq. ID	jC-atXP31C147B12T7s1
Method	BLASTN
NCBI GI	g4519183
BLAST score	34
E value	5.0e-10
Match length	62
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence
Seq. No.	176683
Seq. ID	jC-atXP31C147B23T7d2
Method	BLASTN
NCBI GI	g4544381
BLAST score	215
E value	1.0e-117
Match length	531
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence
Seq. No.	176684
Seq. ID	jC-atXP31C147B23T7s1
Method	BLASTN
NCBI GI	g4544381
BLAST score	199
E value	1.0e-108
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence
Seq. No.	176685
Seq. ID	jC-atXP31C147D12T7d2
Method	BLASTX
NCBI GI	g2244990
BLAST score	481
E value	3.0e-48
Match length	169
% identity	60

NCBI Description	(Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No.	176686
Seq. ID	jC-atXP31C147D14T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	257
E value	3.0e-46
Match length	190
% identity	59
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	176687
Seq. ID	jC-atXP32C144N17T7d2
Method	BLASTN
NCBI GI	g4539309
BLAST score	246
E value	1.0e-135
Match length	484
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	176688
Seq. ID	jC-atXP32C146N20T7d2
Method	BLASTX
NCBI GI	g2494266
BLAST score	455
E value	1.0e-53
Match length	167
% identity	67
NCBI Description	GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917) LepA [Synechocystis sp.]

Seq. No.	176689
Seq. ID	jC-atXP32C146N2T7s1
Method	BLASTX
NCBI GI	g3513730
BLAST score	268
E value	1.0e-23
Match length	59
% identity	83
NCBI Description	(AF080118) No definition line found [Arabidopsis thaliana]

Seq. No.	176690
Seq. ID	jC-atXP32C146P14T7d2
Method	BLASTX
NCBI GI	g3688182
BLAST score	464
E value	1.0e-46
Match length	237
% identity	50
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No.	176691
Seq. ID	jC-atXP32C146P16T7d2
Method	BLASTN
NCBI GI	g4539309
BLAST score	80
E value	7.0e-37
Match length	418
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	176692
Seq. ID	jC-atXP32C146P1T7d2
Method	BLASTX
NCBI GI	g4539301
BLAST score	210
E value	3.0e-16
Match length	144
% identity	42
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	176693
Seq. ID	jC-atXP32C146P4T7d2
Method	BLASTX
NCBI GI	g3445207
BLAST score	150
E value	1.0e-15
Match length	127
% identity	47
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	176694
Seq. ID	jC-atXP32C147E14T7d2
Method	BLASTX
NCBI GI	g1362008
BLAST score	193
E value	4.0e-14
Match length	79
% identity	14
NCBI Description	ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No.	176695
Seq. ID	jC-atXP32C147E1T7d2
Method	BLASTN
NCBI GI	g4539309
BLAST score	381
E value	0.0e+00
Match length	441
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	176696
Seq. ID	jC-atXP32C147E23T7d2
Method	BLASTN

NCBI GI	g3800746
BLAST score	35
E value	7.0e-10
Match length	39
% identity	97
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	176697
Seq. ID	jC-atXP32C147F10T7d2
Method	BLASTN
NCBI GI	g1335926
BLAST score	37
E value	3.0e-11
Match length	49
% identity	94
NCBI Description	Synthetic E. coli Tn3-derived transposon OMP decarboxylase (URA3) and tetracycline efflux protein (tet) genes, complete cds, and beta-galactosidase gene (lacZ), partial cds

Seq. No.	176698
Seq. ID	jC-atXP32C147F20T7d2
Method	BLASTN
NCBI GI	g2828185
BLAST score	37
E value	4.0e-11
Match length	125
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	176699
Seq. ID	jC-atXP32C147G11T7d2
Method	BLASTX
NCBI GI	g135467
BLAST score	52
E value	2.0e-70
Match length	155
% identity	89
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	176700
Seq. ID	jC-atXP32C147G24T7d2
Method	BLASTX
NCBI GI	g2586083
BLAST score	270
E value	3.0e-23
Match length	105
% identity	49
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	176701
Seq. ID	jC-atXP32C147G24T7s1

Method	BLASTX
NCBI GI	g4586061
BLAST score	474
E value	1.0e-47
Match length	86
% identity	100
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	176702
Seq. ID	jC-atXP32C147H14T7d2
Method	BLASTX
NCBI GI	g4324597
BLAST score	212
E value	3.0e-21
Match length	123
% identity	56
NCBI Description	(AF106324) sodium proton exchanger Nhx1 [Arabidopsis thaliana]

Seq. No.	176703
Seq. ID	jC-atXP32C147H20T7d2
Method	BLASTN
NCBI GI	g4538918
BLAST score	69
E value	4.0e-30
Match length	403
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)

Seq. No.	176704
Seq. ID	jC-atXP32C147I23T7d2
Method	BLASTN
NCBI GI	g1946354
BLAST score	262
E value	1.0e-145
Match length	541
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	176705
Seq. ID	jC-atXP32C147K3T7d2
Method	BLASTN
NCBI GI	g3941523
BLAST score	34
E value	3.0e-09
Match length	38
% identity	97
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	176706
Seq. ID	jC-atXP32C147K6T7d2
Method	BLASTN
NCBI GI	g2576326
BLAST score	50

E value	8.0e-19
Match length	71
% identity	31
NCBI Description	Phaseolus vulgaris tRNA-Pro (AGG), tRNA-Pro (UGG) genes

Seq. No.	176707
Seq. ID	jC-atXP32C147L15T7d2
Method	BLASTX
NCBI GI	g4544449
BLAST score	46
E value	5.0e-39
Match length	102
% identity	87
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	176708
Seq. ID	jC-atXP32C147L18T7d2
Method	BLASTN
NCBI GI	g3309173
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds

Seq. No.	176709
Seq. ID	jC-atXP32C147L20T7d2
Method	BLASTX
NCBI GI	g1657617
BLAST score	60
E value	2.0e-98
Match length	239
% identity	79
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	176710
Seq. ID	jC-atXP32C147L23T7d2
Method	BLASTN
NCBI GI	g469109
BLAST score	197
E value	1.0e-106
Match length	364
% identity	89
NCBI Description	A.thaliana (Columbia) Di19 mRNA

Seq. No.	176711
Seq. ID	jC-atXP32C147L7T7d2
Method	BLASTX
NCBI GI	g4262180
BLAST score	270
E value	3.0e-88
Match length	175
% identity	92
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	176712
Seq. ID	jC-atXP32C147M15T7d2
Method	BLASTN
NCBI GI	g3421122
BLAST score	56
E value	2.0e-22
Match length	385
% identity	84
NCBI Description	Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA, complete cds

Seq. No.	176713
Seq. ID	jC-atXP32C147M2T7d2
Method	BLASTX
NCBI GI	g1890315
BLAST score	69
E value	6.1e+00
Match length	96
% identity	65
NCBI Description	(Y11790) peroxidase ATP25a [Arabidopsis thaliana]

Seq. No.	176714
Seq. ID	jC-atXP32C147M6T7d2
Method	BLASTX
NCBI GI	g1657617
BLAST score	788
E value	6.0e-84
Match length	194
% identity	87
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	176715
Seq. ID	jC-atXP32C147O10T7d2
Method	BLASTN
NCBI GI	g2351067
BLAST score	46
E value	2.0e-16
Match length	233
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	176716
Seq. ID	jC-atXP32C147O23T7d2
Method	BLASTX
NCBI GI	g399013
BLAST score	490
E value	4.0e-49
Match length	142
% identity	71
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)

adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	176717
Seq. ID	jC-atXP32C147O24T7d2
Method	BLASTX
NCBI GI	g3152557
BLAST score	177
E value	4.0e-52
Match length	195
% identity	59
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. EST gb_T76227 comes from this gene. [Arabidopsis thaliana]

Seq. No.	176718
Seq. ID	jC-atXP32C147P21T7d2
Method	BLASTX
NCBI GI	g2642429
BLAST score	357
E value	2.0e-33
Match length	120
% identity	28
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	176719
Seq. ID	jC-atXP32C148A12T7d2
Method	BLASTX
NCBI GI	g1944518
BLAST score	258
E value	4.0e-22
Match length	119
% identity	53
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	176720
Seq. ID	jC-atXP32C149C5T7d2
Method	BLASTX
NCBI GI	g141305
BLAST score	167
E value	2.0e-11
Match length	72
% identity	54
NCBI Description	YPT1-RELATED PROTEIN 2 >gi_101034_pir__S12790 GTP-binding protein ypt2 - fission yeast (Schizosaccharomyces pombe) >gi_5144_emb_CAA36707_ (X52469) ypt2 gene product (AA 1-200) [Schizosaccharomyces pombe] >gi_5150_emb_CAA37045_ (X52864) ypt-related protein (AA 1-200) [Schizosaccharomyces pombe] >gi_2414662_emb_CAB16405_ (Z99262) ypt1-related protein 2. [Schizosaccharomyces pombe]

Seq. No. 176721

Seq. ID	jC-atXP32C149C7T7d2
Method	BLASTN
NCBI GI	g2815404
BLAST score	38
E value	1.0e-11
Match length	314
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	176722
Seq. ID	jC-atXP33C144O11T7s2
Method	BLASTX
NCBI GI	g2462756
BLAST score	169
E value	8.0e-12
Match length	108
% identity	43
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	176723
Seq. ID	jC-atXP33C148C13T7s2
Method	BLASTN
NCBI GI	g3738275
BLAST score	234
E value	1.0e-129
Match length	464
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176724
Seq. ID	jC-atXP33C148C14T7s2
Method	BLASTN
NCBI GI	g3108025
BLAST score	187
E value	1.0e-100
Match length	510
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	176725
Seq. ID	jC-atXP33C148C6T7s2
Method	BLASTX
NCBI GI	g629669
BLAST score	273
E value	5.0e-24
Match length	111
% identity	43
NCBI Description	hypothetical protein - tomato

Seq. No.	176726
Seq. ID	jC-atXP33C148D1T7s2
Method	BLASTN
NCBI GI	g3201608
BLAST score	147

E value	4.0e-77
Match length	251
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176727
Seq. ID	jC-atXP33C148I1T7s2
Method	BLASTN
NCBI GI	g2244788
BLAST score	129
E value	2.0e-66
Match length	320
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176728
Seq. ID	jC-atXP33C148M17T7s2
Method	BLASTN
NCBI GI	g2264306
BLAST score	59
E value	9.0e-25
Match length	153
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	176729
Seq. ID	jC-atXP33C149F9T7s2
Method	BLASTN
NCBI GI	g4220645
BLAST score	92
E value	4.0e-44
Match length	372
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	176730
Seq. ID	jC-atXP33C151A14T7s2
Method	BLASTX
NCBI GI	g3769671
BLAST score	224
E value	3.0e-18
Match length	116
% identity	44
NCBI Description	(AF095284) Tic22 [Pisum sativum]

Seq. No.	176731
Seq. ID	jC-atXP33C151A16T7s2
Method	BLASTX
NCBI GI	g1706918
BLAST score	204
E value	6.0e-16
Match length	74
% identity	50

NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	176732
Seq. ID	jC-atXP34C149G22T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176733
Seq. ID	jC-atXP34C149G3T7a1
Method	BLASTX
NCBI GI	g4741956
BLAST score	102
E value	8.0e-04
Match length	142
% identity	54
NCBI Description	(AF134128) Lhcb4:3 protein [Arabidopsis thaliana]

Seq. No.	176734
Seq. ID	jC-atXP34C149H11T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	2.0e-14
Match length	46
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176735
Seq. ID	jC-atXP34C149H1T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	3.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176736
Seq. ID	jC-atXP34C149J20T7a1
Method	BLASTX
NCBI GI	g4835234
BLAST score	148
E value	4.0e-09
Match length	130
% identity	29
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]

Seq. No.	176737
Seq. ID	jC-atXP34C149K24T7a1
Method	BLASTN

NCBI GI	g4455262
BLAST score	34
E value	2.0e-09
Match length	54
% identity	49
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	176738
Seq. ID	jC-atXP34C149L3T7a1
Method	BLASTX
NCBI GI	g3164126
BLAST score	415
E value	2.0e-40
Match length	96
% identity	81
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	176739
Seq. ID	jC-atXP34C149M10T7a1
Method	BLASTX
NCBI GI	g786117
BLAST score	138
E value	9.0e-08
Match length	310
% identity	6
NCBI Description	(L41834) nuclear protein [Ensis minor]

Seq. No.	176740
Seq. ID	jC-atXP34C149N17T7a1
Method	BLASTN
NCBI GI	g2244747
BLAST score	71
E value	3.0e-31
Match length	227
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176741
Seq. ID	jC-atXP34C149O16T7a1
Method	BLASTX
NCBI GI	g132744
BLAST score	114
E value	6.0e-10
Match length	108
% identity	44
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_71230_pir__R5BY17 ribosomal protein L23.e, cytosolic - yeast (Saccharomyces cerevisiae) >gi_4324_emb_CAA25841_ (X01694) ribosomal protein L17 [Saccharomyces cerevisiae] >gi_496691_emb_CAA56018_ (X79489) L23 B x-137 [Saccharomyces cerevisiae] >gi_536142_emb_CAA84908_ (Z35848) ORF YBL087c [Saccharomyces cerevisiae] >gi_603356 (U18916) Rpl17bp: Ribosomal protein, large subunit [Saccharomyces cerevisiae] >gi_622952 (U15653) ribosomal protein L17B [Saccharomyces

cerevisiae]

Seq. No.	176742
Seq. ID	jC-atXP34C149P15T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	3.0e-19
Match length	58
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176743
Seq. ID	jC-atXP34C149P20T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176744
Seq. ID	jC-atXP34C150D7T7a1
Method	BLASTX
NCBI GI	g3510250
BLAST score	601
E value	3.0e-62
Match length	137
% identity	85
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	176745
Seq. ID	jC-atXP34C150E13T7a1
Method	BLASTX
NCBI GI	g2979553
BLAST score	182
E value	5.0e-13
Match length	154
% identity	30
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176746
Seq. ID	jC-atXP34C150E20T7a1
Method	BLASTN
NCBI GI	g3702732
BLAST score	282
E value	1.0e-157
Match length	564
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	176747
Seq. ID	jC-atXP34C150F7T7a1
Method	BLASTX
NCBI GI	g3176669

BLAST score	360
E value	6.0e-34
Match length	119
% identity	55
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	176748
Seq. ID	jC-atXP34C150H24T7a1
Method	BLASTN
NCBI GI	g710625
BLAST score	488
E value	0.0e+00
Match length	560
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	176749
Seq. ID	jC-atXP34C150H2T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176750
Seq. ID	jC-atXP34C150I21T7a1
Method	BLASTN
NCBI GI	g2245031
BLAST score	266
E value	1.0e-147
Match length	565
% identity	47
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	176751
Seq. ID	jC-atXP34C150L12T7a1
Method	BLASTN
NCBI GI	g3738088
BLAST score	180
E value	2.0e-96
Match length	434
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176752
Seq. ID	jC-atXP34C150L22T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	3.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176753
Seq. ID	jC-atXP34C150N20T7a1
Method	BLASTN
NCBI GI	g4159706
BLAST score	451
E value	0.0e+00
Match length	667
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	176754
Seq. ID	jC-atXP34C150N4T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176755
Seq. ID	jC-atXP34C150N4T7d1
Method	BLASTN
NCBI GI	g4159706
BLAST score	42
E value	7.0e-15
Match length	58
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	176756
Seq. ID	jC-atXP34C150N7T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176757
Seq. ID	jC-atXP34C150N9T7a1
Method	BLASTX
NCBI GI	g4335751
BLAST score	143
E value	2.0e-45
Match length	112
% identity	86
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	176758
Seq. ID	jC-atXP34C150O6T7a1
Method	BLASTN

NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176759
Seq. ID	jC-atXP34C150P17T7a1
Method	BLASTX
NCBI GI	g3046700
BLAST score	416
E value	1.0e-40
Match length	134
% identity	72
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	176760
Seq. ID	jC-atXP34C151G15T7a1
Method	BLASTX
NCBI GI	g1572721
BLAST score	162
E value	1.0e-10
Match length	248
% identity	5
NCBI Description	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]

Seq. No.	176761
Seq. ID	jC-atXP34C153B6T7a1
Method	BLASTX
NCBI GI	g1526422
BLAST score	345
E value	3.0e-32
Match length	80
% identity	88
NCBI Description	(D64139) LEA protein in group 5 [Arabidopsis thaliana]

Seq. No.	176762
Seq. ID	jC-atXP34C153C5T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	6.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176763
Seq. ID	jC-atXP34C153D3T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17

Match length	47
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176764
Seq. ID	jC-atXP35C151O10T7s2
Method	BLASTN
NCBI GI	g4220627
BLAST score	48
E value	5.0e-18
Match length	175
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	176765
Seq. ID	jC-atXP35C153G18T7d1
Method	BLASTN
NCBI GI	g3212846
BLAST score	122
E value	3.0e-62
Match length	254
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176766
Seq. ID	jC-atXP35C153H3T7d1
Method	BLASTX
NCBI GI	g1914683
BLAST score	286
E value	1.0e-25
Match length	76
% identity	74
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	176767
Seq. ID	jC-atXP35C153K9T7s2
Method	BLASTN
NCBI GI	g4678705
BLAST score	138
E value	8.0e-72
Match length	210
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	176768
Seq. ID	jC-atXP35C153P10T7s2
Method	BLASTN
NCBI GI	g3063438
BLAST score	225
E value	1.0e-123
Match length	312
% identity	84
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	176769
Seq. ID	jC-atXP35C153P8T7s2
Method	BLASTN
NCBI GI	g3399678
BLAST score	80
E value	4.0e-37
Match length	168
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176770
Seq. ID	jC-atXP35C154C4T7d1
Method	BLASTN
NCBI GI	g4757405
BLAST score	192
E value	1.0e-104
Match length	272
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	176771
Seq. ID	jC-atXP35C154E24T7d1
Method	BLASTN
NCBI GI	g3046851
BLAST score	52
E value	9.0e-21
Match length	129
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	176772
Seq. ID	jC-atXP35C154F12T7s2
Method	BLASTX
NCBI GI	g4263820
BLAST score	147
E value	2.0e-09
Match length	48
% identity	56
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176773
Seq. ID	jC-atXP36C154L2T7d1
Method	BLASTX
NCBI GI	g4586109
BLAST score	164
E value	4.0e-11
Match length	61
% identity	52
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	176774
Seq. ID	jC-atXP36C154O14T7d1
Method	BLASTN

NCBI GI	g3894156
BLAST score	367
E value	0.0e+00
Match length	475
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176775
Seq. ID	jC-atXP36C154P19T7s1
Method	BLASTN
NCBI GI	g2828185
BLAST score	177
E value	4.0e-95
Match length	229
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	176776
Seq. ID	jC-atXP36C155A15T7s1
Method	BLASTX
NCBI GI	g2632061
BLAST score	458
E value	9.0e-46
Match length	92
% identity	96
NCBI Description	(AJ002597) membrane-associated salt-inducible protein like [Arabidopsis thaliana]

Seq. No.	176777
Seq. ID	jC-atXP36C156A22T7d1
Method	BLASTN
NCBI GI	g1850600
BLAST score	100
E value	2.0e-49
Match length	124
% identity	96
NCBI Description	Arabidopsis thaliana Rac-like protein mRNA, complete cds

Seq. No.	176778
Seq. ID	jC-atXP36C156C11T7s1
Method	BLASTN
NCBI GI	g3046854
BLAST score	55
E value	5.0e-22
Match length	229
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	176779
Seq. ID	jC-atXP36C156M7T7s1
Method	BLASTN
NCBI GI	g4589412
BLAST score	136
E value	1.0e-70

Match length	219
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	176780
Seq. ID	jC-atXP37C156G1T7d2
Method	BLASTN
NCBI GI	g4680765
BLAST score	56
E value	2.0e-22
Match length	88
% identity	91
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	176781
Seq. ID	jC-atXP37C157H17T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	1.0e-11
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176782
Seq. ID	jC-atXP37C157H6T7s2
Method	BLASTN
NCBI GI	g2995991
BLAST score	164
E value	3.0e-87
Match length	232
% identity	93
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	176783
Seq. ID	jC-atXP37C157I16T7d2
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	9.0e-22
Match length	67
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176784
Seq. ID	jC-atXP37C157M16T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	38
E value	2.0e-11
Match length	50
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176785
Seq. ID	jC-atXP37C157M1T7d2
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	9.0e-16
Match length	60
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176786
Seq. ID	jC-atXP37C157N18T7d2
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	6.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176787
Seq. ID	jC-atXP37C157O14T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	1.0e-21
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176788
Seq. ID	jC-atXP37C157P24T7d2
Method	BLASTX
NCBI GI	g259447
BLAST score	231
E value	8.0e-19
Match length	122
% identity	40
NCBI Description	(S47409) glycine-rich protein, atGRP {clone atGRP-3} [Arabidopsis thaliana, C24, Peptide, 145 aa] [Arabidopsis thaliana]

Seq. No.	176789
Seq. ID	jC-atXP37C159A11T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176790
Seq. ID	jC-atXP37C159B13T7s2
Method	BLASTN
NCBI GI	g4335744

BLAST score	119
E value	2.0e-60
Match length	209
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176791
Seq. ID	jC-atXP37C159C2T7d2
Method	BLASTN
NCBI GI	g4544405
BLAST score	34
E value	2.0e-09
Match length	118
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	176792
Seq. ID	jC-atXP37C159C8T7d2
Method	BLASTN
NCBI GI	g3169718
BLAST score	271
E value	1.0e-150
Match length	363
% identity	94
NCBI Description	Arabidopsis thaliana mRNA, similar to yeast dcp1, complete cds

Seq. No.	176793
Seq. ID	jC-atXP37C159D24T7d2
Method	BLASTX
NCBI GI	g259447
BLAST score	152
E value	1.0e-09
Match length	32
% identity	78
NCBI Description	(S47409) glycine-rich protein, atGRP {clone atGRP-3} [Arabidopsis thaliana, C24, Peptide, 145 aa] [Arabidopsis thaliana]

Seq. No.	176794
Seq. ID	jC-atXP37C159E10T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	1.0e-09
Match length	55
% identity	93
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176795
Seq. ID	jC-atXP37C159E1T7s2
Method	BLASTX
NCBI GI	g3702332
BLAST score	169
E value	4.0e-12

Match length	47
% identity	68
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	176796
Seq. ID	jC-atXP38C158I19T7d1
Method	BLASTN
NCBI GI	g2182287
BLAST score	49
E value	5.0e-19
Match length	142
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	176797
Seq. ID	jC-atXP38C158J7T7s2
Method	BLASTX
NCBI GI	g1053093
BLAST score	448
E value	2.0e-44
Match length	91
% identity	99
NCBI Description	(U38550) zeta-carotene desaturase precursor [Arabidopsis thaliana]

Seq. No.	176798
Seq. ID	jC-atXP38C160J23T7s2
Method	BLASTN
NCBI GI	g4467131
BLAST score	386
E value	0.0e+00
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	176799
Seq. ID	jC-atXP39C158P6T7s1
Method	BLASTX
NCBI GI	g2129517
BLAST score	326
E value	3.0e-30
Match length	62
% identity	100
NCBI Description	24-sterol C-methyltransferase (EC 2.1.1.41) - Arabidopsis thaliana

Seq. No.	176800
Seq. ID	jC-atXP39C160O1T7s1
Method	BLASTX
NCBI GI	g4218120
BLAST score	301
E value	2.0e-27
Match length	75
% identity	69
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No.	176801
Seq. ID	jC-atXP39C161C17T7s1
Method	BLASTX
NCBI GI	g4454050
BLAST score	570
E value	5.0e-59
Match length	113
% identity	94
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	176802
Seq. ID	jC-atXP39C161D17T7s1
Method	BLASTX
NCBI GI	g3169010
BLAST score	189
E value	4.0e-14
Match length	103
% identity	41
NCBI Description	(AJ006412) putative GTP-binding protein [Homo sapiens]

Seq. No.	176803
Seq. ID	jC-atXP39C161F17T7s1
Method	BLASTN
NCBI GI	g2924733
BLAST score	236
E value	1.0e-130
Match length	296
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	176804
Seq. ID	jC-atXP39C162G7T7s1
Method	BLASTX
NCBI GI	g3080421
BLAST score	395
E value	3.0e-38
Match length	87
% identity	89
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	176805
Seq. ID	jC-atXP39C162I3T7s1
Method	BLASTN
NCBI GI	g3281845
BLAST score	121
E value	5.0e-62
Match length	125
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for LATE ELONGATED HYPOCOTYL MYB transcription factor >gi_4759505_emb_A68428.1_A68428 Sequence 1 from Patent WO9749811

Seq. No.	176806
Seq. ID	jC-atXP3C80D8T7d1

Method	BLASTX
NCBI GI	g4337210
BLAST score	574
E value	2.0e-59
Match length	125
% identity	92
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176807
Seq. ID	jC-atXP3C80E12T7010a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	8.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176808
Seq. ID	jC-atXP3C80F12T7014a1
Method	BLASTX
NCBI GI	g1173624
BLAST score	320
E value	2.0e-29
Match length	95
% identity	61
NCBI Description	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	176809
Seq. ID	jC-atXP3C80F1T7011a1
Method	BLASTN
NCBI GI	g3413696
BLAST score	64
E value	3.0e-27
Match length	248
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176810
Seq. ID	jC-atXP3C80F3T7012a1
Method	BLASTN
NCBI GI	g1036816
BLAST score	137
E value	9.0e-71
Match length	269
% identity	97
NCBI Description	Rhopalosiphum maidis 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence

Seq. No.	176811
Seq. ID	jC-atXP3C80G1T7015a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19

Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176812
Seq. ID	jC-atXP3C81A12T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	60
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176813
Seq. ID	jC-atXP3C81A7T7020a1
Method	BLASTN
NCBI GI	g1872520
BLAST score	233
E value	1.0e-128
Match length	445
% identity	88
NCBI Description	Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) mRNA, complete cds

Seq. No.	176814
Seq. ID	jC-atXP3C81B7T7024a1
Method	BLASTN
NCBI GI	g3335356
BLAST score	256
E value	1.0e-142
Match length	457
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176815
Seq. ID	jC-atXP3C81D1T7027a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176816
Seq. ID	jC-atXP3C81D5T7028a1
Method	BLASTX
NCBI GI	g2982452
BLAST score	222
E value	7.0e-18
Match length	106
% identity	42
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	176817
Seq. ID	jC-atXP3C81H4T7039a1
Method	BLASTX
NCBI GI	g282865
BLAST score	189
E value	6.0e-14
Match length	122
% identity	57
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	176818
Seq. ID	jC-atXP3C82B7T7042a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176819
Seq. ID	jC-atXP3C82D11T7052a1
Method	BLASTN
NCBI GI	g2827644
BLAST score	257
E value	1.0e-142
Match length	406
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	176820
Seq. ID	jC-atXP3C82E10T7075a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176821
Seq. ID	jC-atXP3C82G11T7077a1
Method	BLASTX
NCBI GI	g107422
BLAST score	125
E value	2.0e-06
Match length	212
% identity	8
NCBI Description	proline-rich protein PRB3S (cys) - human (fragment)

Seq. No.	176822

Seq. ID	jC-atXP3C83A2T7054a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176823
Seq. ID	jC-atXP3C83B8T7d1
Method	BLASTN
NCBI GI	g4335711
BLAST score	76
E value	6.0e-35
Match length	173
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176824
Seq. ID	jC-atXP3C83C10T7060a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	7.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176825
Seq. ID	jC-atXP3C83C7T7059a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176826
Seq. ID	jC-atXP3C83G7T7069a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176827
Seq. ID	jC-atXP3C83H12T7074a1
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	7.0e-22
Match length	67

% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176828
Seq. ID	jC-atXP3C83H5T7071a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	51
% identity	92
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176829
Seq. ID	jC-atXP3C84D7T7085a1
Method	BLASTX
NCBI GI	g2246456
BLAST score	181
E value	5.0e-37
Match length	100
% identity	81
NCBI Description	(U71400) S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]

Seq. No.	176830
Seq. ID	jC-atXP3C84F7T7087a1
Method	BLASTN
NCBI GI	g3269280
BLAST score	63
E value	1.0e-26
Match length	111
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	176831
Seq. ID	jC-atXP3C85A5T7088a1
Method	BLASTX
NCBI GI	g4107101
BLAST score	629
E value	1.0e-65
Match length	130
% identity	95
NCBI Description	(AB015142) AHP2 [Arabidopsis thaliana] >gi_4156241_dbj_BAA37110_ (AB012568) ATHP1 [Arabidopsis thaliana]

Seq. No.	176832
Seq. ID	jC-atXP3C85C6T7095a1
Method	BLASTN
NCBI GI	g4757405
BLAST score	96
E value	3.0e-46
Match length	309
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	176833
Seq. ID	jC-atXP40C161I16T7033a1
Method	BLASTX
NCBI GI	g1076331
BLAST score	638
E value	1.0e-66
Match length	132
% identity	94
NCBI Description	histidine transport protein - Arabidopsis thaliana >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter 1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His transporter [Arabidopsis thaliana]

Seq. No.	176834
Seq. ID	jC-atXP40C161I5T7017a1
Method	BLASTX
NCBI GI	g3329623
BLAST score	107
E value	3.0e-04
Match length	232
% identity	7
NCBI Description	(AF078790) No definition line found [Caenorhabditis elegans]

Seq. No.	176835
Seq. ID	jC-atXP40C161J24T7073a1
Method	BLASTX
NCBI GI	g1765899
BLAST score	1175
E value	1.0e-129
Match length	216
% identity	98
NCBI Description	(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. No.	176836
Seq. ID	jC-atXP40C161J9T7041a1
Method	BLASTX
NCBI GI	g2894306
BLAST score	67
E value	8.0e-19
Match length	92
% identity	53
NCBI Description	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No.	176837
Seq. ID	jC-atXP40C161K10T7d1
Method	BLASTN
NCBI GI	g3241927
BLAST score	114
E value	1.0e-57
Match length	185
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	176838
Seq. ID	jC-atXP40C161L8T7058a1
Method	BLASTX
NCBI GI	g3785983
BLAST score	183
E value	3.0e-13
Match length	56
% identity	61
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176839
Seq. ID	jC-atXP40C161M12T7019a1
Method	BLASTX
NCBI GI	g132102
BLAST score	91
E value	1.9e-02
Match length	161
% identity	15
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	176840
Seq. ID	jC-atXP40C161P2T7067a1
Method	BLASTN
NCBI GI	g531828
BLAST score	57
E value	4.0e-23
Match length	65
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176841
Seq. ID	jC-atXP40C162I21T7005a1
Method	BLASTN
NCBI GI	g4165340
BLAST score	66
E value	2.0e-28
Match length	305
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176842
Seq. ID	jC-atXP40C162J3T7037a1
Method	BLASTN
NCBI GI	g3046847
BLAST score	395
E value	0.0e+00
Match length	597
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	176843
Seq. ID	jC-atXP40C162J6T7045a1
Method	BLASTN
NCBI GI	g4581161
BLAST score	255
E value	1.0e-141
Match length	534
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	176844
Seq. ID	jC-atXP40C162K12T7006a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	82
E value	9.0e-38
Match length	130
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	176845
Seq. ID	jC-atXP40C162K19T7030a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176846
Seq. ID	jC-atXP40C162M10T7015a1
Method	BLASTX
NCBI GI	g2244911
BLAST score	259
E value	4.0e-22
Match length	112
% identity	53
NCBI Description	(Z97339) similar to indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	176847
Seq. ID	jC-atXP40C163C16T7008a1
Method	BLASTN
NCBI GI	g2864607
BLAST score	89
E value	3.0e-42
Match length	137
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	176848
Seq. ID	jC-atXP40C164A11T7004a1
Method	BLASTX

NCBI GI	g4193320
BLAST score	318
E value	5.0e-29
Match length	108
% identity	57
NCBI Description	(AF045473) histone deacetylase [Zea mays]

Seq. No.	176849
Seq. ID	jC-atXP41C162N22T7s1
Method	BLASTX
NCBI GI	g4587535
BLAST score	569
E value	9.0e-59
Match length	103
% identity	100
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. EST gb_R29935 comes from this gene. [Arabidopsis thaliana]

Seq. No.	176850
Seq. ID	jC-atXP41C162P15T7d1
Method	BLASTX
NCBI GI	g2194137
BLAST score	523
E value	2.0e-53
Match length	113
% identity	87
NCBI Description	(AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	176851
Seq. ID	jC-atXP41C162P15T7s1
Method	BLASTN
NCBI GI	g2182286
BLAST score	398
E value	0.0e+00
Match length	454
% identity	96
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	176852
Seq. ID	jC-atXP41C164I3T7s1
Method	BLASTN
NCBI GI	g4539309
BLAST score	36
E value	5.0e-11
Match length	112
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	176853
Seq. ID	jC-atXP41C164N14T7s1
Method	BLASTN
NCBI GI	g2924653
BLAST score	301

E value	1.0e-169
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	176854
Seq. ID	jC-atXP41C166A2T7s1
Method	BLASTN
NCBI GI	g2477521
BLAST score	132
E value	3.0e-68
Match length	263
% identity	70
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176855
Seq. ID	jC-atXP41C166D20T7s1
Method	BLASTN
NCBI GI	g3128139
BLAST score	142
E value	5.0e-74
Match length	323
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	176856
Seq. ID	jC-atXP43C167P12T7s1
Method	BLASTN
NCBI GI	g4063735
BLAST score	142
E value	4.0e-74
Match length	210
% identity	92
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	176857
Seq. ID	jC-atXP43C168E3T7003d1
Method	BLASTX
NCBI GI	g1350930
BLAST score	207
E value	5.0e-16
Match length	74
% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	176858
Seq. ID	jC-atXP43C168F20T7s1
Method	BLASTN
NCBI GI	g3766106
BLAST score	204
E value	1.0e-111
Match length	236
% identity	60

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176859
Seq. ID	jC-atXP43C168H2T7018d1
Method	BLASTX
NCBI GI	g2605714
BLAST score	267
E value	2.0e-45
Match length	143
% identity	71
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	176860
Seq. ID	jC-atXP43C168I17T7073d1
Method	BLASTX
NCBI GI	g3212852
BLAST score	156
E value	1.0e-15
Match length	164
% identity	59
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	176861
Seq. ID	jC-atXP43C169C10T7095d1
Method	BLASTX
NCBI GI	g2119156
BLAST score	99
E value	2.0e-10
Match length	365
% identity	9
NCBI Description	collagen alpha chain - tube worm (Riftia pachyptila) (fragment)

Seq. No.	176862
Seq. ID	jC-atXP43C169D19T7s1
Method	BLASTN
NCBI GI	g3212846
BLAST score	190
E value	1.0e-103
Match length	198
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176863
Seq. ID	jC-atXP43C169D23T7055d1
Method	BLASTN
NCBI GI	g4454004
BLAST score	192
E value	1.0e-103
Match length	308
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	176864
Seq. ID	jC-atXP43C169E3T7047d1
Method	BLASTX
NCBI GI	g132110
BLAST score	573
E value	6.0e-59
Match length	162
% identity	72
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	176865
Seq. ID	jC-atXP43C169N1T7s1
Method	BLASTN
NCBI GI	g4467131
BLAST score	46
E value	2.0e-17
Match length	73
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	176866
Seq. ID	jC-atXP43C169N3T7028d1
Method	BLASTX
NCBI GI	g1076366
BLAST score	712
E value	2.0e-83
Match length	162
% identity	97
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	176867
Seq. ID	jC-atXP43C169O15T7059d1
Method	BLASTX
NCBI GI	g2501064
BLAST score	511
E value	1.0e-51
Match length	145
% identity	76
NCBI Description	PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270) Similar to threonyl-tRNA synthetase; coded for by A. thaliana cDNA R65376 [Arabidopsis thaliana]

Seq. No.	176868
Seq. ID	jC-atXP43C169O2T7067d1
Method	BLASTN

NCBI GI	g4680765
BLAST score	36
E value	3.0e-10
Match length	72
% identity	88
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	176869
Seq. ID	jC-atXP43C169P13T7043d1
Method	BLASTX
NCBI GI	g2244869
BLAST score	174
E value	4.0e-12
Match length	98
% identity	45
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176870
Seq. ID	jC-atXP43C170A21T7093d1
Method	BLASTX
NCBI GI	g284068
BLAST score	129
E value	1.0e-06
Match length	247
% identity	11
NCBI Description	DNA-binding protein 5 - human

Seq. No.	176871
Seq. ID	jC-atXP43C170B13T7077d1
Method	BLASTN
NCBI GI	g2618601
BLAST score	288
E value	1.0e-161
Match length	350
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	176872
Seq. ID	jC-atXP44C168K2T7090a1
Method	BLASTX
NCBI GI	g3135693
BLAST score	320
E value	3.0e-29
Match length	136
% identity	45
NCBI Description	(AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No.	176873
Seq. ID	jC-atXP44C169K23T7033a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	9.0e-10
Match length	54
% identity	91

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176874
Seq. ID	jC-atXP44C169K4T7001a1
Method	BLASTN
NCBI GI	g4587677
BLAST score	578
E value	0.0e+00
Match length	657
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T22C12 genomic sequence, complete sequence
Seq. No.	176875
Seq. ID	jC-atXP44C169K6T7009a1
Method	BLASTX
NCBI GI	g2246532
BLAST score	151
E value	3.0e-09
Match length	237
% identity	6
NCBI Description	(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]
Seq. No.	176876
Seq. ID	jC-atXP44C169M13T7026a1
Method	BLASTX
NCBI GI	g4454032
BLAST score	118
E value	7.0e-16
Match length	136
% identity	41
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]
Seq. No.	176877
Seq. ID	jC-atXP44C170G10T7075a1
Method	BLASTX
NCBI GI	g3482975
BLAST score	629
E value	2.0e-65
Match length	121
% identity	98
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	176878
Seq. ID	jC-atXP44C170J3T7037a1
Method	BLASTX
NCBI GI	g1076314
BLAST score	601
E value	3.0e-62
Match length	140
% identity	86
NCBI Description	cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis thaliana (fragment) >gi_499166_emb_CAA56143_ (X79707) CYS1 [Arabidopsis thaliana]
Seq. No.	176879

Seq. ID	jC-atXP44C170J8T7045a1
Method	BLASTN
NCBI GI	g2696018
BLAST score	391
E value	0.0e+00
Match length	525
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	176880
Seq. ID	jC-atXP44C171C10T7086a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	9.0e-22
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176881
Seq. ID	jC-atXP44C171C1T7078a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	9.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176882
Seq. ID	jC-atXP44C171D22T7063a1
Method	BLASTN
NCBI GI	g3928074
BLAST score	146
E value	5.0e-76
Match length	409
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176883
Seq. ID	jC-atXP44C171E13T7095a1
Method	BLASTX
NCBI GI	g113222
BLAST score	290
E value	9.0e-26
Match length	73
% identity	77
NCBI Description	ACTIN 1 >gi_295885_emb_CAA33874_ (X15865) actin [Oryza sativa]

Seq. No.	176884
Seq. ID	jC-atXP44C171F22T7048a1
Method	BLASTX
NCBI GI	g421989

BLAST score	500
E value	2.0e-50
Match length	172
% identity	56
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]

Seq. No.	176885
Seq. ID	jC-atXP44C171F7T7024a1
Method	BLASTX
NCBI GI	g3319341
BLAST score	429
E value	5.0e-42
Match length	133
% identity	65
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No.	176886
Seq. ID	jC-atXP45C170L20T7041a1
Method	BLASTN
NCBI GI	g3738275
BLAST score	59
E value	2.0e-24
Match length	309
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176887
Seq. ID	jC-atXP45C170L24T7049a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	3.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176888
Seq. ID	jC-atXP45C170L8T7025a1
Method	BLASTN
NCBI GI	g2262097
BLAST score	185
E value	1.0e-99
Match length	284
% identity	91
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	176889
Seq. ID	jC-atXP45C170M2T7057a1
Method	BLASTN
NCBI GI	g4756963
BLAST score	131
E value	2.0e-67

Match length	335
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	176890
Seq. ID	jC-atXP45C170M6T7065a1
Method	BLASTN
NCBI GI	g4756963
BLAST score	141
E value	2.0e-73
Match length	250
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	176891
Seq. ID	jC-atXP45C170N12T7010a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176892
Seq. ID	jC-atXP45C170N7T7081a1
Method	BLASTX
NCBI GI	g2262162
BLAST score	187
E value	7.0e-14
Match length	120
% identity	42
NCBI Description	(AC002329) hypothetical protein similar to A. thaliana protein F19K23.19 [Arabidopsis thaliana]

Seq. No.	176893
Seq. ID	jC-atXP45C170N9T7089a1
Method	BLASTN
NCBI GI	g1429224
BLAST score	39
E value	2.0e-12
Match length	262
% identity	80
NCBI Description	A.thaliana mRNA for peroxidase ATP15a, clone EST 151A15T7

Seq. No.	176894
Seq. ID	jC-atXP45C170O16T7066a1
Method	BLASTN
NCBI GI	g4006885
BLAST score	418
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	176895
Seq. ID	jC-atXP45C170O17T7074a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	8.0e-15
Match length	47
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176896
Seq. ID	jC-atXP45C170O7T7034a1
Method	BLASTX
NCBI GI	g2462824
BLAST score	214
E value	5.0e-17
Match length	77
% identity	65
NCBI Description	(AF000657) similar to Jun activation domain binding protein [Arabidopsis thaliana] >gi_2791885 (AF042334) JAB1 [Arabidopsis thaliana]

Seq. No.	176897
Seq. ID	jC-atXP45C170P5T7090a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176898
Seq. ID	jC-atXP45C170P6T7003a1
Method	BLASTN
NCBI GI	g2760166
BLAST score	68
E value	7.0e-30
Match length	287
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]

Seq. No.	176899
Seq. ID	jC-atXP45C171I13T7091a1
Method	BLASTN
NCBI GI	g3702724
BLAST score	110
E value	9.0e-55
Match length	218
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	176900
Seq. ID	jC-atXP45C171I15T7004a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	7.0e-17
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176901
Seq. ID	jC-atXP45C171I7T7083a1
Method	BLASTN
NCBI GI	g3702724
BLAST score	39
E value	2.0e-12
Match length	217
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	176902
Seq. ID	jC-atXP45C171J1T7028a1
Method	BLASTN
NCBI GI	g4775269
BLAST score	103
E value	1.0e-50
Match length	259
% identity	86
NCBI Description	Arabidopsis thaliana srp30 gene, exons 1-12

Seq. No.	176903
Seq. ID	jC-atXP45C171K15T7076a1
Method	BLASTX
NCBI GI	g4115921
BLAST score	213
E value	6.0e-17
Match length	116
% identity	46
NCBI Description	(AF118222) F3H7.4 gene product [Arabidopsis thaliana] >gi_4539434_emb_CAB40022.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	176904
Seq. ID	jC-atXP45C171K21T7084a1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19
Match length	70
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176905
Seq. ID	jC-atXP45C171L22T7029a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21

Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176906
Seq. ID	jC-atXP45C171L8T7092a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	47
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176907
Seq. ID	jC-atXP45C171M19T7069a1
Method	BLASTN
NCBI GI	g1523795
BLAST score	64
E value	2.0e-27
Match length	172
% identity	84
NCBI Description	A.thaliana mRNA for cytochrome P450

Seq. No.	176908
Seq. ID	jC-atXP45C171N11T7085a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	3.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176909
Seq. ID	jC-atXP45C171N2T7077a1
Method	BLASTX
NCBI GI	g4079632
BLAST score	309
E value	3.0e-28
Match length	81
% identity	80
NCBI Description	(AJ131722) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176910
Seq. ID	jC-atXP45C171O22T7040a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176911
Seq. ID	jC-atXP45C171O23T7048a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176912
Seq. ID	jC-atXP45C171O2T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176913
Seq. ID	jC-atXP45C172A1T7027a1
Method	BLASTN
NCBI GI	g531832
BLAST score	37
E value	2.0e-11
Match length	37
% identity	100
NCBI Description	Cloning vector pSport2, complete sequence

Seq. No.	176914
Seq. ID	jC-atXP45C172A5T7043a1
Method	BLASTN
NCBI GI	g540252
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	176915
Seq. ID	jC-atXP45C172A7T7059a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	3.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176916
Seq. ID	jC-atXP45C172A9T7046a1
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	8.0e-15
Match length	43
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176917
Seq. ID	jC-atXP45C172B14T7086a1
Method	BLASTX
NCBI GI	g4079632
BLAST score	294
E value	2.0e-26
Match length	104
% identity	65
NCBI Description	(AJ131722) hypothetical protein [Arabidopsis thaliana]

Seq. No.	176918
Seq. ID	jC-atXP45C172C16T7063a1
Method	BLASTN
NCBI GI	g540252
BLAST score	46
E value	7.0e-17
Match length	46
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	176919
Seq. ID	jC-atXP45C172C23T7d1
Method	BLASTX
NCBI GI	g4539657
BLAST score	127
E value	4.0e-18
Match length	62
% identity	63
NCBI Description	(AF061282) serine-type carboxypeptidase [Sorghum bicolor]

Seq. No.	176920
Seq. ID	jC-atXP45C172E12T7016a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	3.0e-16
Match length	49
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176921
Seq. ID	jC-atXP45C172E15T7024a1
Method	BLASTX
NCBI GI	g2146740
BLAST score	257
E value	4.0e-22
Match length	79
% identity	63
NCBI Description	inner mitochondrial membrane protein - Arabidopsis thaliana >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No.	176922
Seq. ID	jC-atXP46C172E20T7051d1
Method	BLASTX
NCBI GI	g1041706

BLAST score	56
E value	2.0e-14
Match length	124
% identity	44
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176923
Seq. ID	jC-atXP46C172F10T7083d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	925
E value	1.0e-100
Match length	176
% identity	96
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176924
Seq. ID	jC-atXP46C172F13T7091a1
Method	BLASTN
NCBI GI	g633027
BLAST score	62
E value	8.0e-26
Match length	150
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for protein phosphatase 2C

Seq. No.	176925
Seq. ID	jC-atXP46C172F13T7091d1
Method	BLASTX
NCBI GI	g1352681
BLAST score	329
E value	8.0e-36
Match length	160
% identity	59
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	176926
Seq. ID	jC-atXP46C172F15T7004a1
Method	BLASTN
NCBI GI	g3860243
BLAST score	75
E value	1.0e-33
Match length	352
% identity	67
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176927
Seq. ID	jC-atXP46C172F15T7004d1
Method	BLASTX
NCBI GI	g3860261
BLAST score	339

E value	2.0e-31
Match length	113
% identity	69
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	176928
Seq. ID	jC-atXP46C172F16T7012a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176929
Seq. ID	jC-atXP46C172H14T7076a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	3.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176930
Seq. ID	jC-atXP46C172H14T7076d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	75
E value	1.0e-19
Match length	184
% identity	40
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176931
Seq. ID	jC-atXP46C173B10T7009d1
Method	BLASTX
NCBI GI	g3980411
BLAST score	76
E value	1.2e+00
Match length	217
% identity	9
NCBI Description	(AC004561) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	176932
Seq. ID	jC-atXP46C173B7T7001a1
Method	BLASTN
NCBI GI	g3860243
BLAST score	132
E value	1.0e-67
Match length	384
% identity	63

NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176933
Seq. ID	jC-atXP46C173B7T7001d1
Method	BLASTX
NCBI GI	g3860261
BLAST score	286
E value	3.0e-25
Match length	113
% identity	59
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	176934
Seq. ID	jC-atXP46C173C3T7025d1
Method	BLASTX
NCBI GI	g1041706
BLAST score	78
E value	6.0e-10
Match length	98
% identity	47
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176935
Seq. ID	jC-atXP46C173D15T7065d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	401
E value	8.0e-70
Match length	195
% identity	72
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176936
Seq. ID	jC-atXP46C173D23T7073d1
Method	BLASTX
NCBI GI	g1041706
BLAST score	436
E value	7.0e-43
Match length	174
% identity	57
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176937
Seq. ID	jC-atXP46C173E14T7010a1
Method	BLASTN
NCBI GI	g3702732
BLAST score	277
E value	1.0e-154
Match length	601
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	176938
Seq. ID	jC-atXP46C173E7T7081a1
Method	BLASTN
NCBI GI	g3461834
BLAST score	91
E value	2.0e-43
Match length	198
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176939
Seq. ID	jC-atXP46C173F11T7026d1
Method	BLASTX
NCBI GI	g2146741
BLAST score	687
E value	2.0e-72
Match length	180
% identity	74
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	176940
Seq. ID	jC-atXP46C173G14T7058d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	684
E value	1.0e-76
Match length	169
% identity	80
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176941
Seq. ID	jC-atXP46C173G3T7050d1
Method	BLASTX
NCBI GI	g3860261
BLAST score	314
E value	1.0e-28
Match length	115
% identity	63
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	176942
Seq. ID	jC-atXP46C173H17T7090a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	5.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176943
Seq. ID	jC-atXP46C173H17T7090d1
Method	BLASTX
NCBI GI	g1041706
BLAST score	708
E value	1.0e-78
Match length	159
% identity	87
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176944
Seq. ID	jC-atXP46C173H21T7003d1
Method	BLASTX
NCBI GI	g3860261
BLAST score	293
E value	4.0e-26
Match length	115
% identity	60
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	176945
Seq. ID	jC-atXP46C173H9T7074d1
Method	BLASTX
NCBI GI	g1041706
BLAST score	322
E value	2.0e-36
Match length	118
% identity	69
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176946
Seq. ID	jC-atXP46C173J14T7085d1
Method	BLASTX
NCBI GI	g1041706
BLAST score	412
E value	5.0e-40
Match length	160
% identity	56
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	176947
Seq. ID	jC-atXP46C173J17T7093d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	60
E value	1.0e-38
Match length	181
% identity	57
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176948
Seq. ID	jC-atXP46C173J9T7077a1
Method	BLASTN
NCBI GI	g4159700

BLAST score	121
E value	4.0e-61
Match length	417
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	176949
Seq. ID	jC-atXP46C173J9T7077d1
Method	BLASTN
NCBI GI	g4159700
BLAST score	51
E value	2.0e-19
Match length	199
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	176950
Seq. ID	jC-atXP46C173K22T7006d1
Method	BLASTX
NCBI GI	g4309738
BLAST score	1098
E value	1.0e-120
Match length	211
% identity	100
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	176951
Seq. ID	jC-atXP46C173M10T7030a1
Method	BLASTX
NCBI GI	g2262167
BLAST score	343
E value	6.0e-32
Match length	150
% identity	51
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	176952
Seq. ID	jC-atXP46C174A1T7015a1
Method	BLASTX
NCBI GI	g3461837
BLAST score	343
E value	5.0e-32
Match length	136
% identity	59
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176953
Seq. ID	jC-atXP46C174A1T7015d1
Method	BLASTX
NCBI GI	g2828241
BLAST score	148
E value	5.0e-12

Match length	134
% identity	41
NCBI Description	(AJ000885) Expansin [Brassica napus]

Seq. No.	176954
Seq. ID	jC-atXP46C174B1T7023d1
Method	BLASTX
NCBI GI	g1486472
BLAST score	104
E value	2.0e-54
Match length	171
% identity	73
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	176955
Seq. ID	jC-atXP46C174B22T7047a1
Method	BLASTX
NCBI GI	g1255425
BLAST score	189
E value	2.0e-13
Match length	391
% identity	4
NCBI Description	(U53154) No definition line found [Caenorhabditis elegans]

Seq. No.	176956
Seq. ID	jC-atXP46C174B22T7047d1
Method	BLASTX
NCBI GI	g3874243
BLAST score	91
E value	1.2e-02
Match length	155
% identity	13
NCBI Description	(Z70204) similar to PHD-finger.; cDNA EST EMBL:T00556 comes from this gene; cDNA EST yk344f7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	176957
Seq. ID	jC-atXP46C174C14T7063d1
Method	BLASTX
NCBI GI	g585349
BLAST score	91
E value	1.0e-18
Match length	93
% identity	53
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 1 (CK II) >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >gi_391603_dbj_BAA01090_ (D10246) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	176958
Seq. ID	jC-atXP46C174D9T7079d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	813
E value	5.0e-87

Match length	157
% identity	94
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	176959
Seq. ID	jC-atXP46C174E1T7095d1
Method	BLASTN
NCBI GI	g4309747
BLAST score	92
E value	7.0e-44
Match length	509
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176960
Seq. ID	jC-atXP46C174G14T7056a1
Method	BLASTX
NCBI GI	g132102
BLAST score	361
E value	5.0e-34
Match length	161
% identity	51
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	176961
Seq. ID	jC-atXP47C176A10T7d2
Method	BLASTX
NCBI GI	g2119846
BLAST score	506
E value	1.0e-51
Match length	96
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	176962
Seq. ID	jC-atXP48C175F5T7s2
Method	BLASTX
NCBI GI	g3115852
BLAST score	158
E value	6.0e-11
Match length	39
% identity	85
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	176963
Seq. ID	jC-atXP48C177E14T7s2
Method	BLASTX
NCBI GI	g3043443
BLAST score	188
E value	1.0e-14
Match length	45
% identity	33
NCBI Description	(AJ005257) unnamed protein product [Homo sapiens]

Seq. No.	176964
Seq. ID	jC-atXP48C177E6T7d2
Method	BLASTX
NCBI GI	g3157927
BLAST score	187
E value	3.0e-14
Match length	55
% identity	64
NCBI Description	(AC002131) Contains similarity to GDP-dissociation inhibitor gb_L07918 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	176965
Seq. ID	jC-atXP48C178D6T7s2
Method	BLASTN
NCBI GI	g2924652
BLAST score	93
E value	4.0e-45
Match length	157
% identity	46
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	176966
Seq. ID	jC-atXP49C177J14T7042a1
Method	BLASTX
NCBI GI	g127045
BLAST score	550
E value	3.0e-56
Match length	127
% identity	84
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	176967
Seq. ID	jC-atXP49C177L9T7027a1
Method	BLASTN
NCBI GI	g4454587
BLAST score	91
E value	3.0e-43
Match length	301

% identity	72
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	176968
Seq. ID	jC-atXP49C177N17T7075a1
Method	BLASTX
NCBI GI	g4510373
BLAST score	292
E value	5.0e-26
Match length	108
% identity	54
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	176969
Seq. ID	jC-atXP49C177N23T7004a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176970
Seq. ID	jC-atXP49C177P13T7052a1
Method	BLASTX
NCBI GI	g4210330
BLAST score	683
E value	7.0e-72
Match length	137
% identity	94
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	176971
Seq. ID	jC-atXP49C177P9T7036a1
Method	BLASTN
NCBI GI	g4733952
BLAST score	66
E value	2.0e-28
Match length	287
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	176972
Seq. ID	jC-atXP49C178H19T7041a1
Method	BLASTN
NCBI GI	g4454587
BLAST score	64
E value	3.0e-27
Match length	96
% identity	92
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	176973
Seq. ID	jC-atXP49C178K4T7086a1
Method	BLASTX
NCBI GI	g2979555
BLAST score	561
E value	1.0e-57
Match length	123
% identity	85
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	176974
Seq. ID	jC-atXP49C178N4T7031a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	1.0e-23
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176975
Seq. ID	jC-atXP49C178P2T7021a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	1.0e-23
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176976
Seq. ID	jC-atXP49C178P8T7037a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176977
Seq. ID	jC-atXP49C179B19T7016a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	105
E value	1.0e-51
Match length	353
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	176978
Seq. ID	jC-atXP49C180A7T7085a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	47

E value	5.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176979
Seq. ID	jC-atXP49C180B2T7014a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	8.0e-24
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176980
Seq. ID	jC-atXP4C85D7T7005a1
Method	BLASTN
NCBI GI	g3482964
BLAST score	278
E value	1.0e-155
Match length	517
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	176981
Seq. ID	jC-atXP4C86B11T7014a1
Method	BLASTX
NCBI GI	g1350522
BLAST score	151
E value	2.0e-09
Match length	82
% identity	45
NCBI Description	(L47115) late embryogenesis abundant protein [Picea glauca]

Seq. No.	176982
Seq. ID	jC-atXP4C86D5T7016a1
Method	BLASTX
NCBI GI	g285741
BLAST score	201
E value	2.0e-15
Match length	137
% identity	40
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	176983
Seq. ID	jC-atXP4C86E4T7020a1
Method	BLASTX
NCBI GI	g2738248
BLAST score	319
E value	3.0e-29
Match length	92
% identity	74
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	176984
Seq. ID	jC-atXP4C86E8T7021a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	176985
Seq. ID	jC-atXP4C86F12T7026a1
Method	BLASTX
NCBI GI	g4206789
BLAST score	429
E value	4.0e-42
Match length	121
% identity	69
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	176986
Seq. ID	jC-atXP4C86F6T7023a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176987
Seq. ID	jC-atXP4C86F8T7024a1
Method	BLASTN
NCBI GI	g886425
BLAST score	301
E value	1.0e-168
Match length	622
% identity	98
NCBI Description	A.thaliana GPRP gene

Seq. No.	176988
Seq. ID	jC-atXP4C87E9T7031a1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176989
Seq. ID	jC-atXP4C87H10T7039a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50

E value	8.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176990
Seq. ID	jC-atXP4C87H6T7037a1
Method	BLASTN
NCBI GI	g3883125
BLAST score	220
E value	1.0e-120
Match length	248
% identity	96
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, complete cds

Seq. No.	176991
Seq. ID	jC-atXP4C88A20T7056a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	1.0e-20
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	176992
Seq. ID	jC-atXP4C88A8T7041a1
Method	BLASTX
NCBI GI	g2497733
BLAST score	607
E value	6.0e-63
Match length	118
% identity	98
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	176993
Seq. ID	jC-atXP4C88C3T7042a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	176994
Seq. ID	jC-atXP4C88D7T7043a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	1.0e-22
Match length	64
% identity	97

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	176995
Seq. ID	jC-atXP4C88E1T7046a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176996
Seq. ID	jC-atXP4C88E2T7047a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	8.0e-22
Match length	59
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176997
Seq. ID	jC-atXP4C88G19T7d1
Method	BLASTN
NCBI GI	g2351063
BLAST score	37
E value	8.0e-12
Match length	115
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]
Seq. No.	176998
Seq. ID	jC-atXP4C88H13T7071a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	176999
Seq. ID	jC-atXP4C88L11T7089a1
Method	BLASTX
NCBI GI	g4098647
BLAST score	360
E value	5.0e-34
Match length	120
% identity	62
NCBI Description	(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]
Seq. No.	177000
Seq. ID	jC-atXP4C88L20T7093a1

Method	BLASTN
NCBI GI	g598848
BLAST score	55
E value	9.0e-22
Match length	63
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	177001
Seq. ID	jC-atXP50C179F6T7067d1
Method	BLASTN
NCBI GI	g2739359
BLAST score	110
E value	8.0e-55
Match length	142
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177002
Seq. ID	jC-atXP50C179H12T7052d1
Method	BLASTX
NCBI GI	g2500376
BLAST score	201
E value	2.0e-15
Match length	120
% identity	28
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	177003
Seq. ID	jC-atXP50C179H24T7084d1
Method	BLASTX
NCBI GI	g3219355
BLAST score	375
E value	6.0e-36
Match length	130
% identity	62
NCBI Description	(AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]

Seq. No.	177004
Seq. ID	jC-atXP50C179H6T7028d1
Method	BLASTN
NCBI GI	g3738313
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177005
Seq. ID	jC-atXP50C179H9T7044d1
Method	BLASTX
NCBI GI	g2801536
BLAST score	222
E value	4.0e-35

Match length	154
% identity	53
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	177006
Seq. ID	jC-atXP50C179J7T7053d1
Method	BLASTN
NCBI GI	g4490291
BLAST score	61
E value	1.0e-25
Match length	354
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	177007
Seq. ID	jC-atXP50C179K16T7048d1
Method	BLASTX
NCBI GI	g3157947
BLAST score	138
E value	5.0e-11
Match length	105
% identity	25
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	177008
Seq. ID	jC-atXP50C179L20T7096d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	177009
Seq. ID	jC-atXP50C179L2T7080d1
Method	BLASTX
NCBI GI	g3130051
BLAST score	352
E value	3.0e-33
Match length	144
% identity	51
NCBI Description	(AL023518) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	177010
Seq. ID	jC-atXP50C180C16T7s1
Method	BLASTN
NCBI GI	g4455321
BLAST score	34
E value	5.0e-10

Match length	114
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	177011
Seq. ID	jC-atXP50C180D9T7s1
Method	BLASTN
NCBI GI	g533708
BLAST score	69
E value	8.0e-31
Match length	125
% identity	89
NCBI Description	Arabidopsis thaliana Columbia homeotic APETALA2 protein (APETALA2) mRNA, complete cds

Seq. No.	177012
Seq. ID	jC-atXP50C180E15T7057d1
Method	BLASTN
NCBI GI	g3869069
BLAST score	198
E value	1.0e-107
Match length	308
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	177013
Seq. ID	jC-atXP50C180E9T7049d1
Method	BLASTX
NCBI GI	g2499811
BLAST score	479
E value	4.0e-48
Match length	120
% identity	76
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	177014
Seq. ID	jC-atXP50C180F1T7065d1
Method	BLASTN
NCBI GI	g3869069
BLAST score	60
E value	6.0e-25
Match length	194
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	177015
Seq. ID	jC-atXP50C180F6T7081d1
Method	BLASTX
NCBI GI	g1402908
BLAST score	234
E value	7.0e-27
Match length	131

% identity	60
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	177016
Seq. ID	jC-atXP50C180G20T7058d1
Method	BLASTX
NCBI GI	g3219355
BLAST score	75
E value	6.0e-17
Match length	130
% identity	41
NCBI Description	(AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]

Seq. No.	177017
Seq. ID	jC-atXP50C180G7T7042d1
Method	BLASTN
NCBI GI	g4519188
BLAST score	126
E value	2.0e-64
Match length	246
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	177018
Seq. ID	jC-atXP50C180I18T7069d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	281
E value	2.0e-27
Match length	109
% identity	70
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	177019
Seq. ID	jC-atXP50C180J21T7s1
Method	BLASTX
NCBI GI	g3859599
BLAST score	301
E value	2.0e-27
Match length	71
% identity	75
NCBI Description	(AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]

Seq. No.	177020
Seq. ID	jC-atXP50C180K16T7s1
Method	BLASTX
NCBI GI	g168524
BLAST score	268
E value	1.0e-23
Match length	56

% identity	86
NCBI Description	(M31483) glyceraldehyde-3-phosphate dehydrogenase precursor [Zea mays]

Seq. No.	177021
Seq. ID	jC-atXP50C180K17T7062d1
Method	BLASTX
NCBI GI	g1076634
BLAST score	359
E value	4.0e-34
Match length	147
% identity	49
NCBI Description	protein-serine/threonine kinase NPK15 - common tobacco >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No.	177022
Seq. ID	jC-atXP50C180K9T7038d1
Method	BLASTX
NCBI GI	g1565225
BLAST score	262
E value	1.0e-22
Match length	104
% identity	54
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	177023
Seq. ID	jC-atXP50C181A12T7023d1
Method	BLASTX
NCBI GI	g4235430
BLAST score	255
E value	6.0e-22
Match length	110
% identity	52
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	177024
Seq. ID	jC-atXP51C181D21T7s1
Method	BLASTN
NCBI GI	g3985958
BLAST score	235
E value	1.0e-129
Match length	331
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	177025
Seq. ID	jC-atXP51C181G8T7s1
Method	BLASTN
NCBI GI	g3738313
BLAST score	253
E value	1.0e-140
Match length	368
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177026
Seq. ID	jC-atXP52C181K21T7s2
Method	BLASTN
NCBI GI	g3785968
BLAST score	54
E value	5.0e-22
Match length	104
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177027
Seq. ID	jC-atXP52C181M9T7s2
Method	BLASTX
NCBI GI	g2493738
BLAST score	182
E value	3.0e-13
Match length	65
% identity	54
NCBI Description	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) >gi_1377852 (U55059) ClpP [Yersinia enterocolitica]

Seq. No.	177028
Seq. ID	jC-atXP52C183K2T7s2
Method	BLASTN
NCBI GI	g2656028
BLAST score	335
E value	0.0e+00
Match length	343
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	177029
Seq. ID	jC-atXP53C183K20T7066a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177030
Seq. ID	jC-atXP53C183K22T7074a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177031
Seq. ID	jC-atXP53C183N22T7059d1

Method	BLASTX
NCBI GI	g4741962
BLAST score	299
E value	5.0e-27
Match length	92
% identity	43
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	177032
Seq. ID	jC-atXP53C183N7T7043a1
Method	BLASTN
NCBI GI	g4757409
BLAST score	117
E value	6.0e-59
Match length	330
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	177033
Seq. ID	jC-atXP53C183O15T7083d1
Method	BLASTX
NCBI GI	g16374
BLAST score	364
E value	1.0e-34
Match length	106
% identity	67
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	177034
Seq. ID	jC-atXP53C183O5T7067d1
Method	BLASTX
NCBI GI	g4115943
BLAST score	513
E value	4.0e-52
Match length	96
% identity	100
NCBI Description	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]

Seq. No.	177035
Seq. ID	jC-atXP53C184A18T7001a1
Method	BLASTN
NCBI GI	g3869073
BLAST score	199
E value	1.0e-108
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	177036
Seq. ID	jC-atXP53C184C23T7081a1
Method	BLASTN

NCBI GI	g531828
BLAST score	34
E value	1.0e-09
Match length	34
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177037
Seq. ID	jC-atXP53C184G13T7029a1
Method	BLASTN
NCBI GI	g4454447
BLAST score	150
E value	1.0e-78
Match length	327
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177038
Seq. ID	jC-atXP53C184G4T7021a1
Method	BLASTN
NCBI GI	g2373402
BLAST score	68
E value	9.0e-30
Match length	223
% identity	89
NCBI Description	Arabidopsis thaliana mRNA, partial cds

Seq. No.	177039
Seq. ID	jC-atXP53C184H16T7053a1
Method	BLASTN
NCBI GI	g2924733
BLAST score	67
E value	3.0e-29
Match length	278
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	177040
Seq. ID	jC-atXP53C184I7T7093d1
Method	BLASTX
NCBI GI	g1694976
BLAST score	252
E value	2.0e-21
Match length	69
% identity	80
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	177041
Seq. ID	jC-atXP53C184J1T7030a1
Method	BLASTN
NCBI GI	g4335711
BLAST score	58
E value	7.0e-24

Match length	123
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177042
Seq. ID	jC-atXP53C184K1T7054d1
Method	BLASTN
NCBI GI	g2264320
BLAST score	39
E value	1.0e-12
Match length	104
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	177043
Seq. ID	jC-atXP53C184L2T7070d1
Method	BLASTX
NCBI GI	g81615
BLAST score	166
E value	2.0e-11
Match length	129
% identity	41
NCBI Description	G-box-binding factor 1 - Arabidopsis thaliana >gi_16286_emb_CAA45356_ (X63894) G-box binding factor 1 [Arabidopsis thaliana]

Seq. No.	177044
Seq. ID	jC-atXP53C185A21T7060a1
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	7.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	177045
Seq. ID	jC-atXP53C185A23T7068d1
Method	BLASTN
NCBI GI	g16285
BLAST score	42
E value	1.0e-14
Match length	42
% identity	100
NCBI Description	A.thaliana mRNA GBF1 for G-box binding factor

Seq. No.	177046
Seq. ID	jC-atXP53C185A7T7044a1
Method	BLASTX
NCBI GI	g4539335
BLAST score	285
E value	2.0e-25
Match length	73
% identity	63
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	177047
Seq. ID	jC-atXP53C185B13T7092a1
Method	BLASTN
NCBI GI	g1871173
BLAST score	110
E value	7.0e-55
Match length	238
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	177048
Seq. ID	jC-atXP53C185C24T7023a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	48
E value	8.0e-18
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177049
Seq. ID	jC-atXP53C185C24T7023d1
Method	BLASTN
NCBI GI	g4454022
BLAST score	93
E value	1.0e-44
Match length	198
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	177050
Seq. ID	jC-atXP53C185D15T7047a1
Method	BLASTN
NCBI GI	g16335
BLAST score	127
E value	6.0e-65
Match length	361
% identity	85
NCBI Description	Arabidopsis thaliana mRNA for 3-hydroxy-3-methylglutaryl CoA reductase (EC 1.1.1.34)

Seq. No.	177051
Seq. ID	jC-atXP53C185F10T7079d1
Method	BLASTX
NCBI GI	g3482924
BLAST score	700
E value	5.0e-74
Match length	138
% identity	100
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	177052

Seq. ID	jC-atXP53C185F11T7087d1
Method	BLASTN
NCBI GI	g16181
BLAST score	43
E value	7.0e-15
Match length	187
% identity	88
NCBI Description	A.thaliana gene for tonoplast intrinsic protein alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis thaliana tonoplast intrinsic protein (alpha-TIP) gene, complete cds

Seq. No.	177053
Seq. ID	jC-atXP54C184O13T7049a1
Method	BLASTN
NCBI GI	g2264320
BLAST score	84
E value	3.0e-39
Match length	124
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	177054
Seq. ID	jC-atXP54C184P11T7089d1
Method	BLASTN
NCBI GI	g3869075
BLAST score	132
E value	5.0e-68
Match length	380
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	177055
Seq. ID	jC-atXP54C185I9T7091a1
Method	BLASTX
NCBI GI	g2529665
BLAST score	434
E value	7.0e-43
Match length	108
% identity	80
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	177056
Seq. ID	jC-atXP54C185I9T7091d1
Method	BLASTX
NCBI GI	g2529665
BLAST score	176
E value	1.0e-12
Match length	117
% identity	36
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No. 177057

Seq. ID	jC-atXP54C185K4T7020a1
Method	BLASTN
NCBI GI	g2791999
BLAST score	36
E value	1.0e-10
Match length	111
% identity	86
NCBI Description	Arabidopsis thaliana mRNA for ribosomal protein L4

Seq. No.	177058
Seq. ID	jC-atXP54C185M3T7036d1
Method	BLASTN
NCBI GI	g3241920
BLAST score	60
E value	5.0e-25
Match length	119
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	177059
Seq. ID	jC-atXP54C185N21T7092a1
Method	BLASTX
NCBI GI	g2511576
BLAST score	196
E value	6.0e-15
Match length	61
% identity	61
NCBI Description	(Y13177) multicatalytic endopeptidase [Arabidopsis thaliana]

Seq. No.	177060
Seq. ID	jC-atXP54C185N2T7060a1
Method	BLASTN
NCBI GI	g2804257
BLAST score	52
E value	3.0e-20
Match length	76
% identity	92
NCBI Description	Arabidopsis thaliana DNA for phosphoglycerate dehydrogenase, complete cds

Seq. No.	177061
Seq. ID	jC-atXP54C185N3T7068d1
Method	BLASTX
NCBI GI	g4580455
BLAST score	525
E value	9.0e-57
Match length	145
% identity	85
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	177062
Seq. ID	jC-atXP54C185N5T7076a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34

E value	2.0e-09
Match length	38
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177063
Seq. ID	jC-atXP54C186A11T7050d1
Method	BLASTX
NCBI GI	g1542941
BLAST score	60
E value	2.0e-09
Match length	105
% identity	44
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	177064
Seq. ID	jC-atXP54C186A19T7058a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177065
Seq. ID	jC-atXP54C186A22T7074a1
Method	BLASTN
NCBI GI	g2564046
BLAST score	43
E value	7.0e-15
Match length	67
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	177066
Seq. ID	jC-atXP54C186A24T7082d1
Method	BLASTN
NCBI GI	g2088638
BLAST score	179
E value	5.0e-96
Match length	371
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177067
Seq. ID	jC-atXP54C186A4T7026a1
Method	BLASTX
NCBI GI	g131011
BLAST score	125
E value	1.0e-06
Match length	159
% identity	5
NCBI Description	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-D)

Seq. No.	177068
Seq. ID	jC-atXP54C186B23T7035a1
Method	BLASTN
NCBI GI	g3985949
BLAST score	79
E value	2.0e-36
Match length	276
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	177069
Seq. ID	jC-atXP54C186C10T7051a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	1.0e-22
Match length	63
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177070
Seq. ID	jC-atXP54C186C3T7043a1
Method	BLASTN
NCBI GI	g2264305
BLAST score	129
E value	4.0e-66
Match length	426
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	177071
Seq. ID	jC-atXP54C186C3T7043d1
Method	BLASTX
NCBI GI	g4539292
BLAST score	472
E value	2.0e-47
Match length	128
% identity	75
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	177072
Seq. ID	jC-atXP54C186D1T7075d1
Method	BLASTX
NCBI GI	g4580455
BLAST score	329
E value	1.0e-30
Match length	150
% identity	56
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	177073
Seq. ID	jC-atXP54C186D23T7077a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	39
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177074
Seq. ID	jC-atXP54C186E12T7014a1
Method	BLASTN
NCBI GI	g642161
BLAST score	144
E value	3.0e-75
Match length	243
% identity	90
NCBI Description	A.thaliana gene for chloroplast ribosomal protein S13

Seq. No.	177075
Seq. ID	jC-atXP54C186E14T7022d1
Method	BLASTN
NCBI GI	g2865461
BLAST score	67
E value	3.0e-29
Match length	123
% identity	89
NCBI Description	Arabidopsis thaliana lactate dehydrogenase (LDH1) gene, complete cds

Seq. No.	177076
Seq. ID	jC-atXP54C186E15T7030a1
Method	BLASTN
NCBI GI	g4455348
BLAST score	205
E value	1.0e-111
Match length	292
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	177077
Seq. ID	jC-atXP54C186E2T7085a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177078
Seq. ID	jC-atXP54C186F21T7031d1
Method	BLASTN
NCBI GI	g4678291
BLAST score	60
E value	3.0e-25
Match length	115

% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	177079
Seq. ID	jC-atXP54C186H11T7008d1
Method	BLASTX
NCBI GI	g629602
BLAST score	141
E value	3.0e-28
Match length	107
% identity	64
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	177080
Seq. ID	jC-atXP54C187A14T7061a1
Method	BLASTN
NCBI GI	g1145694
BLAST score	100
E value	6.0e-49
Match length	124
% identity	97
NCBI Description	Arabidopsis thaliana actin (ACT3) gene, complete cds

Seq. No.	177081
Seq. ID	jC-atXP54C188I22T7062a1
Method	BLASTX
NCBI GI	g746540
BLAST score	145
E value	6.0e-09
Match length	72
% identity	40
NCBI Description	(U23521) No definition line found [Caenorhabditis elegans]

Seq. No.	177082
Seq. ID	jC-atXP54C188I23T7070a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177083
Seq. ID	jC-atXP54C188I8T7046d1
Method	BLASTN
NCBI GI	g2618677
BLAST score	111
E value	2.0e-55
Match length	263
% identity	90
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177084
Seq. ID	jC-atXP55C186J11T7s2
Method	BLASTN
NCBI GI	g2924734
BLAST score	134
E value	4.0e-69
Match length	341
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	177085
Seq. ID	jC-atXP55C186J13T7d2
Method	BLASTX
NCBI GI	g3273198
BLAST score	289
E value	8.0e-26
Match length	58
% identity	100
NCBI Description	(AB010916) responce reactor2 [Arabidopsis thaliana] >gi_4678318_emb_CAB41129.1_ (AL049658) responce reactor2 [Arabidopsis thaliana]

Seq. No.	177086
Seq. ID	jC-atXP55C187O3T7s2
Method	BLASTN
NCBI GI	g166695
BLAST score	96
E value	8.0e-47
Match length	188
% identity	88
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	177087
Seq. ID	jC-atXP57C190G14T7d1
Method	BLASTX
NCBI GI	g3915023
BLAST score	209
E value	3.0e-17
Match length	57
% identity	68
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	177088
Seq. ID	jC-atXP57C190G1T7005a1
Method	BLASTN
NCBI GI	g2673901
BLAST score	100
E value	8.0e-49
Match length	323
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177089
Seq. ID	jC-atXP57C190H21T7010a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	55
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177090
Seq. ID	jC-atXP57C190H3T7007a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	72
E value	3.0e-32
Match length	72
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	177091
Seq. ID	jC-atXP57C190I17T7015a1
Method	BLASTX
NCBI GI	g4587685
BLAST score	49
E value	3.0e-27
Match length	98
% identity	71
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	177092
Seq. ID	jC-atXP57C190I5T7011a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	41
E value	5.0e-14
Match length	41
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177093
Seq. ID	jC-atXP57C190J12T7018a1
Method	BLASTN
NCBI GI	g1877523
BLAST score	65
E value	5.0e-28
Match length	93
% identity	92
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	177094
Seq. ID	jC-atXP57C190O11T7042a1
Method	BLASTN

NCBI GI	g2290120
BLAST score	47
E value	2.0e-17
Match length	47
% identity	100
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177095
Seq. ID	jC-atXP57C190O14T7043a1
Method	BLASTN
NCBI GI	g4803835
BLAST score	154
E value	5.0e-81
Match length	287
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No.	177096
Seq. ID	jC-atXP57C190O9T7041a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	7.0e-21
Match length	65
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177097
Seq. ID	jC-atXP57C190P9T7045a1
Method	BLASTN
NCBI GI	g4163996
BLAST score	201
E value	1.0e-109
Match length	285
% identity	93
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	177098
Seq. ID	jC-atXP57C191F16T7058a1
Method	BLASTX
NCBI GI	g2072626
BLAST score	346
E value	2.0e-32
Match length	81
% identity	88
NCBI Description	(Y12904) hypothetical protein [Arabidopsis thaliana] >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor II homolog [Arabidopsis thaliana]

Seq. No.	177099
Seq. ID	jC-atXP57C191I13T7068a1
Method	BLASTN
NCBI GI	g2266411

BLAST score	65
E value	4.0e-28
Match length	219
% identity	88
NCBI Description	Arabidopsis thaliana GST11 gene

Seq. No.	177100
Seq. ID	jC-atXP57C191J2T7072a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	41
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177101
Seq. ID	jC-atXP57C191K16T7075a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177102
Seq. ID	jC-atXP57C191K19T7076a1
Method	BLASTN
NCBI GI	g4519791
BLAST score	348
E value	0.0e+00
Match length	416
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for Asp1, complete cds

Seq. No.	177103
Seq. ID	jC-atXP57C192A2T7049a1
Method	BLASTN
NCBI GI	g2656031
BLAST score	217
E value	1.0e-118
Match length	337
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	177104
Seq. ID	jC-atXP57C192A9T7d1
Method	BLASTN
NCBI GI	g2815519
BLAST score	196
E value	1.0e-106
Match length	208
% identity	99
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	177105
Seq. ID	jC-atXP57C192C12T7083a1
Method	BLASTN
NCBI GI	g4337186
BLAST score	59
E value	2.0e-24
Match length	136
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177106
Seq. ID	jC-atXP57C192K23T7090a1
Method	BLASTX
NCBI GI	g3785999
BLAST score	451
E value	8.0e-45
Match length	83
% identity	100
NCBI Description	(AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	177107
Seq. ID	jC-atXP58C191N4T7s3
Method	BLASTN
NCBI GI	g2924651
BLAST score	144
E value	2.0e-75
Match length	172
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	177108
Seq. ID	jC-atXP58C191O13T7s3
Method	BLASTN
NCBI GI	g3046847
BLAST score	252
E value	1.0e-139
Match length	328
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	177109
Seq. ID	jC-atXP58C193D6T7s3
Method	BLASTX
NCBI GI	g2464865
BLAST score	175
E value	6.0e-13
Match length	32
% identity	100
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	177110
Seq. ID	jC-atXP58C194C22T7s3

Method	BLASTX
NCBI GI	g4079632
BLAST score	344
E value	3.0e-32
Match length	70
% identity	99
NCBI Description	(AJ131722) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177111
Seq. ID	jC-atXP58C194E3T7s3
Method	BLASTN
NCBI GI	g3510347
BLAST score	160
E value	7.0e-85
Match length	280
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	177112
Seq. ID	jC-atXP59C192J2T7d1
Method	BLASTX
NCBI GI	g4455364
BLAST score	239
E value	5.0e-20
Match length	134
% identity	37
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	177113
Seq. ID	jC-atXP59C192J2T7s1
Method	BLASTX
NCBI GI	g4191796
BLAST score	315
E value	6.0e-29
Match length	97
% identity	56
NCBI Description	(AC005917) putative senescence-associated protein 5 [Arabidopsis thaliana]

Seq. No.	177114
Seq. ID	jC-atXP59C193J13T7s1
Method	BLASTN
NCBI GI	g3449323
BLAST score	45
E value	1.0e-16
Match length	93
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	177115
Seq. ID	jC-atXP59C193K23T7s1
Method	BLASTN
NCBI GI	g4567237
BLAST score	118

E value	1.0e-59
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	177116
Seq. ID	jC-atXP59C196C2T7s1
Method	BLASTX
NCBI GI	g4314378
BLAST score	398
E value	2.0e-39
Match length	71
% identity	97
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	177117
Seq. ID	jC-atXP5C88M6T7002a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	8.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177118
Seq. ID	jC-atXP5C88N18T7007a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177119
Seq. ID	jC-atXP5C88N1T7005a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	9.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177120
Seq. ID	jC-atXP5C88N23T7008a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177121

Seq. ID	jC-atXP5C88N6T7006a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177122
Seq. ID	jC-atXP5C88O4T7010a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	50
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177123
Seq. ID	jC-atXP5C88P8T7014a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177124
Seq. ID	jC-atXP5C89B5T7020a1
Method	BLASTN
NCBI GI	g4220640
BLAST score	138
E value	3.0e-71
Match length	467
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	177125
Seq. ID	jC-atXP5C89B9T7021a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177126
Seq. ID	jC-atXP5C89D12T7026a1
Method	BLASTX
NCBI GI	g3941543
BLAST score	945
E value	1.0e-102
Match length	187

% identity	99
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	177127
Seq. ID	jC-atXP5C89E5T7030a1
Method	BLASTX
NCBI GI	g4584521
BLAST score	430
E value	4.0e-42
Match length	157
% identity	61
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	177128
Seq. ID	jC-atXP5C89F7T7033a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	3.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177129
Seq. ID	jC-atXP5C89G21T7035a1
Method	BLASTN
NCBI GI	g4510360
BLAST score	534
E value	0.0e+00
Match length	671
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	177130
Seq. ID	jC-atXP5C89H13T7036a1
Method	BLASTX
NCBI GI	g1362019
BLAST score	616
E value	6.0e-64
Match length	158
% identity	78
NCBI Description	zinc finger protein 6 - Arabidopsis thaliana >gi_790683 (L39649) zinc finger protein [Arabidopsis thaliana]

Seq. No.	177131
Seq. ID	jC-atXP5C89J14T7044a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177132
Seq. ID	jC-atXP5C89J8T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	8.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177133
Seq. ID	jC-atXP5C89M16T7063a1
Method	BLASTX
NCBI GI	g2462840
BLAST score	330
E value	2.0e-30
Match length	105
% identity	65
NCBI Description	(AF000657) cytochrome C [Arabidopsis thaliana]

Seq. No.	177134
Seq. ID	jC-atXP5C89N21T7d1
Method	BLASTX
NCBI GI	g2459446
BLAST score	202
E value	2.0e-16
Match length	50
% identity	80
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	177135
Seq. ID	jC-atXP5C90D3T7d1
Method	BLASTX
NCBI GI	g4585990
BLAST score	152
E value	2.0e-10
Match length	66
% identity	9
NCBI Description	(AC005287) Very similar to disease resistance proteins [Arabidopsis thaliana]

Seq. No.	177136
Seq. ID	jC-atXP5C90E24T7096a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177137
Seq. ID	jC-atXP60C196K17T7018a1
Method	BLASTX
NCBI GI	g2144912
BLAST score	136

E value	7.0e-08
Match length	151
% identity	8
NCBI Description	salivary proline-rich glycoprotein precursor PRB4 (large allele) - human

Seq. No.	177138
Seq. ID	jC-atXP60C196N5T7034a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	7.0e-15
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177139
Seq. ID	jC-atXP60C197D21T7009a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177140
Seq. ID	jC-atXP60C197G2T7041a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177141
Seq. ID	jC-atXP60C197I10T7089a1
Method	BLASTX
NCBI GI	g1402878
BLAST score	418
E value	5.0e-41
Match length	101
% identity	78
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	177142
Seq. ID	jC-atXP60C197K1T7074a1
Method	BLASTN
NCBI GI	g4249393
BLAST score	33
E value	8.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177143
Seq. ID	jC-atXP60C197K1T7074d1
Method	BLASTN
NCBI GI	g4249393
BLAST score	133
E value	2.0e-68
Match length	406
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177144
Seq. ID	jC-atXP60C197L1T7082a1
Method	BLASTX
NCBI GI	g3334116
BLAST score	144
E value	2.0e-20
Match length	93
% identity	61
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_1297066_emb_CAA65119_ (X95863) adenine nucleotide translocator [Triticum turgidum]

Seq. No.	177145
Seq. ID	jC-atXP60C197M21T7027a1
Method	BLASTX
NCBI GI	g3184292
BLAST score	319
E value	2.0e-29
Match length	52
% identity	100
NCBI Description	(AC004136) putative nucleic acid binding protein, 5' partial [Arabidopsis thaliana]

Seq. No.	177146
Seq. ID	jC-atXP60C197M9T7011a1
Method	BLASTN
NCBI GI	g4102702
BLAST score	90
E value	6.0e-43
Match length	310
% identity	83
NCBI Description	Arabidopsis thaliana ribulose-5-phosphate-3-epimerase mRNA, complete cds

Seq. No.	177147
Seq. ID	jC-atXP60C197M9T7011d1
Method	BLASTN
NCBI GI	g4102702
BLAST score	77
E value	3.0e-35
Match length	252
% identity	83
NCBI Description	Arabidopsis thaliana ribulose-5-phosphate-3-epimerase mRNA, complete cds

Seq. No.	177148
Seq. ID	jC-atXP60C198A2T7051a1
Method	BLASTN
NCBI GI	g598848
BLAST score	52
E value	4.0e-20
Match length	60
% identity	97
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	177149
Seq. ID	jC-atXP60C198A2T7051d1
Method	BLASTX
NCBI GI	g4220481
BLAST score	297
E value	8.0e-27
Match length	116
% identity	47
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	177150
Seq. ID	jC-atXP60C198E23T7085d1
Method	BLASTX
NCBI GI	g1076287
BLAST score	291
E value	4.0e-26
Match length	102
% identity	61
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	177151
Seq. ID	jC-atXP60C198F21T7038a1
Method	BLASTN
NCBI GI	g4006815
BLAST score	230
E value	1.0e-126
Match length	319
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177152
Seq. ID	jC-atXP60C198F7T7022a1
Method	BLASTX
NCBI GI	g3164140
BLAST score	225
E value	2.0e-18
Match length	55
% identity	73
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	177153
Seq. ID	jC-atXP60C198F8T7030d1
Method	BLASTX

NCBI GI	g1914683
BLAST score	103
E value	5.0e-04
Match length	130
% identity	32
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	177154
Seq. ID	jC-atXP60C198H11T7078d1
Method	BLASTX
NCBI GI	g4220528
BLAST score	252
E value	2.0e-21
Match length	120
% identity	54
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	177155
Seq. ID	jC-atXP60C198J20T7015d1
Method	BLASTX
NCBI GI	g132102
BLAST score	198
E value	4.0e-15
Match length	143
% identity	30
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	177156
Seq. ID	jC-atXP60C198J24T7023d1
Method	BLASTN
NCBI GI	g4220640
BLAST score	269
E value	1.0e-149
Match length	397
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	177157
Seq. ID	jC-atXP60C198M20T7079a1
Method	BLASTX
NCBI GI	g113028
BLAST score	265
E value	3.0e-44
Match length	136
% identity	74
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68214_pir__WZECIC isocitrate lyase (EC 4.1.3.1) - Escherichia coli >gi_40888_emb_CAA30974_ (X12431) isocitrate lyase [Escherichia coli] >gi_396350 (U00006) isocitrate lyase [Escherichia coli] >gi_1790445 (AE000474)

isocitrate lyase [Escherichia coli]

Seq. No.	177158
Seq. ID	jC-atXP60C198N17T7016a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	4.0e-20
Match length	63
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177159
Seq. ID	jC-atXP60C198N17T7016d1
Method	BLASTN
NCBI GI	g3702739
BLAST score	114
E value	3.0e-57
Match length	369
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	177160
Seq. ID	jC-atXP60C198O12T7040a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	2.0e-23
Match length	61
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177161
Seq. ID	jC-atXP60C198O12T7040d1
Method	BLASTX
NCBI GI	g972921
BLAST score	368
E value	4.0e-35
Match length	96
% identity	79
NCBI Description	(U18411) IAA9 [Arabidopsis thaliana] >gi_2832666_emb_CAA16692_ (AL021684) auxin-induced protein IAA9 [Arabidopsis thaliana]

Seq. No.	177162
Seq. ID	jC-atXP60C198O15T7048a1
Method	BLASTN
NCBI GI	g540252
BLAST score	52
E value	4.0e-20
Match length	60
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	177163
Seq. ID	jC-atXP60C199D3T7091d1
Method	BLASTN
NCBI GI	g3449331
BLAST score	120
E value	9.0e-61
Match length	261
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	177164
Seq. ID	jC-atXP60C199F23T7088a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177165
Seq. ID	jC-atXP60C199G24T7096d1
Method	BLASTN
NCBI GI	g2262097
BLAST score	184
E value	6.0e-99
Match length	319
% identity	91
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	177166
Seq. ID	jC-atXP60C199I11T7028a1
Method	BLASTX
NCBI GI	g3980238
BLAST score	134
E value	2.0e-09
Match length	70
% identity	53
NCBI Description	(Z21677) ribosomal protein L18 [Thermotoga maritima]

Seq. No.	177167
Seq. ID	jC-atXP60C199I15T7036a1
Method	BLASTN
NCBI GI	g3985958
BLAST score	272
E value	1.0e-151
Match length	427
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	177168
Seq. ID	jC-atXP60C199I15T7036d1
Method	BLASTN
NCBI GI	g3985958

BLAST score	98
E value	1.0e-47
Match length	291
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	177169
Seq. ID	jC-atXP60C199J23T7060d1
Method	BLASTX
NCBI GI	g1621539
BLAST score	224
E value	2.0e-33
Match length	134
% identity	65
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	177170
Seq. ID	jC-atXP60C199J4T7044d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	177171
Seq. ID	jC-atXP60C199K20T7076a1
Method	BLASTX
NCBI GI	g4538963
BLAST score	382
E value	1.0e-36
Match length	105
% identity	73
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	177172
Seq. ID	jC-atXP60C199K20T7076d1
Method	BLASTN
NCBI GI	g4538949
BLAST score	60
E value	7.0e-25
Match length	104
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	177173
Seq. ID	jC-atXP60C199L3T7092a1
Method	BLASTX
NCBI GI	g3193309
BLAST score	171
E value	5.0e-12

Match length	65
% identity	52
NCBI Description	(AF069300) No definition line found [Arabidopsis thaliana]

Seq. No.	177174
Seq. ID	jC-atXP60C199L5T7005d1
Method	BLASTN
NCBI GI	g4567237
BLAST score	52
E value	3.0e-20
Match length	96
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	177175
Seq. ID	jC-atXP60C200A10T7037d1
Method	BLASTN
NCBI GI	g4589414
BLAST score	306
E value	1.0e-172
Match length	453
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	177176
Seq. ID	jC-atXP60C200A22T7045a1
Method	BLASTN
NCBI GI	g2244901
BLAST score	414
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177177
Seq. ID	jC-atXP60C200A4T7013a1
Method	BLASTN
NCBI GI	g531828
BLAST score	47
E value	3.0e-17
Match length	47
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177178
Seq. ID	jC-atXP60C200A4T7013d1
Method	BLASTX
NCBI GI	g4678264
BLAST score	75
E value	8.6e-01
Match length	145
% identity	64
NCBI Description	(AL049657) putative protein [Arabidopsis thaliana]

Seq. No.	177179
Seq. ID	jC-atXP60C200A5T7021d1
Method	BLASTX
NCBI GI	g3212879
BLAST score	390
E value	1.0e-37
Match length	81
% identity	89
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	177180
Seq. ID	jC-atXP60C200C5T7061d1
Method	BLASTN
NCBI GI	g2288979
BLAST score	74
E value	3.0e-33
Match length	298
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177181
Seq. ID	jC-atXP61C199M7T7d1
Method	BLASTX
NCBI GI	g1176658
BLAST score	327
E value	3.0e-30
Match length	128
% identity	50
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	177182
Seq. ID	jC-atXP61C200F4T7d1
Method	BLASTN
NCBI GI	g2828278
BLAST score	112
E value	1.0e-56
Match length	140
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	177183
Seq. ID	jC-atXP61C201D3T7s1
Method	BLASTX
NCBI GI	g3043882
BLAST score	170
E value	4.0e-12
Match length	82
% identity	34
NCBI Description	(U95842) transmembrane protein Tmp7 [Lactococcus lactis]

Seq. No.	177184
Seq. ID	jC-atXP61C201E2T7s1

Method	BLASTX
NCBI GI	g544045
BLAST score	191
E value	2.0e-14
Match length	127
% identity	29
NCBI Description	CEPHAMYCIN EXPORT PROTEIN CMCT >gi_581413_emb_CAA78375_ (Z13973) cmcT [Streptomyces lactamdurans]

Seq. No.	177185
Seq. ID	jC-atXP61C201E9T7d1
Method	BLASTX
NCBI GI	g2832616
BLAST score	246
E value	4.0e-21
Match length	111
% identity	59
NCBI Description	(AL021711) heat shock transcription factor - like protein [Arabidopsis thaliana]

Seq. No.	177186
Seq. ID	jC-atXP61C201F2T7s1
Method	BLASTN
NCBI GI	g2828180
BLAST score	94
E value	9.0e-46
Match length	155
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	177187
Seq. ID	jC-atXP61C201F9T7s1
Method	BLASTX
NCBI GI	g4544427
BLAST score	223
E value	2.0e-18
Match length	43
% identity	91
NCBI Description	(AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	177188
Seq. ID	jC-atXP62C201L19T7d2
Method	BLASTX
NCBI GI	g3249098
BLAST score	242
E value	2.0e-20
Match length	115
% identity	51
NCBI Description	(AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481 and gb_N64971 come from this gene. [Arabidopsis thaliana]

Seq. No.	177189
Seq. ID	jC-atXP62C201N16T7d2
Method	BLASTN
NCBI GI	g16131

BLAST score	284
E value	1.0e-158
Match length	320
% identity	97
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment

Seq. No.	177190
Seq. ID	jC-atXP62C201N18T7020a1
Method	BLASTN
NCBI GI	g862639
BLAST score	46
E value	7.0e-17
Match length	61
% identity	95
NCBI Description	Arabidopsis thaliana MADS-box protein AGL11 (AGL11) mRNA, complete cds

Seq. No.	177191
Seq. ID	jC-atXP62C201P18T7015a1
Method	BLASTX
NCBI GI	g548655
BLAST score	191
E value	2.0e-14
Match length	72
% identity	58
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	177192
Seq. ID	jC-atXP62C202E9T7001a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	43
E value	7.0e-15
Match length	67
% identity	91
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177193
Seq. ID	jC-atXP62C202J1T7081a1
Method	BLASTX
NCBI GI	g3096947
BLAST score	376
E value	5.0e-36
Match length	116
% identity	68
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	177194
Seq. ID	jC-atXP62C202L17T7d2
Method	BLASTX
NCBI GI	g4567199

BLAST score	98
E value	2.0e-97
Match length	185
% identity	55
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	177195
Seq. ID	jC-atXP62C202P19T7013a1
Method	BLASTN
NCBI GI	g4678219
BLAST score	56
E value	1.0e-22
Match length	262
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	177196
Seq. ID	jC-atXP62C202P19T7d2
Method	BLASTX
NCBI GI	g4678222
BLAST score	638
E value	1.0e-66
Match length	163
% identity	80
NCBI Description	(AC007135) unknown protein [Arabidopsis thaliana]

Seq. No.	177197
Seq. ID	jC-atXP62C203C3T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	45
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177198
Seq. ID	jC-atXP62C203D10T7d2
Method	BLASTX
NCBI GI	g3421087
BLAST score	976
E value	1.0e-106
Match length	204
% identity	96
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	177199
Seq. ID	jC-atXP62C203D3T7062a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	49
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177200
Seq. ID	jC-atXP62C203F16T7080a1
Method	BLASTN
NCBI GI	g4585891
BLAST score	119
E value	3.0e-60
Match length	179
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	177201
Seq. ID	jC-atXP62C204A16T7047a1
Method	BLASTN
NCBI GI	g4585891
BLAST score	179
E value	6.0e-96
Match length	360
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	177202
Seq. ID	jC-atXP62C204C16T7024a1
Method	BLASTX
NCBI GI	g4206767
BLAST score	99
E value	2.0e-23
Match length	54
% identity	94
NCBI Description	(AF104330) glycine-rich protein 3 short isoform [Arabidopsis thaliana]

Seq. No.	177203
Seq. ID	jC-atXP62C204E19T7056a1
Method	BLASTN
NCBI GI	g4006933
BLAST score	51
E value	1.0e-19
Match length	314
% identity	84
NCBI Description	Arabidopsis thaliana mRNA for glutathione transferase

Seq. No.	177204
Seq. ID	jC-atXP63C203G9T7s2
Method	BLASTN
NCBI GI	g4733952
BLAST score	91
E value	5.0e-44
Match length	151
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	177205
Seq. ID	jC-atXP63C203H11T7s2

Method	BLASTN
NCBI GI	g4741939
BLAST score	133
E value	8.0e-69
Match length	141
% identity	99
NCBI Description	Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds

Seq. No.	177206
Seq. ID	jC-atXP63C203I10T7d2
Method	BLASTX
NCBI GI	g4415924
BLAST score	233
E value	2.0e-19
Match length	43
% identity	100
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	177207
Seq. ID	jC-atXP63C203P1T7s2
Method	BLASTX
NCBI GI	g2460200
BLAST score	199
E value	2.0e-15
Match length	63
% identity	57
NCBI Description	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No.	177208
Seq. ID	jC-atXP63C204G16T7s2
Method	BLASTN
NCBI GI	g3080352
BLAST score	446
E value	0.0e+00
Match length	475
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	177209
Seq. ID	jC-atXP63C204G2T7s2
Method	BLASTN
NCBI GI	g4757410
BLAST score	111
E value	9.0e-56
Match length	196
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	177210
Seq. ID	jC-atXP63C204K18T7s2
Method	BLASTN
NCBI GI	g4468103

BLAST score	118
E value	8.0e-60
Match length	276
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	177211
Seq. ID	jC-atXP63C204K1T7s2
Method	BLASTN
NCBI GI	g4539448
BLAST score	85
E value	2.0e-40
Match length	153
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	177212
Seq. ID	jC-atXP63C204L11T7s2
Method	BLASTX
NCBI GI	g1613900
BLAST score	157
E value	2.0e-10
Match length	78
% identity	41
NCBI Description	(U73168) partial CDS, human putative tumor suppressor (U23946) [Homo sapiens]

Seq. No.	177213
Seq. ID	jC-atXP63C204M13T7d2
Method	BLASTN
NCBI GI	g4159709
BLAST score	306
E value	1.0e-172
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	177214
Seq. ID	jC-atXP63C205E8T7d2
Method	BLASTX
NCBI GI	g2832625
BLAST score	734
E value	4.0e-78
Match length	156
% identity	85
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	177215
Seq. ID	jC-atXP63C205E8T7s2
Method	BLASTX
NCBI GI	g629669
BLAST score	218
E value	1.0e-17
Match length	90

% identity	43
NCBI Description	hypothetical protein - tomato

Seq. No.	177216
Seq. ID	jC-atXP63C205E9T7d2
Method	BLASTN
NCBI GI	g4262221
BLAST score	204
E value	1.0e-111
Match length	329
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177217
Seq. ID	jC-atXP64C205L7T7d1
Method	BLASTX
NCBI GI	g4539010
BLAST score	220
E value	6.0e-18
Match length	133
% identity	29
NCBI Description	(AL049481) putative DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	177218
Seq. ID	jC-atXP64C207I1T7d1
Method	BLASTX
NCBI GI	g3834323
BLAST score	305
E value	1.0e-27
Match length	161
% identity	39
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	177219
Seq. ID	jC-atXP65C206M1T7s1
Method	BLASTN
NCBI GI	g4757392
BLAST score	81
E value	8.0e-38
Match length	169
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	177220
Seq. ID	jC-atXP65C206M3T7081d1
Method	BLASTX
NCBI GI	g1620371
BLAST score	778
E value	5.0e-83
Match length	183
% identity	83
NCBI Description	(Y08782) peroxidase ATP23a [Arabidopsis thaliana]

Seq. No.	177221

Seq. ID	jC-atXP65C206N18T7026d1
Method	BLASTX
NCBI GI	g3128176
BLAST score	233
E value	2.0e-21
Match length	148
% identity	47
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	177222
Seq. ID	jC-atXP65C206N24T7050d1
Method	BLASTX
NCBI GI	g3128176
BLAST score	228
E value	3.0e-27
Match length	180
% identity	45
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	177223
Seq. ID	jC-atXP65C206P1T7082d1
Method	BLASTX
NCBI GI	g3877105
BLAST score	191
E value	3.0e-14
Match length	167
% identity	13
NCBI Description	(Z79755) Similarity to Bovine Grave's disease carrier protein (SW:GDC_BOVIN); cDNA EST EMBL:D69947 comes from this gene [Caenorhabditis elegans]

Seq. No.	177224
Seq. ID	jC-atXP65C206P5T7090d1
Method	BLASTN
NCBI GI	g547390
BLAST score	34
E value	3.0e-09
Match length	81
% identity	88
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	177225
Seq. ID	jC-atXP65C207N18T7060d1
Method	BLASTN
NCBI GI	g1848276
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Human telomerase-associated protein TP-1 mRNA, complete cds

Seq. No.	177226
Seq. ID	jC-atXP65C207N3T7s1
Method	BLASTN
NCBI GI	g4757399
BLAST score	129
E value	1.0e-66

Match length	189
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	177227
Seq. ID	jC-atXP65C207P16T7084d1
Method	BLASTN
NCBI GI	g1848276
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Human telomerase-associated protein TP-1 mRNA, complete cds

Seq. No.	177228
Seq. ID	jC-atXP65C208A7T7s1
Method	BLASTN
NCBI GI	g2832689
BLAST score	265
E value	1.0e-147
Match length	277
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	177229
Seq. ID	jC-atXP65C208B15T7053d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	177230
Seq. ID	jC-atXP65C208D10T7085d1
Method	BLASTX
NCBI GI	g399900
BLAST score	916
E value	3.0e-99
Match length	188
% identity	95
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	177231
Seq. ID	jC-atXP65C208D17T7022d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	1.0e-11

Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177232
Seq. ID	jC-atXP65C208I8T7031d1
Method	BLASTX
NCBI GI	g2832641
BLAST score	309
E value	5.0e-28
Match length	92
% identity	100
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	177233
Seq. ID	jC-atXP65C209A2T7027d1
Method	BLASTN
NCBI GI	g3242970
BLAST score	203
E value	1.0e-110
Match length	427
% identity	87
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	177234
Seq. ID	jC-atXP65C209B3T7s1
Method	BLASTN
NCBI GI	g2924652
BLAST score	244
E value	1.0e-135
Match length	244
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	177235
Seq. ID	jC-atXP65C209D13T7s1
Method	BLASTN
NCBI GI	g4757410
BLAST score	38
E value	2.0e-12
Match length	50
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	177236
Seq. ID	jC-atXP65C209D19T7048d1
Method	BLASTX
NCBI GI	g2894379
BLAST score	151
E value	2.0e-09
Match length	70
% identity	43

NCBI Description	(Y14573) ring finger protein [Hordeum vulgare]

Seq. No.	177237
Seq. ID	jC-atXP65C209E11T7064d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177238
Seq. ID	jC-atXP65C209F12T7088d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	6.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177239
Seq. ID	jC-atXP65C209F23T7096d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	6.0e-13
Match length	44
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	177240
Seq. ID	jC-atXP65C209F6T7072d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	39
E value	1.0e-12
Match length	43
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	177241
Seq. ID	jC-atXP65C209F6T7s1
Method	BLASTN
NCBI GI	g3241922
BLAST score	209
E value	1.0e-114
Match length	384
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	177242
Seq. ID	jC-atXP66C208M1T7049a1
Method	BLASTX
NCBI GI	g1490554
BLAST score	337
E value	2.0e-31
Match length	64
% identity	100
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	177243
Seq. ID	jC-atXP66C208M23T7065a1
Method	BLASTN
NCBI GI	g2494106
BLAST score	146
E value	3.0e-76
Match length	273
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177244
Seq. ID	jC-atXP66C208M3T7057a1
Method	BLASTN
NCBI GI	g531828
BLAST score	49
E value	2.0e-18
Match length	68
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177245
Seq. ID	jC-atXP66C208N8T7073a1
Method	BLASTN
NCBI GI	g2564045
BLAST score	142
E value	7.0e-74
Match length	293
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	177246
Seq. ID	jC-atXP66C208O11T7018a1
Method	BLASTN
NCBI GI	g4582444
BLAST score	217
E value	1.0e-118
Match length	410
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	177247
Seq. ID	jC-atXP66C208O7T7010a1
Method	BLASTN

NCBI GI	g531828
BLAST score	52
E value	3.0e-20
Match length	68
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177248
Seq. ID	jC-atXP66C208P20T7042a1
Method	BLASTX
NCBI GI	g4539452
BLAST score	95
E value	1.0e-17
Match length	66
% identity	67
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	177249
Seq. ID	jC-atXP66C209G13T7001a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	155
E value	1.0e-81
Match length	314
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	177250
Seq. ID	jC-atXP66C209H10T7033a1
Method	BLASTN
NCBI GI	g2828184
BLAST score	220
E value	1.0e-120
Match length	384
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	177251
Seq. ID	jC-atXP66C209L20T7015a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177252
Seq. ID	jC-atXP66C209P16T7039a1
Method	BLASTN
NCBI GI	g2947056
BLAST score	48
E value	9.0e-18
Match length	207

% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177253
Seq. ID	jC-atXP66C210A23T7074a1
Method	BLASTN
NCBI GI	g4220627
BLAST score	129
E value	4.0e-66
Match length	284
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	177254
Seq. ID	jC-atXP66C210A23T7d1
Method	BLASTN
NCBI GI	g4220627
BLAST score	83
E value	4.0e-39
Match length	143
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	177255
Seq. ID	jC-atXP66C210B4T7082a1
Method	BLASTX
NCBI GI	g3851636
BLAST score	196
E value	6.0e-15
Match length	65
% identity	60
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	177256
Seq. ID	jC-atXP66C210C17T7011a1
Method	BLASTN
NCBI GI	g2281628
BLAST score	104
E value	3.0e-51
Match length	218
% identity	90
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.2 mRNA, partial cds

Seq. No.	177257
Seq. ID	jC-atXP66C210C23T7019a1
Method	BLASTN
NCBI GI	g4220627
BLAST score	224
E value	1.0e-123
Match length	264
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	177258
Seq. ID	jC-atXP66C210F5T7067a1
Method	BLASTN
NCBI GI	g531828
BLAST score	34
E value	2.0e-09
Match length	54
% identity	91
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177259
Seq. ID	jC-atXP66C210G15T7028a1
Method	BLASTX
NCBI GI	g4490316
BLAST score	152
E value	8.0e-10
Match length	59
% identity	58
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	177260
Seq. ID	jC-atXP66C210H21T7084a1
Method	BLASTX
NCBI GI	g1419090
BLAST score	345
E value	2.0e-32
Match length	85
% identity	76
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	177261
Seq. ID	jC-atXP66C210H3T7044a1
Method	BLASTX
NCBI GI	g3935150
BLAST score	334
E value	4.0e-31
Match length	61
% identity	100
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No.	177262
Seq. ID	jC-atXP66C210H5T7052a1
Method	BLASTX
NCBI GI	g3551131
BLAST score	448
E value	2.0e-44
Match length	91
% identity	92
NCBI Description	(AB012044) plasma membrane aquaporin (PAQ1) [Raphanus sativus]

Seq. No.	177263
Seq. ID	jC-atXP66C210I12T7005a1
Method	BLASTX

NCBI GI g4559391
BLAST score 203
E value 9.0e-16
Match length 44
% identity 80
NCBI Description (AC006526) putative auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 177264
Seq. ID jC-atXP66C210K20T7053a1
Method BLASTN
NCBI GI g3128136
BLAST score 316
E value 1.0e-177
Match length 418
% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No. 177265
Seq. ID jC-atXP66C210L16T7085a1
Method BLASTN
NCBI GI g2290120
BLAST score 37
E value 3.0e-11
Match length 64
% identity 92
NCBI Description HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No. 177266
Seq. ID jC-atXP66C210M17T7022a1
Method BLASTX
NCBI GI g3334323
BLAST score 396
E value 2.0e-38
Match length 78
% identity 97
NCBI Description GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_ (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No. 177267
Seq. ID jC-atXP66C210N14T7046a1
Method BLASTN
NCBI GI g2564045
BLAST score 153
E value 2.0e-80
Match length 375
% identity 84
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No. 177268
Seq. ID jC-atXP66C210N5T7030a1

Method	BLASTX
NCBI GI	g585382
BLAST score	261
E value	1.0e-22
Match length	71
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG) >gi_322536_pir__S30570 laminin receptor homolog - Arabidopsis thaliana >gi_16380_emb_CAA48794_ (X69056) laminin receptor homologue [Arabidopsis thaliana]

Seq. No.	177269
Seq. ID	jC-atXP66C210N8T7038a1
Method	BLASTN
NCBI GI	g4733953
BLAST score	103
E value	1.0e-50
Match length	279
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	177270
Seq. ID	jC-atXP66C211A4T7055a1
Method	BLASTN
NCBI GI	g3212102
BLAST score	40
E value	5.0e-13
Match length	235
% identity	80
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	177271
Seq. ID	jC-atXP66C211E14T7032a1
Method	BLASTX
NCBI GI	g2500378
BLAST score	247
E value	6.0e-21
Match length	72
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	177272
Seq. ID	jC-atXP66C211F3T7040a1
Method	BLASTX
NCBI GI	g3121844
BLAST score	197
E value	5.0e-15
Match length	47
% identity	81
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_1652668_dbj_BAA17588_ (D90907) phosphatidate cytidylyltransferase [Synechocystis sp.]

Seq. No.	177273
Seq. ID	jC-atXP66C211F6T7048a1
Method	BLASTN
NCBI GI	g3212102
BLAST score	103
E value	1.0e-50
Match length	331
% identity	87
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	177274
Seq. ID	jC-atXP66C211G18T7064a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	3.0e-20
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177275
Seq. ID	jC-atXP66C211I3T7072a1
Method	BLASTX
NCBI GI	g131263
BLAST score	79
E value	2.0e-23
Match length	139
% identity	47
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_72662_pir__F2VFD1 photosystem II protein D1 precursor - fava bean chloroplast >gi_12381_emb_CAA35688_ (X17694) Q-B protein (AA 1-353) [Vicia faba]

Seq. No.	177276
Seq. ID	jC-atXP67C211N2T7009a1
Method	BLASTN
NCBI GI	g2392762
BLAST score	162
E value	8.0e-86
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana BAC T32N15 from chromsome III near 54 cM, complete sequence

Seq. No.	177277
Seq. ID	jC-atXP67C212C22T7050a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	4.0e-14
Match length	50
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177278
Seq. ID	jC-atXP67C212D11T7066a1
Method	BLASTN
NCBI GI	g598848
BLAST score	53
E value	1.0e-20
Match length	61
% identity	98
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	177279
Seq. ID	jC-atXP67C212D5T7d1
Method	BLASTN
NCBI GI	g4589415
BLAST score	137
E value	2.0e-71
Match length	189
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	177280
Seq. ID	jC-atXP67C212F12T7027a1
Method	BLASTN
NCBI GI	g540252
BLAST score	55
E value	6.0e-22
Match length	59
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	177281
Seq. ID	jC-atXP67C213D1T7028a1
Method	BLASTN
NCBI GI	g2914688
BLAST score	127
E value	6.0e-65
Match length	235
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177282
Seq. ID	jC-atXP67C213G1T7037a1
Method	BLASTX
NCBI GI	g2995384
BLAST score	119
E value	3.0e-28
Match length	108
% identity	67
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	177283
Seq. ID	jC-atXP67C213J5T7022a1
Method	BLASTX
NCBI GI	g3015514

BLAST score	350
E value	6.0e-33
Match length	71
% identity	100
NCBI Description	(U72351) ADPG pyrophosphorylase small subunit [Arabidopsis thaliana]

Seq. No.	177284
Seq. ID	jC-atXP67C213M24T7055a1
Method	BLASTN
NCBI GI	g3319339
BLAST score	313
E value	1.0e-176
Match length	361
% identity	97
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	177285
Seq. ID	jC-atXP67C213O3T7008a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	331
E value	0.0e+00
Match length	439
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	177286
Seq. ID	jC-atXP67C213P4T7056a1
Method	BLASTX
NCBI GI	g4559372
BLAST score	240
E value	5.0e-20
Match length	51
% identity	92
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]

Seq. No.	177287
Seq. ID	jC-atXP67C214H10T7044a1
Method	BLASTX
NCBI GI	g4210449
BLAST score	200
E value	2.0e-15
Match length	40
% identity	100
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	177288
Seq. ID	jC-atXP67C214H17T7052a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	4.0e-10
Match length	51

% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177289
Seq. ID	jC-atXP67C214J17T7076a1
Method	BLASTN
NCBI GI	g4335744
BLAST score	47
E value	4.0e-17
Match length	95
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177290
Seq. ID	jC-atXP68C214D4T7s1
Method	BLASTN
NCBI GI	g4049332
BLAST score	248
E value	1.0e-137
Match length	252
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	177291
Seq. ID	jC-atXP68C214F11T7d1
Method	BLASTX
NCBI GI	g115385
BLAST score	568
E value	3.0e-59
Match length	124
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	177292
Seq. ID	jC-atXP68C214L11T7d1
Method	BLASTX
NCBI GI	g1523800
BLAST score	249
E value	2.0e-21
Match length	127
% identity	43
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No.	177293
Seq. ID	jC-atXP68C217A19T7s1
Method	BLASTX
NCBI GI	g4490708
BLAST score	333
E value	3.0e-31
Match length	67
% identity	100
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	177294
Seq. ID	jC-atXP68C217A3T7s1
Method	BLASTN
NCBI GI	g2995991
BLAST score	252
E value	1.0e-139
Match length	365
% identity	92
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	177295
Seq. ID	jC-atXP68C218F9T7s1
Method	BLASTN
NCBI GI	g3702315
BLAST score	126
E value	9.0e-65
Match length	190
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177296
Seq. ID	jC-atXP68C218H7T7s1
Method	BLASTX
NCBI GI	g2244989
BLAST score	431
E value	7.0e-43
Match length	84
% identity	100
NCBI Description	(Z97340) strong similarity to naringenin 3-dioxygenase [Arabidopsis thaliana]

Seq. No.	177297
Seq. ID	jC-atXP69C217D15T7025d1
Method	BLASTX
NCBI GI	g1209703
BLAST score	133
E value	4.0e-12
Match length	79
% identity	54
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	177298
Seq. ID	jC-atXP69C217D21T7033a1
Method	BLASTN
NCBI GI	g1655479
BLAST score	43
E value	8.0e-15
Match length	127
% identity	83
NCBI Description	Arabidopsis thaliana mRNA for gamma subunit of mitochondrial F1-ATPase, complete cds

Seq. No.	177299
Seq. ID	jC-atXP69C217G10T7073a1

Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	6.0e-19
Match length	58
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177300
Seq. ID	jC-atXP69C217G11T7081a1
Method	BLASTX
NCBI GI	g1350720
BLAST score	262
E value	1.0e-22
Match length	59
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	177301
Seq. ID	jC-atXP69C217G17T7089a1
Method	BLASTX
NCBI GI	g4586264
BLAST score	314
E value	9.0e-29
Match length	62
% identity	95
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	177302
Seq. ID	jC-atXP69C217G1T7065a1
Method	BLASTN
NCBI GI	g2351066
BLAST score	215
E value	1.0e-117
Match length	267
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	177303
Seq. ID	jC-atXP69C217L1T7059a1
Method	BLASTX
NCBI GI	g3650034
BLAST score	391
E value	8.0e-38
Match length	96
% identity	79
NCBI Description	(AC005396) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	177304
Seq. ID	jC-atXP69C217L4T7067d1
Method	BLASTX
NCBI GI	g3024021
BLAST score	91

E value	2.0e-19
Match length	109
% identity	51
NCBI Description	INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D) >gi_2225883_dbj_BAA20878_ (AB004825) eukaryotic initiation factor 5A4 [Solanum tuberosum]

Seq. No.	177305
Seq. ID	jC-atXP69C217M4T7083d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177306
Seq. ID	jC-atXP69C217M7T7091a1
Method	BLASTX
NCBI GI	g4586264
BLAST score	212
E value	7.0e-17
Match length	55
% identity	75
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	177307
Seq. ID	jC-atXP69C217M7T7091d1
Method	BLASTX
NCBI GI	g4586264
BLAST score	294
E value	3.0e-26
Match length	135
% identity	51
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	177308
Seq. ID	jC-atXP69C217M8T7004a1
Method	BLASTX
NCBI GI	g3790567
BLAST score	328
E value	2.0e-30
Match length	66
% identity	85
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	177309
Seq. ID	jC-atXP69C217N4T7020d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	34
E value	3.0e-09

Match length	38
% identity	97
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	177310
Seq. ID	jC-atXP69C217N7T7036a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	2.0e-12
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177311
Seq. ID	jC-atXP69C217O4T7060a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	8.0e-21
Match length	69
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177312
Seq. ID	jC-atXP69C217P10T7084a1
Method	BLASTX
NCBI GI	g1350930
BLAST score	361
E value	3.0e-34
Match length	77
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	177313
Seq. ID	jC-atXP69C218L15T7058a1
Method	BLASTX
NCBI GI	g1800279
BLAST score	147
E value	3.0e-09
Match length	30
% identity	100
NCBI Description	(U81238) putative Cys3His zinc finger protein ATCTH [Arabidopsis thaliana]

Seq. No.	177314
Seq. ID	jC-atXP69C218L8T7042a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	55
E value	5.0e-22
Match length	67
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177315
Seq. ID	jC-atXP69C218N23T7082a1
Method	BLASTX
NCBI GI	g2497259
BLAST score	188
E value	5.0e-14
Match length	70
% identity	60
NCBI Description	ISOCITRATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP) >gi_166386 (M93672) isocitrate dehydrogenase [Medicago sativa]

Seq. No.	177316
Seq. ID	jC-atXP69C218N23T7082d1
Method	BLASTX
NCBI GI	g542060
BLAST score	49
E value	1.0e-12
Match length	93
% identity	47
NCBI Description	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) - common tobacco

Seq. No.	177317
Seq. ID	jC-atXP69C218N24T7090a1
Method	BLASTX
NCBI GI	g479386
BLAST score	229
E value	7.0e-19
Match length	74
% identity	68
NCBI Description	isocitrate dehydrogenase - soybean

Seq. No.	177318
Seq. ID	jC-atXP69C218N24T7090d1
Method	BLASTX
NCBI GI	g3641398
BLAST score	101
E value	9.0e-12
Match length	78
% identity	41
NCBI Description	(AF020038) NADP-dependent isocitrate dehydrogenase [Homo sapiens]

Seq. No.	177319
Seq. ID	jC-atXP69C218O20T7011a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	59
E value	2.0e-24
Match length	165
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 177320

Seq. ID	jC-atXP69C218O20T7011d1
Method	BLASTN
NCBI GI	g2244991
BLAST score	296
E value	1.0e-165
Match length	648
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177321
Seq. ID	jC-atXP69C219A23T7014a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177322
Seq. ID	jC-atXP69C219A23T7014d1
Method	BLASTX
NCBI GI	g3790567
BLAST score	869
E value	1.0e-93
Match length	157
% identity	100
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	177323
Seq. ID	jC-atXP69C219C8T7093a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	1.0e-19
Match length	62
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	177324
Seq. ID	jC-atXP69C219C8T7093d1
Method	BLASTN
NCBI GI	g1848276
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Human telomerase-associated protein TP-1 mRNA, complete cds

Seq. No.	177325
Seq. ID	jC-atXP69C219D17T7045a1
Method	BLASTN
NCBI GI	g2264320
BLAST score	68

E value	1.0e-29
Match length	104
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	177326
Seq. ID	jC-atXP69C219D5T7029a1
Method	BLASTN
NCBI GI	g790678
BLAST score	120
E value	9.0e-61
Match length	282
% identity	89
NCBI Description	Arabidopsis thaliana zinc finger protein 4 (ZFP4) mRNA, complete cds

Seq. No.	177327
Seq. ID	jC-atXP69C219E3T7061a1
Method	BLASTN
NCBI GI	g790678
BLAST score	229
E value	1.0e-126
Match length	265
% identity	97
NCBI Description	Arabidopsis thaliana zinc finger protein 4 (ZFP4) mRNA, complete cds

Seq. No.	177328
Seq. ID	jC-atXP69C219G5T7030a1
Method	BLASTN
NCBI GI	g3869072
BLAST score	105
E value	8.0e-52
Match length	301
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	177329
Seq. ID	jC-atXP69C219I21T7070d1
Method	BLASTX
NCBI GI	g2109293
BLAST score	137
E value	1.0e-96
Match length	192
% identity	91
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	177330
Seq. ID	jC-atXP69C219J10T7078a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	35
E value	5.0e-10
Match length	35

% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177331
Seq. ID	jC-atXP69C219K1T7086a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	4.0e-11
Match length	40
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177332
Seq. ID	jC-atXP69C219L11T7015a1
Method	BLASTX
NCBI GI	g2146773
BLAST score	247
E value	6.0e-21
Match length	88
% identity	57
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046268 (U26944) senescence-associated protein [Arabidopsis thaliana]

Seq. No.	177333
Seq. ID	jC-atXP69C219L11T7015d1
Method	BLASTX
NCBI GI	g2129729
BLAST score	160
E value	5.0e-90
Match length	181
% identity	94
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046270 (U26945) senescence-associated protein [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana] >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen1 [Arabidopsis thaliana]

Seq. No.	177334
Seq. ID	jC-atXP69C219L18T7023a1
Method	BLASTX
NCBI GI	g2982266
BLAST score	169
E value	8.0e-12
Match length	83
% identity	48
NCBI Description	(AF051216) probable fibrillarin [Picea mariana]

Seq. No.	177335
Seq. ID	jC-atXP69C219L22T7031a1
Method	BLASTN
NCBI GI	g2252848
BLAST score	154
E value	5.0e-81
Match length	294

% identity	88
NCBI Description	Arabidopsis thaliana BAC TM018A10
Seq. No.	177336
Seq. ID	jC-atXP69C219L23T7039d1
Method	BLASTX
NCBI GI	g2129933
BLAST score	56
E value	1.0e-13
Match length	102
% identity	52
NCBI Description	myb-related transcription factor TMH27 - tomato >gi_1167484_emb_CAA64614_ (X95296) transcription factor [Lycopersicon esculentum]
Seq. No.	177337
Seq. ID	jC-atXP69C219L5T7007a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	7.0e-21
Match length	69
% identity	96
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	177338
Seq. ID	jC-atXP69C219L5T7007d1
Method	BLASTX
NCBI GI	g3790567
BLAST score	185
E value	2.0e-13
Match length	139
% identity	37
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]
Seq. No.	177339
Seq. ID	jC-atXP69C219N4T7071d1
Method	BLASTX
NCBI GI	g2129729
BLAST score	910
E value	2.0e-98
Match length	182
% identity	97
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046270 (U26945) senescence-associated protein [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana] >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen1 [Arabidopsis thaliana]
Seq. No.	177340
Seq. ID	jC-atXP69C219O19T7008a1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19

Match length	62
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177341
Seq. ID	jC-atXP69C219O19T7008d1
Method	BLASTN
NCBI GI	g3510347
BLAST score	40
E value	7.0e-13
Match length	244
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	177342
Seq. ID	jC-atXP69C219P5T7016a1
Method	BLASTX
NCBI GI	g4827050
BLAST score	185
E value	1.0e-13
Match length	60
% identity	53
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No.	177343
Seq. ID	jC-atXP69C220A1T7048a1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	1.0e-19
Match length	70
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177344
Seq. ID	jC-atXP69C220A1T7048d1
Method	BLASTX
NCBI GI	g2196466
BLAST score	68
E value	9.0e-14
Match length	154
% identity	45
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	177345
Seq. ID	jC-atXP69C220B13T7072a1
Method	BLASTN
NCBI GI	g2760167
BLAST score	135
E value	1.0e-69
Match length	286

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	177346
Seq. ID	jC-atXP69C220B14T7080a1
Method	BLASTN
NCBI GI	g598848
BLAST score	45
E value	5.0e-16
Match length	49
% identity	98
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	177347
Seq. ID	jC-atXP69C220G13T7092a1
Method	BLASTN
NCBI GI	g3451055
BLAST score	168
E value	2.0e-89
Match length	281
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	177348
Seq. ID	jC-atXP69C220G17T7005d1
Method	BLASTX
NCBI GI	g231995
BLAST score	223
E value	7.0e-27
Match length	134
% identity	50
NCBI Description	DEHYDRIN RAB18 >gi_282880_pir__S28021 rab18 protein - Arabidopsis thaliana >gi_16451_emb_CAA48178_ (X68042) RAB18 [Arabidopsis thaliana]

Seq. No.	177349
Seq. ID	jC-atXP69C220G21T7021a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	5.0e-10
Match length	42
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177350
Seq. ID	jC-atXP69C220G21T7021d1
Method	BLASTN
NCBI GI	g3869072
BLAST score	52
E value	6.0e-20
Match length	124
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	177351
Seq. ID	jC-atXP6C90H7T7s1
Method	BLASTX
NCBI GI	g2317906
BLAST score	220
E value	5.0e-18
Match length	43
% identity	98
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	177352
Seq. ID	jC-atXP6C90J5T7s1
Method	BLASTN
NCBI GI	g2281628
BLAST score	89
E value	9.0e-43
Match length	125
% identity	93
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.2 mRNA, partial cds

Seq. No.	177353
Seq. ID	jC-atXP6C91E21T7s1
Method	BLASTN
NCBI GI	g2739359
BLAST score	243
E value	1.0e-134
Match length	275
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177354
Seq. ID	jC-atXP70C220D23T7025a1
Method	BLASTX
NCBI GI	g3924594
BLAST score	248
E value	9.0e-35
Match length	107
% identity	73
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	177355
Seq. ID	jC-atXP70C220E11T7041a1
Method	BLASTX
NCBI GI	g3924594
BLAST score	513
E value	4.0e-52
Match length	104
% identity	62
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	177356
Seq. ID	jC-atXP70C220E4T7057a1
Method	BLASTN
NCBI GI	g2244991
BLAST score	67
E value	3.0e-29
Match length	91
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177357
Seq. ID	jC-atXP70C220H8T7034a1
Method	BLASTN
NCBI GI	g4335711
BLAST score	93
E value	1.0e-44
Match length	125
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177358
Seq. ID	jC-atXP70C220I14T7074a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	7.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177359
Seq. ID	jC-atXP70C220I19T7082a1
Method	BLASTX
NCBI GI	g4678357
BLAST score	490
E value	2.0e-49
Match length	96
% identity	96
NCBI Description	(AL049659) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	177360
Seq. ID	jC-atXP70C220I2T7066a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	37
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177361
Seq. ID	jC-atXP70C220L1T7029a1
Method	BLASTN
NCBI GI	g4589419

BLAST score	275
E value	1.0e-153
Match length	401
% identity	56
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	177362
Seq. ID	jC-atXP70C220M10T7069a1
Method	BLASTN
NCBI GI	g3355463
BLAST score	67
E value	3.0e-29
Match length	129
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177363
Seq. ID	jC-atXP70C220O3T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	7.0e-21
Match length	53
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177364
Seq. ID	jC-atXP70C220P16T7086a1
Method	BLASTN
NCBI GI	g4519190
BLAST score	58
E value	9.0e-24
Match length	242
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	177365
Seq. ID	jC-atXP70C220P19T7094a1
Method	BLASTN
NCBI GI	g3641835
BLAST score	200
E value	1.0e-108
Match length	268
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	177366
Seq. ID	jC-atXP70C220P22T7007a1
Method	BLASTN
NCBI GI	g531828
BLAST score	37
E value	3.0e-11
Match length	41

% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177367
Seq. ID	jC-atXP70C221B17T7075a1
Method	BLASTX
NCBI GI	g132110
BLAST score	121
E value	3.0e-13
Match length	82
% identity	50
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	177368
Seq. ID	jC-atXP70C221C16T7020a1
Method	BLASTN
NCBI GI	g2914688
BLAST score	77
E value	3.0e-35
Match length	125
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177369
Seq. ID	jC-atXP70C221D7T7036a1
Method	BLASTN
NCBI GI	g1764099
BLAST score	104
E value	3.0e-51
Match length	193
% identity	93
NCBI Description	Arabidopsis thaliana GDP-D-mannose-4,6-dehydratase (MUR1) mRNA, complete cds

Seq. No.	177370
Seq. ID	jC-atXP70C222A11T7031a1
Method	BLASTX
NCBI GI	g3482931
BLAST score	181
E value	4.0e-13
Match length	53
% identity	68
NCBI Description	(AC003970) germin-like protein [Arabidopsis thaliana]

Seq. No.	177371
Seq. ID	jC-atXP70C222A16T7047a1
Method	BLASTN
NCBI GI	g3548797
BLAST score	56
E value	1.0e-22
Match length	84

% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177372
Seq. ID	jC-atXP70C222C18T7024a1
Method	BLASTN
NCBI GI	g2264302
BLAST score	84
E value	3.0e-39
Match length	339
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	177373
Seq. ID	jC-atXP70C222C19T7032a1
Method	BLASTX
NCBI GI	g464985
BLAST score	142
E value	1.0e-08
Match length	71
% identity	45
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	177374
Seq. ID	jC-atXP70C222C6T7087a1
Method	BLASTN
NCBI GI	g4263694
BLAST score	234
E value	1.0e-129
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177375
Seq. ID	jC-atXP70C222C9T7008a1
Method	BLASTX
NCBI GI	g4263711
BLAST score	211
E value	1.0e-16
Match length	128
% identity	41
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	177376
Seq. ID	jC-atXP70C222D13T7040a1
Method	BLASTN
NCBI GI	g928933
BLAST score	56
E value	2.0e-22
Match length	214

% identity	84
NCBI Description	A.thaliana mRNA for gamma-glutamyl transpeptidase

Seq. No.	177377
Seq. ID	jC-atXP70C222F17T7088a1
Method	BLASTX
NCBI GI	g1354272
BLAST score	273
E value	6.0e-24
Match length	54
% identity	93
NCBI Description	(U51036) aspartic proteinase [Arabidopsis thaliana]

Seq. No.	177378
Seq. ID	jC-atXP70C222F22T7096a1
Method	BLASTX
NCBI GI	g2078350
BLAST score	339
E value	1.0e-31
Match length	87
% identity	78
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	177379
Seq. ID	jC-atXP71C221I2T7058d1
Method	BLASTX
NCBI GI	g114089
BLAST score	795
E value	3.0e-90
Match length	178
% identity	98
NCBI Description	RAS-RELATED PROTEIN ARA-4 >gi_81633_pir__JS0641 GTP-binding protein ara-4 - Arabidopsis thaliana >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein [Arabidopsis thaliana] >gi_3763922 (AC004450) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	177380
Seq. ID	jC-atXP71C221J9T7090d1
Method	BLASTN
NCBI GI	g2343110
BLAST score	33
E value	1.0e-08
Match length	41
% identity	95
NCBI Description	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds

Seq. No.	177381
Seq. ID	jC-atXP71C221K10T7s2
Method	BLASTX
NCBI GI	g3695384
BLAST score	509
E value	1.0e-51
Match length	147
% identity	76
NCBI Description	(AF096370) contains similarity to the helix-loop-helix

DNA-binding domain (Pfam: PF00010 HLH, E-value: 0.0046) [Arabidopsis thaliana]

Seq. No.	177382
Seq. ID	jC-atXP71C221K7T7011d1
Method	BLASTX
NCBI GI	g786117
BLAST score	183
E value	7.0e-13
Match length	399
% identity	13
NCBI Description	(L41834) nuclear protein [Ensis minor]

Seq. No.	177383
Seq. ID	jC-atXP71C222G7T7001d1
Method	BLASTN
NCBI GI	g3341671
BLAST score	352
E value	0.0e+00
Match length	400
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177384
Seq. ID	jC-atXP71C222G9T7s2
Method	BLASTN
NCBI GI	g2570223
BLAST score	189
E value	1.0e-102
Match length	279
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177385
Seq. ID	jC-atXP71C222J10T7073d1
Method	BLASTN
NCBI GI	g732561
BLAST score	59
E value	3.0e-24
Match length	152
% identity	88
NCBI Description	A.thaliana rpl15 gene for plastid ribosomal protein CL15

Seq. No.	177386
Seq. ID	jC-atXP71C222L16T7028d1
Method	BLASTN
NCBI GI	g4589434
BLAST score	72
E value	3.0e-32
Match length	141
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	177387

Seq. ID	jC-atXP71C222L5T7012d1
Method	BLASTX
NCBI GI	g3264805
BLAST score	1028
E value	1.0e-112
Match length	195
% identity	99
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	177388
Seq. ID	jC-atXP71C222M22T7084d1
Method	BLASTX
NCBI GI	g3122572
BLAST score	707
E value	1.0e-74
Match length	206
% identity	67
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	177389
Seq. ID	jC-atXP71C222N3T7s2
Method	BLASTX
NCBI GI	g121075
BLAST score	255
E value	3.0e-22
Match length	49
% identity	96
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	177390
Seq. ID	jC-atXP71C222P10T7s2
Method	BLASTN
NCBI GI	g2264317
BLAST score	223
E value	1.0e-122
Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	177391
Seq. ID	jC-atXP71CF1A6T7086d1
Method	BLASTN
NCBI GI	g4263753

BLAST score	60
E value	7.0e-25
Match length	202
% identity	86
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	177392
Seq. ID	jC-atXP71CF1B4T7055d1
Method	BLASTN
NCBI GI	g3790586
BLAST score	158
E value	3.0e-83
Match length	363
% identity	87
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHF2a mRNA, complete cds

Seq. No.	177393
Seq. ID	jC-atXP71CF1B7T7071d1
Method	BLASTX
NCBI GI	g2760328
BLAST score	177
E value	1.0e-12
Match length	76
% identity	53
NCBI Description	(AC002130) F1N21.13 [Arabidopsis thaliana]

Seq. No.	177394
Seq. ID	jC-atXP71CF1C3T7087d1
Method	BLASTX
NCBI GI	g4033469
BLAST score	178
E value	1.0e-31
Match length	184
% identity	45
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	177395
Seq. ID	jC-atXP71CF1C8T7008d1
Method	BLASTX
NCBI GI	g3264805
BLAST score	241
E value	5.0e-20
Match length	176
% identity	39
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	177396
Seq. ID	jC-atXP72C221M23T7s1
Method	BLASTX
NCBI GI	g2078350
BLAST score	362

E value	3.0e-34
Match length	91
% identity	81
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	177397
Seq. ID	jC-atXP72C221O18T7s1
Method	BLASTN
NCBI GI	g2182285
BLAST score	77
E value	2.0e-35
Match length	258
% identity	81
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177398
Seq. ID	jC-atXP72C221P12T7s1
Method	BLASTN
NCBI GI	g2244901
BLAST score	34
E value	5.0e-10
Match length	94
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177399
Seq. ID	jC-atXP73C223E17T7b1
Method	BLASTN
NCBI GI	g2618683
BLAST score	103
E value	2.0e-50
Match length	172
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177400
Seq. ID	jC-atXP73C223E17T7d2
Method	BLASTX
NCBI GI	g2506443
BLAST score	170
E value	1.0e-11
Match length	55
% identity	65
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	177401

Seq. ID	jC-atXP73C223E22T7b1
Method	BLASTN
NCBI GI	g1877523
BLAST score	338
E value	0.0e+00
Match length	440
% identity	96
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	177402
Seq. ID	jC-atXP73C223F21T7b1
Method	BLASTN
NCBI GI	g1877523
BLAST score	460
E value	0.0e+00
Match length	507
% identity	99
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	177403
Seq. ID	jC-atXP73C223F21T7d2
Method	BLASTX
NCBI GI	g2062157
BLAST score	222
E value	9.0e-18
Match length	60
% identity	35
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	177404
Seq. ID	jC-atXP73C223F9T7b1
Method	BLASTX
NCBI GI	g399013
BLAST score	259
E value	5.0e-94
Match length	224
% identity	54
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	177405
Seq. ID	jC-atXP73C223L7T7b1
Method	BLASTX
NCBI GI	g4753651
BLAST score	611
E value	1.0e-68
Match length	161
% identity	84
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis

thaliana]

Seq. No.	177406
Seq. ID	jC-atXP73C223L7T7d2
Method	BLASTX
NCBI GI	g4753651
BLAST score	680
E value	2.0e-71
Match length	157
% identity	83
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	177407
Seq. ID	jC-atXP73C224A7T7b1
Method	BLASTN
NCBI GI	g405130
BLAST score	244
E value	1.0e-134
Match length	264
% identity	98
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	177408
Seq. ID	jC-atXP73C224B2T7d2
Method	BLASTN
NCBI GI	g4584841
BLAST score	518
E value	0.0e+00
Match length	636
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	177409
Seq. ID	jC-atXP73C224B4T7b1
Method	BLASTX
NCBI GI	g124157
BLAST score	212
E value	1.0e-16
Match length	140
% identity	36
NCBI Description	INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE) >gi_184556 (M21188) insulin-degrading enzyme [Homo sapiens]

Seq. No.	177410
Seq. ID	jC-atXP73C224B6T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	5.0e-19
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177411
Seq. ID	jC-atXP73C224C3T7b1
Method	BLASTX
NCBI GI	g461899
BLAST score	721
E value	2.0e-76
Match length	160
% identity	91
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	177412
Seq. ID	jC-atXP73C224E2T7d2
Method	BLASTN
NCBI GI	g3264774
BLAST score	131
E value	4.0e-67
Match length	497
% identity	89
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	177413
Seq. ID	jC-atXP73CF2F2T7b1
Method	BLASTX
NCBI GI	g3775985
BLAST score	206
E value	5.0e-22
Match length	76
% identity	78
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	177414
Seq. ID	jC-atXP73CF2F3T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	71
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177415
Seq. ID	jC-atXP73CF2F5T7d2
Method	BLASTX
NCBI GI	g3882355
BLAST score	284
E value	1.0e-27
Match length	100
% identity	61
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis

thaliana]

Seq. No.	177416
Seq. ID	jC-atXP73CF3A11T7d2
Method	BLASTX
NCBI GI	g2244839
BLAST score	279
E value	3.0e-29
Match length	203
% identity	14
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177417
Seq. ID	jC-atXP73CF3B10T7d2
Method	BLASTX
NCBI GI	g1669387
BLAST score	1243
E value	1.0e-137
Match length	240
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	177418
Seq. ID	jC-atXP73CF3B1T7d2
Method	BLASTX
NCBI GI	g3914666
BLAST score	843
E value	8.0e-94
Match length	236
% identity	80
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565) ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	177419
Seq. ID	jC-atXP73CF3C4T7d2
Method	BLASTX
NCBI GI	g4467139
BLAST score	116
E value	6.0e-61
Match length	210
% identity	58
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	177420
Seq. ID	jC-atXP73CF3C5T7d2
Method	BLASTX
NCBI GI	g3850573
BLAST score	1081
E value	1.0e-118
Match length	228
% identity	91
NCBI Description	(AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from

this gene. [Arabidopsis thaliana]

Seq. No.	177421
Seq. ID	jC-atXP73CF3C8T7d2
Method	BLASTX
NCBI GI	g2924523
BLAST score	224
E value	5.0e-18
Match length	236
% identity	9
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	177422
Seq. ID	jC-atXP74C223L16T7011d1
Method	BLASTX
NCBI GI	g1173345
BLAST score	365
E value	6.0e-55
Match length	138
% identity	83
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	177423
Seq. ID	jC-atXP74C223L17T7019d1
Method	BLASTX
NCBI GI	g3249095
BLAST score	783
E value	2.0e-83
Match length	204
% identity	80
NCBI Description	(AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No.	177424
Seq. ID	jC-atXP74C223N6T7083d1
Method	BLASTX
NCBI GI	g2245020
BLAST score	71
E value	5.0e-15
Match length	221
% identity	32
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	177425
Seq. ID	jC-atXP74C224F7T7041d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	715
E value	1.0e-75

Match length	193
% identity	67
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	177426
Seq. ID	jC-atXP74C224H10T7073d1
Method	BLASTX
NCBI GI	g3264805
BLAST score	1231
E value	1.0e-136
Match length	239
% identity	99
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	177427
Seq. ID	jC-atXP74C224H21T7010d1
Method	BLASTX
NCBI GI	g228938
BLAST score	83
E value	6.0e-09
Match length	337
% identity	8
NCBI Description	Hyp-rich glycoprotein [Zea diploperennis]

Seq. No.	177428
Seq. ID	jC-atXP74C224J9T7034d1
Method	BLASTX
NCBI GI	g2245093
BLAST score	197
E value	7.0e-15
Match length	111
% identity	48
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	177429
Seq. ID	jC-atXP74C224K10T7066d1
Method	BLASTX
NCBI GI	g4090884
BLAST score	382
E value	2.0e-36
Match length	159
% identity	57
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	177430
Seq. ID	jC-atXP74C224K21T7074d1
Method	BLASTN
NCBI GI	g4586241
BLAST score	282
E value	1.0e-157
Match length	594
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	177431
Seq. ID	jC-atXP74C224K5T7058d1
Method	BLASTX
NCBI GI	g3319347
BLAST score	928
E value	1.0e-100
Match length	195
% identity	89
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	177432
Seq. ID	jC-atXP74C224N21T7079d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	3.0e-09
Match length	46
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177433
Seq. ID	jC-atXP74C224O20T7095d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	81
E value	3.0e-01
Match length	145
% identity	18
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	177434
Seq. ID	jC-atXP74C224P6T7016d1
Method	BLASTX
NCBI GI	g480725
BLAST score	343
E value	4.0e-32
Match length	119
% identity	55
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	177435
Seq. ID	jC-atXP74C225D23T7022d1
Method	BLASTX
NCBI GI	g1402908
BLAST score	1077
E value	1.0e-118
Match length	230
% identity	91
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)

peroxidase [Arabidopsis thaliana]

Seq. No.	177436
Seq. ID	jC-atXP74C225E18T7038d1
Method	BLASTX
NCBI GI	g1076393
BLAST score	1046
E value	1.0e-114
Match length	210
% identity	100
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	177437
Seq. ID	jC-atXP74C225G17T7007d1
Method	BLASTX
NCBI GI	g480725
BLAST score	255
E value	1.0e-21
Match length	153
% identity	29
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	177438
Seq. ID	jC-atXP74C225G23T7023d1
Method	BLASTN
NCBI GI	g3869072
BLAST score	303
E value	1.0e-170
Match length	672
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	177439
Seq. ID	jC-atXP74C226A20T7072d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	97
E value	6.0e-40
Match length	181
% identity	50
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	177440
Seq. ID	jC-atXP74C226A23T7088d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	205
E value	1.0e-17
Match length	176
% identity	29

NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	177441
Seq. ID	jC-atXP75C225I21T7d1
Method	BLASTX
NCBI GI	g2055273
BLAST score	207
E value	2.0e-16
Match length	39
% identity	97
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	177442
Seq. ID	jC-atXP75C226E3T7d1
Method	BLASTX
NCBI GI	g2252849
BLAST score	543
E value	1.0e-55
Match length	160
% identity	68
NCBI Description	(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]

Seq. No.	177443
Seq. ID	jC-atXP75C226E3T7s1
Method	BLASTN
NCBI GI	g2252848
BLAST score	51
E value	1.0e-19
Match length	208
% identity	83
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	177444
Seq. ID	jC-atXP75C226G7T7s1
Method	BLASTN
NCBI GI	g4559375
BLAST score	328
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	177445
Seq. ID	jC-atXP75C226K23T7s1
Method	BLASTN
NCBI GI	g3367567
BLAST score	382
E value	0.0e+00
Match length	429
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	177446
Seq. ID	jC-atXP75C227O21T7d1

Method	BLASTX
NCBI GI	g99698
BLAST score	235
E value	9.0e-20
Match length	88
% identity	58
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	177447
Seq. ID	jC-atXP75C227O23T7s1
Method	BLASTN
NCBI GI	g472874
BLAST score	65
E value	2.0e-28
Match length	85
% identity	94
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 1c

Seq. No.	177448
Seq. ID	jC-atXP75C228F3T7d1
Method	BLASTN
NCBI GI	g4314354
BLAST score	91
E value	5.0e-44
Match length	143
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177449
Seq. ID	jC-atXP76C226P10T7d1
Method	BLASTX
NCBI GI	g1170373
BLAST score	922
E value	1.0e-100
Match length	182
% identity	99
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177450
Seq. ID	jC-atXP76C227D6T7s1
Method	BLASTX
NCBI GI	g4056457
BLAST score	201
E value	1.0e-15
Match length	52
% identity	79
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	177451
Seq. ID	jC-atXP76C227L21T7s1
Method	BLASTN

NCBI GI	g3869067
BLAST score	186
E value	1.0e-100
Match length	275
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	177452
Seq. ID	jC-atXP76C227L7T7s1
Method	BLASTX
NCBI GI	g3912919
BLAST score	591
E value	3.0e-61
Match length	120
% identity	100
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177453
Seq. ID	jC-atXP76C227N6T7s1
Method	BLASTN
NCBI GI	g928809
BLAST score	34
E value	1.0e-09
Match length	147
% identity	83
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq3) gene

Seq. No.	177454
Seq. ID	jC-atXP76C228G7T7s1
Method	BLASTN
NCBI GI	g4741928
BLAST score	64
E value	2.0e-27
Match length	152
% identity	86
NCBI Description	Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds

Seq. No.	177455
Seq. ID	jC-atXP76C228H2T7s1
Method	BLASTN
NCBI GI	g3859658
BLAST score	254
E value	1.0e-141
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	177456
Seq. ID	jC-atXP77C228K12T7s1
Method	BLASTN
NCBI GI	g4538949
BLAST score	76
E value	7.0e-35
Match length	213

% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	177457
Seq. ID	jC-atXP77C228K20T7s1
Method	BLASTN
NCBI GI	g3608126
BLAST score	158
E value	2.0e-83
Match length	402
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177458
Seq. ID	jC-atXP77C229D15T7d1
Method	BLASTN
NCBI GI	g2597829
BLAST score	73
E value	4.0e-33
Match length	141
% identity	88
NCBI Description	Arabidopsis thaliana CBL1 gene

Seq. No.	177459
Seq. ID	jC-atXP77C229F10T7d1
Method	BLASTN
NCBI GI	g4006940
BLAST score	36
E value	2.0e-11
Match length	52
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for voltage-dependent anion-selective channel protein

Seq. No.	177460
Seq. ID	jC-atXP77C229I22T7s1
Method	BLASTN
NCBI GI	g4220633
BLAST score	379
E value	0.0e+00
Match length	447
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	177461
Seq. ID	jC-atXP77C229J13T7s1
Method	BLASTN
NCBI GI	g2246620
BLAST score	53
E value	2.0e-21
Match length	113
% identity	93
NCBI Description	Arabidopsis thaliana salt-stress induced tonoplast intrinsic protein mRNA, complete cds

Seq. No.	177462
Seq. ID	jC-atXP77C229J19T7s1
Method	BLASTN
NCBI GI	g3449327
BLAST score	103
E value	4.0e-51
Match length	151
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	177463
Seq. ID	jC-atXP77C229J6T7s1
Method	BLASTX
NCBI GI	g2632254
BLAST score	306
E value	6.0e-28
Match length	87
% identity	67
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	177464
Seq. ID	jC-atXP77C230E10T7s1
Method	BLASTN
NCBI GI	g2828182
BLAST score	111
E value	1.0e-55
Match length	183
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	177465
Seq. ID	jC-atXP77C230E7T7s1
Method	BLASTN
NCBI GI	g2924651
BLAST score	175
E value	8.0e-94
Match length	255
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	177466
Seq. ID	jC-atXP77C230F1T7s1
Method	BLASTN
NCBI GI	g2832611
BLAST score	119
E value	3.0e-60
Match length	359
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	177467
Seq. ID	jC-atXP77C230H20T7s1

Method	BLASTN
NCBI GI	g2656032
BLAST score	429
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	177468
Seq. ID	jC-atXP77C230I23T7s1
Method	BLASTN
NCBI GI	g4490322
BLAST score	201
E value	1.0e-109
Match length	333
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for nitrate transporter, partial

Seq. No.	177469
Seq. ID	jC-atXP78C229K13T7b1
Method	BLASTX
NCBI GI	g2245093
BLAST score	47
E value	1.0e-44
Match length	157
% identity	71
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	177470
Seq. ID	jC-atXP78C229K15T7b1
Method	BLASTN
NCBI GI	g2342673
BLAST score	172
E value	1.0e-91
Match length	340
% identity	96
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177471
Seq. ID	jC-atXP78C229L21T7b1
Method	BLASTX
NCBI GI	g1706772
BLAST score	787
E value	3.0e-84
Match length	155
% identity	96
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana]

	>gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]
Seq. No.	177472
Seq. ID	jC-atXP78CF4C12T7b1
Method	BLASTN
NCBI GI	g1621538
BLAST score	101
E value	2.0e-49
Match length	256
% identity	93
NCBI Description	Arabidopsis thaliana annexin-like protein mRNA, complete cds
Seq. No.	177473
Seq. ID	jC-atXP78CF4D5T7b1
Method	BLASTX
NCBI GI	g3983125
BLAST score	283
E value	4.0e-25
Match length	83
% identity	75
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]
Seq. No.	177474
Seq. ID	jC-atXP78CF4E3T7b1
Method	BLASTX
NCBI GI	g2062163
BLAST score	85
E value	8.0e-18
Match length	144
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	177475
Seq. ID	jC-atXP78CF4E7T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	52
E value	3.0e-20
Match length	92
% identity	89
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)
Seq. No.	177476
Seq. ID	jC-atXP78CF4G2T7b1
Method	BLASTX
NCBI GI	g2129597
BLAST score	232
E value	2.0e-22
Match length	84
% identity	64
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis

thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	177477
Seq. ID	jC-atXP78CF4G4T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	7.0e-12
Match length	75
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177478
Seq. ID	jC-atXP78CF5B6T7b1
Method	BLASTX
NCBI GI	g2781354
BLAST score	107
E value	1.0e-04
Match length	89
% identity	25
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	177479
Seq. ID	jC-atXP78CF5C11T7b1
Method	BLASTX
NCBI GI	g4006941
BLAST score	577
E value	1.0e-59
Match length	139
% identity	82
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	177480
Seq. ID	jC-atXP78CF5D10T7b1
Method	BLASTN
NCBI GI	g2225992
BLAST score	38
E value	8.0e-12
Match length	38
% identity	100
NCBI Description	Nicotiana tabacum mRNA for ferredoxin-NADP reductase

Seq. No.	177481
Seq. ID	jC-atXP78CF5D9T7b1
Method	BLASTN
NCBI GI	g2804255
BLAST score	40
E value	5.0e-13
Match length	98
% identity	84
NCBI Description	Oryctolagus cuniculus mRNA for interferon gamma, complete cds

Seq. No.	177482

Seq. ID	jC-atXP78CF5G2T7b1
Method	BLASTX
NCBI GI	g1565225
BLAST score	637
E value	1.0e-66
Match length	144
% identity	85
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	177483
Seq. ID	jC-atXP78CF5H5T7b1
Method	BLASTX
NCBI GI	g4204274
BLAST score	266
E value	4.0e-23
Match length	104
% identity	56
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	177484
Seq. ID	jC-atXP78CF6F3T7b1
Method	BLASTX
NCBI GI	g1109600
BLAST score	730
E value	2.0e-77
Match length	145
% identity	94
NCBI Description	(D16628) ATsEH [Arabidopsis thaliana] >gi_2760840 (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]

Seq. No.	177485
Seq. ID	jC-atXP79C230M13T7b1
Method	BLASTX
NCBI GI	g3859607
BLAST score	71
E value	5.0e-42
Match length	103
% identity	89
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=.21, N=1) [Arabidopsis thaliana]

Seq. No.	177486
Seq. ID	jC-atXP79C230N13T7d2
Method	BLASTX
NCBI GI	g3859607
BLAST score	526
E value	2.0e-53
Match length	129
% identity	81
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=.21, N=1) [Arabidopsis thaliana]

Seq. No.	177487
Seq. ID	jC-atXP79C230O17T7d2
Method	BLASTX
NCBI GI	g4378848

BLAST score	277
E value	2.0e-24
Match length	94
% identity	57
NCBI Description	(AF124349) hydrolase [Zymomonas mobilis]

Seq. No.	177488
Seq. ID	jC-atXP79C230O22T7b1
Method	BLASTX
NCBI GI	g131528
BLAST score	305
E value	2.0e-27
Match length	164
% identity	30
NCBI Description	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) >gi_35768_emb_CAA43973_ (X62006) polypirimidine tract binding protein [Homo sapiens] >gi_35774_emb_CAA43056_ (X60648) polypyrimidine tract-binding protein (pPTB) [Homo sapiens] >gi_4096061 (AC006273) PTB_HUMAN; PTB; HETEROGENEOUS NUCLEA; HNRNP I; 57 KD RNA-BINDING PROTEIN PPTB-1 [Homo sapiens]

Seq. No.	177489
Seq. ID	jC-atXP79C230P9T7b1
Method	BLASTX
NCBI GI	g2851508
BLAST score	688
E value	2.0e-72
Match length	135
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	177490
Seq. ID	jC-atXP79C231F6T7b1
Method	BLASTX
NCBI GI	g4586256
BLAST score	586
E value	1.0e-60
Match length	140
% identity	83
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	177491
Seq. ID	jC-atXP79C231I12T7b1
Method	BLASTX
NCBI GI	g2661422
BLAST score	928
E value	1.0e-100
Match length	188
% identity	96
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein

[Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_
(AL023094) Putative S-phase-specific ribosomal protein
[Arabidopsis thaliana]

Seq. No.	177492
Seq. ID	jC-atXP79C237B2T7d2
Method	BLASTN
NCBI GI	g1890153
BLAST score	276
E value	1.0e-154
Match length	448
% identity	91
NCBI Description	A.thaliana mRNA for alpha-mannosidase precursor

Seq. No.	177493
Seq. ID	jC-atXP79C237C3T7b1
Method	BLASTX
NCBI GI	g2252859
BLAST score	306
E value	8.0e-28
Match length	136
% identity	51
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	177494
Seq. ID	jC-atXP79C237C3T7d2
Method	BLASTN
NCBI GI	g1871173
BLAST score	417
E value	0.0e+00
Match length	535
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	177495
Seq. ID	jC-atXP79C237D8T7b1
Method	BLASTX
NCBI GI	g285741
BLAST score	202
E value	2.0e-15
Match length	222
% identity	32
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	177496
Seq. ID	jC-atXP79C237F6T7d2
Method	BLASTX
NCBI GI	g3242721
BLAST score	556
E value	5.0e-57
Match length	156
% identity	79
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No. 177497

Seq. ID	jC-atXP79C237H12T7d2
Method	BLASTX
NCBI GI	g4567225
BLAST score	469
E value	8.0e-47
Match length	88
% identity	100
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	177498
Seq. ID	jC-atXP79C238C1T7d2
Method	BLASTX
NCBI GI	g1809305
BLAST score	304
E value	5.0e-49
Match length	165
% identity	68
NCBI Description	(U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315 (U73781) histone H1-3 [Arabidopsis thaliana] >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis thaliana]

Seq. No.	177499
Seq. ID	jC-atXP79C238H10T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	67
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177500
Seq. ID	jC-atXP79C239C7T7d2
Method	BLASTX
NCBI GI	g2388906
BLAST score	414
E value	2.0e-40
Match length	173
% identity	44
NCBI Description	(Z98974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	177501
Seq. ID	jC-atXP79C239D1T7b1
Method	BLASTX
NCBI GI	g1669387
BLAST score	153
E value	1.0e-09
Match length	164
% identity	21
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	177502
Seq. ID	jC-atXP79C239E2T7d2
Method	BLASTX
NCBI GI	g3287687

BLAST score	692
E value	6.0e-73
Match length	153
% identity	93
NCBI Description	(AC003979) Match to sucrose-proton symporter (SUC2) gene gb_X75382 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	177503
Seq. ID	jC-atXP79C240A1T7b1
Method	BLASTX
NCBI GI	g2341034
BLAST score	605
E value	7.0e-63
Match length	126
% identity	95
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	177504
Seq. ID	jC-atXP79C240C21T7b1
Method	BLASTN
NCBI GI	g4028980
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	pCP1(-) SK positive selection cloning vector gltS gene

Seq. No.	177505
Seq. ID	jC-atXP79CF4G9T7b1
Method	BLASTX
NCBI GI	g2809259
BLAST score	700
E value	7.0e-74
Match length	138
% identity	99
NCBI Description	(AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No.	177506
Seq. ID	jC-atXP79CF4H10T7b1
Method	BLASTN
NCBI GI	g4538918
BLAST score	593
E value	0.0e+00
Match length	685
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)

Seq. No.	177507
Seq. ID	jC-atXP79CF4H2T7b1
Method	BLASTN
NCBI GI	g4725940
BLAST score	59
E value	5.0e-24
Match length	83
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17

(ESSA project)

Seq. No.	177508
Seq. ID	jC-atXP79CF4H5T7b1
Method	BLASTX
NCBI GI	g4678332
BLAST score	492
E value	2.0e-49
Match length	136
% identity	64
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	177509
Seq. ID	jC-atXP79CF4H8T7d2
Method	BLASTX
NCBI GI	g2809259
BLAST score	739
E value	2.0e-78
Match length	145
% identity	99
NCBI Description	(AC002560) F21B7.28 [Arabidopsis thaliana]

Seq. No.	177510
Seq. ID	jC-atXP7C91H4T7s1
Method	BLASTN
NCBI GI	g3158393
BLAST score	59
E value	7.0e-25
Match length	119
% identity	87
NCBI Description	Arabidopsis thaliana LRR-containing F-box protein (COI1) mRNA, complete cds

Seq. No.	177511
Seq. ID	jC-atXP7C91I19T7s1
Method	BLASTX
NCBI GI	g132166
BLAST score	262
E value	4.0e-23
Match length	49
% identity	94
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	177512
Seq. ID	jC-atXP7C91J3T7s1
Method	BLASTN
NCBI GI	g4581103
BLAST score	139
E value	2.0e-72
Match length	227
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic

sequence, complete sequence

Seq. No.	177513
Seq. ID	jC-atXP7C91K13T7d1
Method	BLASTX
NCBI GI	g2194119
BLAST score	530
E value	2.0e-54
Match length	104
% identity	95
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	177514
Seq. ID	jC-atXP7C91N10T7s1
Method	BLASTN
NCBI GI	g4090568
BLAST score	153
E value	1.0e-80
Match length	274
% identity	88
NCBI Description	Arabidopsis thaliana Myb-related transcription factor CCA1 gene, complete cds

Seq. No.	177515
Seq. ID	jC-atXP7C91P14T7d1
Method	BLASTN
NCBI GI	g2351062
BLAST score	136
E value	2.0e-70
Match length	242
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	177516
Seq. ID	jC-atXP7C91P23T7d1
Method	BLASTX
NCBI GI	g4581117
BLAST score	516
E value	2.0e-62
Match length	127
% identity	96
NCBI Description	(AC005825) putative ubiquitin-conjugating enzyme E2;GB:T21483 appears to be a partially-spliced transcript from this gene [Arabidopsis thaliana]

Seq. No.	177517
Seq. ID	jC-atXP7C92A5T7s1
Method	BLASTN
NCBI GI	g681901
BLAST score	324
E value	0.0e+00
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No.	177518
Seq. ID	jC-atXP80C231J16T7s1
Method	BLASTN
NCBI GI	g4757390
BLAST score	175
E value	8.0e-94
Match length	253
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	177519
Seq. ID	jC-atXP80C231L9T7s1
Method	BLASTN
NCBI GI	g4249393
BLAST score	391
E value	0.0e+00
Match length	440
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177520
Seq. ID	jC-atXP80C231O3T7d1
Method	BLASTX
NCBI GI	g3421090
BLAST score	696
E value	1.0e-73
Match length	137
% identity	99
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	177521
Seq. ID	jC-atXP80C232B2T7d1
Method	BLASTX
NCBI GI	g3421090
BLAST score	483
E value	2.0e-60
Match length	127
% identity	93
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	177522
Seq. ID	jC-atXP80C232F18T7s1
Method	BLASTN
NCBI GI	g4589451
BLAST score	102
E value	3.0e-50
Match length	227
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T32G24, complete sequence

Seq. No.	177523
Seq. ID	jC-atXP80C240D16T7s1

Method	BLASTN
NCBI GI	g3510344
BLAST score	236
E value	1.0e-130
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	177524
Seq. ID	jC-atXP80C240F1T7s1
Method	BLASTN
NCBI GI	g4589437
BLAST score	438
E value	0.0e+00
Match length	459
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	177525
Seq. ID	jC-atXP80C240F21T7d1
Method	BLASTX
NCBI GI	g3269287
BLAST score	707
E value	6.0e-75
Match length	149
% identity	92
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	177526
Seq. ID	jC-atXP80C240F21T7s1
Method	BLASTX
NCBI GI	g2501812
BLAST score	255
E value	5.0e-22
Match length	51
% identity	98
NCBI Description	(U91509) glycolate oxidase [Arabidopsis thaliana]

Seq. No.	177527
Seq. ID	jC-atXP80C240G20T7s1
Method	BLASTX
NCBI GI	g4510424
BLAST score	632
E value	4.0e-66
Match length	127
% identity	98
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	177528
Seq. ID	jC-atXP80C240N2T7s1
Method	BLASTN
NCBI GI	g2564045
BLAST score	148
E value	1.0e-77
Match length	269

% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	177529
Seq. ID	jC-atXP80C240P2T7s1
Method	BLASTN
NCBI GI	g3128142
BLAST score	482
E value	0.0e+00
Match length	490
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	177530
Seq. ID	jC-atXP81C240J5T7s1
Method	BLASTX
NCBI GI	g4191791
BLAST score	218
E value	9.0e-18
Match length	69
% identity	67
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	177531
Seq. ID	jC-atXP81C240K17T7s1
Method	BLASTN
NCBI GI	g4589122
BLAST score	74
E value	2.0e-33
Match length	246
% identity	87
NCBI Description	Arabidopsis thaliana At14a protein mRNA, complete cds

Seq. No.	177532
Seq. ID	jC-atXP81C240L8T7s1
Method	BLASTN
NCBI GI	g4510360
BLAST score	144
E value	1.0e-75
Match length	168
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	177533
Seq. ID	jC-atXP81C240M3T7s1
Method	BLASTN
NCBI GI	g3068702
BLAST score	234
E value	1.0e-129
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2),

Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	177534
Seq. ID	jC-atXP82C240P16T7b1
Method	BLASTX
NCBI GI	g3138972
BLAST score	1099
E value	1.0e-120
Match length	224
% identity	99
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	177535
Seq. ID	jC-atXP82C240P21T7d3
Method	BLASTX
NCBI GI	g232031
BLAST score	57
E value	2.0e-40
Match length	193
% identity	52
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	177536
Seq. ID	jC-atXP82C240P4T7d3
Method	BLASTX
NCBI GI	g913445
BLAST score	539
E value	6.0e-55
Match length	171
% identity	59
NCBI Description	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No.	177537
Seq. ID	jC-atXP82C241A2T7d3
Method	BLASTN
NCBI GI	g2656024
BLAST score	188
E value	1.0e-101
Match length	574
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	177538
Seq. ID	jC-atXP82CG1C2T7b1
Method	BLASTX
NCBI GI	g1170373
BLAST score	430
E value	3.0e-42

Match length	102
% identity	84
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177539
Seq. ID	jC-atXP82CG1E2T7b1
Method	BLASTN
NCBI GI	g2924654
BLAST score	209
E value	1.0e-113
Match length	347
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]

Seq. No.	177540
Seq. ID	jC-atXP82CG1E2T7d3
Method	BLASTN
NCBI GI	g2924653
BLAST score	240
E value	1.0e-132
Match length	538
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	177541
Seq. ID	jC-atXP82CG1E6T7d3
Method	BLASTX
NCBI GI	g1170373
BLAST score	660
E value	4.0e-69
Match length	149
% identity	88
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177542
Seq. ID	jC-atXP82CG1E7T7d3
Method	BLASTN
NCBI GI	g4467358
BLAST score	47
E value	5.0e-17
Match length	47
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	177543
Seq. ID	jC-atXP82CG1E8T7d3
Method	BLASTN
NCBI GI	g3413510
BLAST score	34

E value	3.0e-09
Match length	42
% identity	95
NCBI Description	Spinacia oleracea mRNA (nuclear-encoded) for chloroplast glucose-6-phosphate isomerase

Seq. No.	177544
Seq. ID	jC-atXP82CG1E9T7d3
Method	BLASTN
NCBI GI	g2618602
BLAST score	53
E value	2.0e-20
Match length	93
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	177545
Seq. ID	jC-atXP82CG1F10T7d3
Method	BLASTX
NCBI GI	g2829918
BLAST score	166
E value	3.0e-11
Match length	98
% identity	47
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	177546
Seq. ID	jC-atXP82CG1F3T7d3
Method	BLASTN
NCBI GI	g4467358
BLAST score	53
E value	1.0e-20
Match length	53
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	177547
Seq. ID	jC-atXP82CG1F8T7d3
Method	BLASTX
NCBI GI	g2760834
BLAST score	519
E value	1.0e-52
Match length	197
% identity	59
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No.	177548
Seq. ID	jC-atXP82CG1G11T7d3
Method	BLASTX
NCBI GI	g4406804
BLAST score	508
E value	3.0e-51
Match length	126
% identity	78

NCBI Description	(AC006304) proline iminopeptidase [Arabidopsis thaliana]
Seq. No.	177549
Seq. ID	jC-atXP82CG1G9T7d3
Method	BLASTX
NCBI GI	g2506139
BLAST score	545
E value	1.0e-55
Match length	157
% identity	68
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]
Seq. No.	177550
Seq. ID	jC-atXP82CG1H11T7d3
Method	BLASTX
NCBI GI	g1710151
BLAST score	1121
E value	1.0e-123
Match length	208
% identity	100
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]
Seq. No.	177551
Seq. ID	jC-atXP82CG1H1T7d3
Method	BLASTX
NCBI GI	g1710151
BLAST score	759
E value	7.0e-88
Match length	209
% identity	73
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]
Seq. No.	177552
Seq. ID	jC-atXP82CG2A12T7b1
Method	BLASTN
NCBI GI	g58066
BLAST score	43
E value	1.0e-14
Match length	74
% identity	92
NCBI Description	pBluescript SK(-) vector DNA, phagemid excised from lambda ZAP
Seq. No.	177553
Seq. ID	jC-atXP82CG2A1T7d3
Method	BLASTN
NCBI GI	g2914688
BLAST score	196
E value	1.0e-106
Match length	457
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	177554

Seq. ID	jC-atXP82CG2A7T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	53
E value	5.0e-21
Match length	57
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177555
Seq. ID	jC-atXP82CG2B10T7d3
Method	BLASTX
NCBI GI	g4587615
BLAST score	707
E value	1.0e-74
Match length	197
% identity	73
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	177556
Seq. ID	jC-atXP82CG2B7T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	4.0e-30
Match length	69
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177557
Seq. ID	jC-atXP82CG2B7T7d3
Method	BLASTN
NCBI GI	g2582640
BLAST score	35
E value	6.0e-10
Match length	39
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177558
Seq. ID	jC-atXP82CG2B8T7b1
Method	BLASTX
NCBI GI	g1170040
BLAST score	322
E value	1.0e-29
Match length	129
% identity	54
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase

[Arabidopsis thaliana]

Seq. No.	177559
Seq. ID	jC-atXP82CG2C1T7d3
Method	BLASTX
NCBI GI	g2997686
BLAST score	696
E value	2.0e-73
Match length	143
% identity	96
NCBI Description	(AF053303) putative transcriptional co-activator [Arabidopsis thaliana] >gi_3513735 (AF080118) contains similarity to RNA polymerase II transcription cofactor p15 [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	177560
Seq. ID	jC-atXP82CG2C2T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	49
E value	4.0e-18
Match length	65
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177561
Seq. ID	jC-atXP82CG2C8T7b1
Method	BLASTX
NCBI GI	g3044214
BLAST score	205
E value	7.0e-16
Match length	89
% identity	51
NCBI Description	(AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	177562
Seq. ID	jC-atXP82CG2D10T7d3
Method	BLASTN
NCBI GI	g4455168
BLAST score	128
E value	2.0e-65
Match length	290
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	177563
Seq. ID	jC-atXP82CG2D2T7d3
Method	BLASTX
NCBI GI	g3913379
BLAST score	126
E value	2.0e-23
Match length	121
% identity	55
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)

>gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	177564
Seq. ID	jC-atXP82CG2E2T7d3
Method	BLASTX
NCBI GI	g3138972
BLAST score	391
E value	6.0e-46
Match length	125
% identity	82
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	177565
Seq. ID	jC-atXP82CG2E7T7b1
Method	BLASTN
NCBI GI	g3492855
BLAST score	36
E value	3.0e-10
Match length	100
% identity	85
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	177566
Seq. ID	jC-atXP82CG2F11T7d3
Method	BLASTN
NCBI GI	g3138971
BLAST score	42
E value	6.0e-14
Match length	87
% identity	95
NCBI Description	Arabidopsis thaliana dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex (LTA1) mRNA, complete cds

Seq. No.	177567
Seq. ID	jC-atXP82CG2F3T7d3
Method	BLASTN
NCBI GI	g4467358
BLAST score	38
E value	1.0e-11
Match length	42
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	177568
Seq. ID	jC-atXP82CG2F6T7b1
Method	BLASTX
NCBI GI	g2146733
BLAST score	445
E value	6.0e-44
Match length	75
% identity	100
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	177569
Seq. ID	jC-atXP82CG2G1T7b1
Method	BLASTX
NCBI GI	g3170241
BLAST score	149
E value	3.0e-09
Match length	55
% identity	45
NCBI Description	(AF042732) TU37B2 [Anopheles gambiae]

Seq. No.	177570
Seq. ID	jC-atXP82CG2G1T7d3
Method	BLASTX
NCBI GI	g3283893
BLAST score	173
E value	2.0e-12
Match length	60
% identity	53
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	177571
Seq. ID	jC-atXP82CG2G3T7b1
Method	BLASTN
NCBI GI	g606949
BLAST score	166
E value	5.0e-88
Match length	500
% identity	89
NCBI Description	Arabidopsis thaliana clone KNAT1 knotted-like homeobox protein gene, partial cds

Seq. No.	177572
Seq. ID	jC-atXP82CG2G3T7d3
Method	BLASTX
NCBI GI	g1170676
BLAST score	394
E value	1.0e-48
Match length	150
% identity	64
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 1 >gi_606950 (U14174) knotted-like homeobox protein [Arabidopsis thaliana] >gi_4689449_gb_AAD27897.1_AC006267_2 (AC006267) KNAT1 homeobox-like protein [Arabidopsis thaliana]

Seq. No.	177573
Seq. ID	jC-atXP83C241A15T7025a1
Method	BLASTN
NCBI GI	g3172156
BLAST score	95
E value	5.0e-46
Match length	216
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177574

Seq. ID	jC-atXP83C241A18T7049a1
Method	BLASTX
NCBI GI	g2088653
BLAST score	189
E value	4.0e-14
Match length	97
% identity	45
NCBI Description	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]

Seq. No.	177575
Seq. ID	jC-atXP83C241A20T7057a1
Method	BLASTX
NCBI GI	g1709203
BLAST score	253
E value	1.0e-21
Match length	66
% identity	67
NCBI Description	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMP 1) (INOSITOL MONOPHOSPHATASE 1) >gi_1098977 (U39444) myo-inositol monophosphatase 1 [Lycopersicon esculentum]

Seq. No.	177576
Seq. ID	jC-atXP83C241A21T7065d1
Method	BLASTX
NCBI GI	g3980396
BLAST score	883
E value	2.0e-95
Match length	164
% identity	99
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	177577
Seq. ID	jC-atXP83C241A22T7073a1
Method	BLASTN
NCBI GI	g2924505
BLAST score	127
E value	5.0e-65
Match length	310
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	177578
Seq. ID	jC-atXP83C241A22T7073d1
Method	BLASTX
NCBI GI	g2924515
BLAST score	348
E value	1.0e-32
Match length	69
% identity	88
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	177579
Seq. ID	jC-atXP83C241A23T7081d1
Method	BLASTX

NCBI GI	g2244866
BLAST score	607
E value	4.0e-63
Match length	133
% identity	87
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177580
Seq. ID	jC-atXP83C241A5T7001d1
Method	BLASTN
NCBI GI	g2351073
BLAST score	47
E value	3.0e-17
Match length	87
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	177581
Seq. ID	jC-atXP83C241K16T7042a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	46
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	177582
Seq. ID	jC-atXP83C241K21T7050a1
Method	BLASTN
NCBI GI	g2642427
BLAST score	66
E value	2.0e-28
Match length	328
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177583
Seq. ID	jC-atXP83C241L11T7066a1
Method	BLASTX
NCBI GI	g3451077
BLAST score	275
E value	3.0e-24
Match length	65
% identity	72
NCBI Description	(AL031326) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	177584
Seq. ID	jC-atXP83C241L21T7074a1
Method	BLASTX
NCBI GI	g1709203
BLAST score	237
E value	9.0e-20
Match length	64

% identity	64
NCBI Description	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMP 1) (INOSITOL MONOPHOSPHATASE 1) >gi_1098977 (U39444) myo-inositol monophosphatase 1 [Lycopersicon esculentum]

Seq. No.	177585
Seq. ID	jC-atXP83C241L3T7058d1
Method	BLASTX
NCBI GI	g4586256
BLAST score	555
E value	5.0e-57
Match length	156
% identity	72
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	177586
Seq. ID	jC-atXP83C241M17T7019a1
Method	BLASTX
NCBI GI	g2895510
BLAST score	266
E value	4.0e-23
Match length	94
% identity	57
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	177587
Seq. ID	jC-atXP83C241M17T7019d1
Method	BLASTX
NCBI GI	g2895510
BLAST score	798
E value	2.0e-85
Match length	174
% identity	92
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	177588
Seq. ID	jC-atXP83CG2G7T7048d1
Method	BLASTN
NCBI GI	g4159708
BLAST score	344
E value	0.0e+00
Match length	400
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	177589
Seq. ID	jC-atXP83CG2G8T7056a1
Method	BLASTN
NCBI GI	g2668397
BLAST score	43
E value	8.0e-15
Match length	51
% identity	98

NCBI Description	Mus musculus mGLT-1 mRNA, complete cds
Seq. No.	177590
Seq. ID	jC-atXP83CG3A4T7043a1
Method	BLASTX
NCBI GI	g3135611
BLAST score	54
E value	9.0e-32
Match length	124
% identity	62
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]
Seq. No.	177591
Seq. ID	jC-atXP83CG3A6T7059a1
Method	BLASTX
NCBI GI	g3746059
BLAST score	371
E value	2.0e-35
Match length	134
% identity	59
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	177592
Seq. ID	jC-atXP83CG3A7T7067d1
Method	BLASTX
NCBI GI	g2369714
BLAST score	144
E value	8.0e-09
Match length	44
% identity	64
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	177593
Seq. ID	jC-atXP83CG3B3T7020a1
Method	BLASTX
NCBI GI	g4193388
BLAST score	457
E value	1.0e-45
Match length	129
% identity	68
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	177594
Seq. ID	jC-atXP83CG3B7T7044a1
Method	BLASTN
NCBI GI	g4106339
BLAST score	279
E value	1.0e-155
Match length	399
% identity	92
NCBI Description	Arabidopsis thaliana protein phosphatase 2A regulatory subunit isoform B' delta mRNA, complete cds
Seq. No.	177595

Seq. ID	jC-atXP83CG3B7T7044d1
Method	BLASTN
NCBI GI	g4106339
BLAST score	185
E value	2.0e-99
Match length	345
% identity	92
NCBI Description	Arabidopsis thaliana protein phosphatase 2A regulatory subunit isoform B' delta mRNA, complete cds

Seq. No.	177596
Seq. ID	jC-atXP83CG3B9T7052a1
Method	BLASTN
NCBI GI	g1399264
BLAST score	166
E value	3.0e-88
Match length	430
% identity	85
NCBI Description	Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 9 (CPK9) mRNA, complete cds

Seq. No.	177597
Seq. ID	jC-atXP83CG3B9T7052d1
Method	BLASTX
NCBI GI	g1399265
BLAST score	315
E value	1.0e-45
Match length	145
% identity	66
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	177598
Seq. ID	jC-atXP83CG3C12T7021a1
Method	BLASTN
NCBI GI	g4314354
BLAST score	46
E value	1.0e-16
Match length	138
% identity	80
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177599
Seq. ID	jC-atXP83CG3C12T7021d1
Method	BLASTN
NCBI GI	g4314354
BLAST score	44
E value	2.0e-15
Match length	72
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177600
Seq. ID	jC-atXP83CG3C6T7092d1
Method	BLASTX

NCBI GI	g4006898
BLAST score	67
E value	5.2e+00
Match length	87
% identity	38
NCBI Description	(Z99708) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	177601
Seq. ID	jC-atXP83CG3C8T7013a1
Method	BLASTN
NCBI GI	g3063438
BLAST score	218
E value	1.0e-119
Match length	335
% identity	93
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	177602
Seq. ID	jC-atXP83CG3D5T7045a1
Method	BLASTN
NCBI GI	g57923
BLAST score	52
E value	4.0e-20
Match length	67
% identity	94
NCBI Description	M.musculus Flk-1 mRNA

Seq. No.	177603
Seq. ID	jC-atXP83CG3D7T7061a1
Method	BLASTN
NCBI GI	g2264309
BLAST score	318
E value	1.0e-179
Match length	426
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	177604
Seq. ID	jC-atXP83CG3D7T7061d1
Method	BLASTN
NCBI GI	g2264309
BLAST score	202
E value	1.0e-109
Match length	290
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	177605
Seq. ID	jC-atXP83CG3D8T7069a1
Method	BLASTX
NCBI GI	g3122271
BLAST score	131
E value	2.0e-07

Match length	136
% identity	30
NCBI Description	IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (KAP ALPHA) >gi_2154717_emb_CAA70703_ (Y09511) Kap alpha protein [Arabidopsis thaliana]

Seq. No.	177606
Seq. ID	jC-atXP83CG3E4T7022a1
Method	BLASTN
NCBI GI	g2668397
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Mus musculus mGLT-1 mRNA, complete cds

Seq. No.	177607
Seq. ID	jC-atXP83CG3E4T7022d1
Method	BLASTX
NCBI GI	g730220
BLAST score	174
E value	2.0e-12
Match length	116
% identity	38
NCBI Description	OXALYL-COA DECARBOXYLASE >gi_1086099_pir__A55219 oxalyl-CoA decarboxylase (EC 4.1.1.8) - Oxalobacter formigenes >gi_150447 (M77128) oxalyl-CoA decarboxylase [Oxalobacter formigenes]

Seq. No.	177608
Seq. ID	jC-atXP83CG3E7T7046a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	387
E value	0.0e+00
Match length	424
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177609
Seq. ID	jC-atXP83CG3F10T7047d1
Method	BLASTX
NCBI GI	g2829923
BLAST score	316
E value	5.0e-29
Match length	101
% identity	63
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	177610
Seq. ID	jC-atXP83CG3F7T7031d1
Method	BLASTN
NCBI GI	g4335744
BLAST score	359
E value	0.0e+00

Match length	470
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177611
Seq. ID	jC-atXP83CG3G11T7016d1
Method	BLASTX
NCBI GI	g2341034
BLAST score	761
E value	4.0e-81
Match length	152
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	177612
Seq. ID	jC-atXP83CG3G12T7024d1
Method	BLASTX
NCBI GI	g2341034
BLAST score	336
E value	2.0e-31
Match length	149
% identity	54
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	177613
Seq. ID	jC-atXP83CG3G2T7063d1
Method	BLASTX
NCBI GI	g3287270
BLAST score	246
E value	2.0e-32
Match length	118
% identity	63
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	177614
Seq. ID	jC-atXP83CG3G4T7079a1
Method	BLASTX
NCBI GI	g2244792
BLAST score	175
E value	2.0e-12
Match length	46
% identity	65
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	177615
Seq. ID	jC-atXP83CG3H2T7040d1
Method	BLASTX
NCBI GI	g1706130
BLAST score	178
E value	8.0e-13
Match length	86
% identity	48
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No.	177616
Seq. ID	jC-atXP84CG4C7T7b1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	5.0e-10
Match length	59
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	177617
Seq. ID	jC-atXP84CG4C9T7b1
Method	BLASTN
NCBI GI	g3985950
BLAST score	84
E value	3.0e-39
Match length	353
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]

Seq. No.	177618
Seq. ID	jC-atXP84CG5A10T7b1
Method	BLASTX
NCBI GI	g132074
BLAST score	540
E value	3.0e-55
Match length	139
% identity	77
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	177619
Seq. ID	jC-atXP84CG5A1T7b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	166
E value	2.0e-11
Match length	75
% identity	49
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	177620
Seq. ID	jC-atXP84CG5A2T7b1
Method	BLASTX
NCBI GI	g2341031
BLAST score	524
E value	2.0e-53
Match length	122
% identity	91
NCBI Description	(AC000104) F19P19.10 [Arabidopsis thaliana]

Seq. No.	177621
Seq. ID	jC-atXP84CG5B1T7b1
Method	BLASTN
NCBI GI	g4756963
BLAST score	54
E value	2.0e-21
Match length	233
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	177622
Seq. ID	jC-atXP84CG5B5T7b1
Method	BLASTN
NCBI GI	g3413696
BLAST score	110
E value	9.0e-55
Match length	274
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177623
Seq. ID	jC-atXP84CG5B6T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	39
E value	2.0e-12
Match length	83
% identity	86
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177624
Seq. ID	jC-atXP84CG5C11T7b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	281
E value	7.0e-25
Match length	97
% identity	64
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	177625
Seq. ID	jC-atXP84CG5C8T7b1
Method	BLASTX
NCBI GI	g3043415
BLAST score	371
E value	2.0e-35
Match length	94
% identity	78
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	177626
Seq. ID	jC-atXP84CG5D12T7b1
Method	BLASTN
NCBI GI	g2338549

BLAST score	38
E value	9.0e-12
Match length	46
% identity	96
NCBI Description	Sparus aurata keratin mRNA, partial cds

Seq. No.	177627
Seq. ID	jC-atXP84CG5E11T7b1
Method	BLASTN
NCBI GI	g1017822
BLAST score	44
E value	2.0e-15
Match length	67
% identity	93
NCBI Description	Human RNA polymerase II subunit (hsRPB8) mRNA, complete cds

Seq. No.	177628
Seq. ID	jC-atXP84CG5E12T7b1
Method	BLASTN
NCBI GI	g4220643
BLAST score	194
E value	1.0e-105
Match length	322
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	177629
Seq. ID	jC-atXP84CG5E5T7b1
Method	BLASTX
NCBI GI	g3176687
BLAST score	165
E value	5.0e-25
Match length	118
% identity	64
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	177630
Seq. ID	jC-atXP84CG5E6T7b1
Method	BLASTX
NCBI GI	g1170373
BLAST score	464
E value	2.0e-46
Match length	128
% identity	74
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177631
Seq. ID	jC-atXP84CG5F7T7b1
Method	BLASTX
NCBI GI	g3367596

BLAST score	519
E value	9.0e-53
Match length	117
% identity	86
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	177632
Seq. ID	jC-atXP84CG5G11T7b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	209
E value	2.0e-16
Match length	77
% identity	52
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	177633
Seq. ID	jC-atXP84CG5G7T7b1
Method	BLASTN
NCBI GI	g166901
BLAST score	116
E value	2.0e-58
Match length	323
% identity	90
NCBI Description	Arabidopsis thaliana beta-5 tubulin (TUB5) gene, complete cds

Seq. No.	177634
Seq. ID	jC-atXP85C241C15T7b1
Method	BLASTX
NCBI GI	g3435279
BLAST score	286
E value	3.0e-25
Match length	156
% identity	49
NCBI Description	(AF082391) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	177635
Seq. ID	jC-atXP85C241D22T7b1
Method	BLASTX
NCBI GI	g1363492
BLAST score	303
E value	3.0e-41
Match length	174
% identity	57
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	177636
Seq. ID	jC-atXP85CG4D6T7b1
Method	BLASTX
NCBI GI	g2760086

BLAST score	301
E value	5.0e-27
Match length	71
% identity	47
NCBI Description	(Y16046) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	177637
Seq. ID	jC-atXP85CG4D8T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	60
E value	7.0e-25
Match length	80
% identity	94
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177638
Seq. ID	jC-atXP85CG4E9T7b1
Method	BLASTN
NCBI GI	g4538895
BLAST score	414
E value	0.0e+00
Match length	494
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	177639
Seq. ID	jC-atXP85CG4F3T7b1
Method	BLASTN
NCBI GI	g2252848
BLAST score	229
E value	1.0e-126
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	177640
Seq. ID	jC-atXP85CG7G12T7b1
Method	BLASTX
NCBI GI	g3122858
BLAST score	870
E value	9.0e-94
Match length	194
% identity	91
NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No.	177641
Seq. ID	jC-atXP85CG7H11T7b1
Method	BLASTX
NCBI GI	g3319350
BLAST score	701
E value	6.0e-74

Match length	133
% identity	98
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	177642
Seq. ID	jC-atXP85CG8B1T7b1
Method	BLASTN
NCBI GI	g572605
BLAST score	72
E value	4.0e-32
Match length	96
% identity	95
NCBI Description	B.napus ACCg8 gene

Seq. No.	177643
Seq. ID	jC-atXP85CG8B5T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	64
E value	4.0e-27
Match length	76
% identity	96
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177644
Seq. ID	jC-atXP85CG8B7T7b1
Method	BLASTX
NCBI GI	g2498277
BLAST score	196
E value	1.0e-14
Match length	207
% identity	6
NCBI Description	CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II) >gi_2136733_pir__I46014 cylicin II - bovine >gi_757754_emb_CAA86753_ (Z46789) cylicin II [Bos taurus]

Seq. No.	177645
Seq. ID	jC-atXP85CG8C3T7b1
Method	BLASTX
NCBI GI	g3776561
BLAST score	276
E value	4.0e-24
Match length	129
% identity	53
NCBI Description	(AC005388) Identical to DNA for acyl carrier protein (ACP) gene A2 gb_X57699 from A. thaliana. ESTs gb_W43252, gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955 come from this gene. [Arabidopsis thaliana]

Seq. No.	177646
Seq. ID	jC-atXP86CF10d2
Method	BLASTX
NCBI GI	g4115943
BLAST score	169
E value	1.0e-11
Match length	186
% identity	20

NCBI Description	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]

Seq. No.	177647
Seq. ID	jC-atXP86CG10A10T7b1
Method	BLASTX
NCBI GI	g2143227
BLAST score	289
E value	2.0e-35
Match length	81
% identity	93
NCBI Description	(Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No.	177648
Seq. ID	jC-atXP86CG10A8T7d2
Method	BLASTN
NCBI GI	g1890153
BLAST score	208
E value	1.0e-113
Match length	459
% identity	87
NCBI Description	A.thaliana mRNA for alpha-mannosidase precursor

Seq. No.	177649
Seq. ID	jC-atXP86CG10A9T7b1
Method	BLASTX
NCBI GI	g131011
BLAST score	82
E value	3.4e-01
Match length	314
% identity	19
NCBI Description	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-D)

Seq. No.	177650
Seq. ID	jC-atXP86CG10B7T7b1
Method	BLASTN
NCBI GI	g4662640
BLAST score	221
E value	1.0e-121
Match length	448
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	177651
Seq. ID	jC-atXP86CG10B7T7d2
Method	BLASTX
NCBI GI	g4662644
BLAST score	371
E value	3.0e-35
Match length	152
% identity	53
NCBI Description	(AC006429) unknown protein [Arabidopsis thaliana]

Seq. No.	177652
Seq. ID	jC-atXP86CG10C3T7b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	54
E value	4.0e-21
Match length	70
% identity	94
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	177653
Seq. ID	jC-atXP86CG10C7T7d2
Method	BLASTX
NCBI GI	g2129579
BLAST score	1026
E value	1.0e-112
Match length	215
% identity	94
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	177654
Seq. ID	jC-atXP86CG10D3T7d2
Method	BLASTX
NCBI GI	g113026
BLAST score	356
E value	2.0e-33
Match length	106
% identity	69
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	177655
Seq. ID	jC-atXP86CG10D8T7d2
Method	BLASTX
NCBI GI	g1906826
BLAST score	368
E value	5.0e-54
Match length	186
% identity	62
NCBI Description	(Y11827) heat shock protein [Arabidopsis thaliana]

Seq. No.	177656
Seq. ID	jC-atXP86CG4F7T7b1
Method	BLASTX
NCBI GI	g3643598
BLAST score	86
E value	7.0e-30
Match length	101
% identity	67
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	177657
Seq. ID	jC-atXP86CG4F7T7d2
Method	BLASTN
NCBI GI	g3643588
BLAST score	284
E value	1.0e-158
Match length	559
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177658
Seq. ID	jC-atXP86CG4G2T7d2
Method	BLASTX
NCBI GI	g231683
BLAST score	264
E value	7.0e-24
Match length	101
% identity	59
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	177659
Seq. ID	jC-atXP86CG4G5T7b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	343
E value	0.0e+00
Match length	677
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	177660
Seq. ID	jC-atXP86CG4G9T7b1
Method	BLASTN
NCBI GI	g2244950
BLAST score	92
E value	6.0e-44
Match length	409
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177661
Seq. ID	jC-atXP86CG4G9T7d2
Method	BLASTX
NCBI GI	g2244979
BLAST score	247
E value	1.0e-20
Match length	163
% identity	44
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	177662
Seq. ID	jC-atXP86CG8C12T7b1
Method	BLASTN
NCBI GI	g639675
BLAST score	35
E value	1.0e-09
Match length	47
% identity	96
NCBI Description	Oryzias latipes mRNA for photolyase, complete cds

Seq. No.	177663
Seq. ID	jC-atXP86CG8C4T7d2
Method	BLASTX
NCBI GI	g2244750
BLAST score	252
E value	3.0e-21
Match length	72
% identity	78
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	177664
Seq. ID	jC-atXP86CG8C6T7b1
Method	BLASTX
NCBI GI	g1160355
BLAST score	172
E value	1.0e-11
Match length	353
% identity	7
NCBI Description	(U33058) UNC-89 [Caenorhabditis elegans]

Seq. No.	177665
Seq. ID	jC-atXP86CG8C7T7b1
Method	BLASTX
NCBI GI	g2736513
BLAST score	160
E value	2.0e-10
Match length	266
% identity	12
NCBI Description	(AF039052) No definition line found [Caenorhabditis elegans]

Seq. No.	177666
Seq. ID	jC-atXP86CG8D10T7b1
Method	BLASTN
NCBI GI	g984755
BLAST score	55
E value	8.0e-22
Match length	63
% identity	97
NCBI Description	O.sativa mRNA for chilling-inducible protein

Seq. No.	177667
Seq. ID	jC-atXP86CG8D11T7d2
Method	BLASTN

NCBI GI	g4159704
BLAST score	95
E value	9.0e-46
Match length	323
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	177668
Seq. ID	jC-atXP86CG8D4T7d2
Method	BLASTX
NCBI GI	g1170034
BLAST score	369
E value	9.0e-52
Match length	119
% identity	92
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	177669
Seq. ID	jC-atXP86CG8E1T7b1
Method	BLASTX
NCBI GI	g3643598
BLAST score	482
E value	3.0e-48
Match length	105
% identity	84
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	177670
Seq. ID	jC-atXP86CG8E5T7b1
Method	BLASTN
NCBI GI	g3785968
BLAST score	198
E value	1.0e-107
Match length	415
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177671
Seq. ID	jC-atXP86CG8E5T7d2
Method	BLASTX
NCBI GI	g3785991
BLAST score	507
E value	3.0e-51
Match length	148
% identity	71
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	177672
Seq. ID	jC-atXP86CG9D11T7d2

Method	BLASTX
NCBI GI	g2827630
BLAST score	190
E value	4.0e-54
Match length	183
% identity	66
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	177673
Seq. ID	jC-atXP86CG9D1T7d2
Method	BLASTN
NCBI GI	g2828278
BLAST score	163
E value	3.0e-86
Match length	541
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	177674
Seq. ID	jC-atXP86CG9D6T7b1
Method	BLASTN
NCBI GI	g4115930
BLAST score	180
E value	2.0e-96
Match length	320
% identity	97
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	177675
Seq. ID	jC-atXP86CG9E6T7d2
Method	BLASTX
NCBI GI	g3549639
BLAST score	1127
E value	1.0e-124
Match length	242
% identity	88
NCBI Description	(AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq. No.	177676
Seq. ID	jC-atXP86CG9E9T7d2
Method	BLASTN
NCBI GI	g4191760
BLAST score	100
E value	1.0e-48
Match length	397
% identity	88
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	177677
Seq. ID	jC-atXP86CG9F1T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	8.0e-22
Match length	59

% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177678
Seq. ID	jC-atXP86CG9F1T7d2
Method	BLASTN
NCBI GI	g1786137
BLAST score	34
E value	3.0e-09
Match length	38
% identity	97
NCBI Description	Petunia hybrida mRNA for PEThy;ZPT3-1, complete cds

Seq. No.	177679
Seq. ID	jC-atXP86CG9F4T7b1
Method	BLASTX
NCBI GI	g3096931
BLAST score	169
E value	2.0e-13
Match length	80
% identity	61
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	177680
Seq. ID	jC-atXP86CG9F7T7d2
Method	BLASTX
NCBI GI	g2117612
BLAST score	97
E value	3.0e-09
Match length	138
% identity	38
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	177681
Seq. ID	jC-atXP86CG9G11T7b1
Method	BLASTN
NCBI GI	g559342
BLAST score	59
E value	2.0e-24
Match length	63
% identity	98
NCBI Description	Human TBXAS1 gene for thromboxane synthase, exon

Seq. No.	177682
Seq. ID	jC-atXP86CG9G6T7b1
Method	BLASTX
NCBI GI	g4803836
BLAST score	598
E value	1.0e-105
Match length	232
% identity	86
NCBI Description	(AB026987) a dynamin-like protein ADL3 [Arabidopsis thaliana]

Seq. No. 177683

Seq. ID	jC-atXP86CG9G7T7b1
Method	BLASTN
NCBI GI	g416320
BLAST score	38
E value	1.0e-11
Match length	54
% identity	93
NCBI Description	Yeast centromere vector pRS415 with LEU2 marker, complete sequence

Seq. No.	177684
Seq. ID	jC-atXP86CG9H10T7d2
Method	BLASTN
NCBI GI	g4220641
BLAST score	330
E value	0.0e+00
Match length	510
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	177685
Seq. ID	jC-atXP86CG9H11T7b1
Method	BLASTN
NCBI GI	g2828278
BLAST score	237
E value	1.0e-130
Match length	464
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	177686
Seq. ID	jC-atXP86CG9H11T7d2
Method	BLASTN
NCBI GI	g2828278
BLAST score	144
E value	7.0e-75
Match length	583
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	177687
Seq. ID	jC-atXP86CG9H1T7b1
Method	BLASTX
NCBI GI	g450880
BLAST score	383
E value	9.0e-37
Match length	90
% identity	84
NCBI Description	(X77199) heat shock cognate 70-1 [Arabidopsis thaliana]

Seq. No.	177688
Seq. ID	jC-atXP87C244F6T7b1
Method	BLASTN
NCBI GI	g3849811

BLAST score	148
E value	2.0e-77
Match length	200
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177689
Seq. ID	jC-atXP87C244G4T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	76
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177690
Seq. ID	jC-atXP87C244H16T7b1
Method	BLASTX
NCBI GI	g3608261
BLAST score	529
E value	6.0e-54
Match length	106
% identity	95
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	177691
Seq. ID	jC-atXP87CG6D4T7b1
Method	BLASTN
NCBI GI	g3776000
BLAST score	247
E value	1.0e-136
Match length	353
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12

Seq. No.	177692
Seq. ID	jC-atXP87CG8E12T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177693
Seq. ID	jC-atXP87CG8F6T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	43
E value	8.0e-15
Match length	99
% identity	90

NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177694
Seq. ID	jC-atXP87CG8G10T7b1
Method	BLASTX
NCBI GI	g2062157
BLAST score	214
E value	5.0e-17
Match length	76
% identity	30
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	177695
Seq. ID	jC-atXP87CG8G9T7b1
Method	BLASTX
NCBI GI	g541858
BLAST score	462
E value	4.0e-46
Match length	89
% identity	92
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	177696
Seq. ID	jC-atXP88C241N24T7s1
Method	BLASTX
NCBI GI	g3204125
BLAST score	223
E value	3.0e-18
Match length	52
% identity	85
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]

Seq. No.	177697
Seq. ID	jC-atXP88C241O20T7d1
Method	BLASTX
NCBI GI	g115783
BLAST score	607
E value	3.0e-63
Match length	114
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	177698
Seq. ID	jC-atXP88C241P2T7s1
Method	BLASTX
NCBI GI	g4680705
BLAST score	162
E value	4.0e-11
Match length	50

% identity	58
NCBI Description	(AF132967) CGI-33 protein [Homo sapiens]

Seq. No.	177699
Seq. ID	jC-atXP88C242C2T7s1
Method	BLASTN
NCBI GI	g4589439
BLAST score	369
E value	0.0e+00
Match length	377
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	177700
Seq. ID	jC-atXP88C242H10T7s1
Method	BLASTN
NCBI GI	g2244829
BLAST score	168
E value	1.0e-89
Match length	321
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177701
Seq. ID	jC-atXP88C242J14T7s1
Method	BLASTX
NCBI GI	g1769849
BLAST score	157
E value	1.0e-10
Match length	53
% identity	64
NCBI Description	(Z75663) chlorophyll a/b binding protein [Apium graveolens]

Seq. No.	177702
Seq. ID	jC-atXP88C244I17T7s1
Method	BLASTN
NCBI GI	g3128142
BLAST score	408
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	177703
Seq. ID	jC-atXP88C244K16T7s1
Method	BLASTX
NCBI GI	g4567208
BLAST score	179
E value	7.0e-13
Match length	103
% identity	45
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	177704

Seq. ID	jC-atXP89C242K4T7s1
Method	BLASTN
NCBI GI	g4455348
BLAST score	246
E value	1.0e-136
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	177705
Seq. ID	jC-atXP89C242K7T7049d1
Method	BLASTN
NCBI GI	g2264317
BLAST score	117
E value	6.0e-59
Match length	310
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	177706
Seq. ID	jC-atXP89C242L11T7s1
Method	BLASTX
NCBI GI	g1134882
BLAST score	320
E value	1.0e-29
Match length	59
% identity	92
NCBI Description	(Z68291) cysteine protease [Pisum sativum]

Seq. No.	177707
Seq. ID	jC-atXP89C242M4T7s1
Method	BLASTN
NCBI GI	g4490717
BLAST score	61
E value	4.0e-26
Match length	137
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	177708
Seq. ID	jC-atXP89C244L15T7066d1
Method	BLASTN
NCBI GI	g3367500
BLAST score	324
E value	0.0e+00
Match length	384
% identity	96
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	177709
Seq. ID	jC-atXP89C244M23T7s1
Method	BLASTX
NCBI GI	g4262157

BLAST score	155
E value	2.0e-10
Match length	64
% identity	48
NCBI Description	(AC005275) putative calmodulin [Arabidopsis thaliana]

Seq. No.	177710
Seq. ID	jC-atXP89C244N2T7s1
Method	BLASTN
NCBI GI	g16270
BLAST score	73
E value	6.0e-33
Match length	283
% identity	86
NCBI Description	A.thaliana enolase gene

Seq. No.	177711
Seq. ID	jC-atXP89C244O21T7019d1
Method	BLASTN
NCBI GI	g3005688
BLAST score	212
E value	1.0e-115
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana AT4 mRNA sequence

Seq. No.	177712
Seq. ID	jC-atXP89C244O21T7s1
Method	BLASTN
NCBI GI	g3005688
BLAST score	102
E value	5.0e-50
Match length	267
% identity	92
NCBI Description	Arabidopsis thaliana AT4 mRNA sequence

Seq. No.	177713
Seq. ID	jC-atXP89C244O24T7027d1
Method	BLASTN
NCBI GI	g3763915
BLAST score	343
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177714
Seq. ID	jC-atXP89C244P12T7051d1
Method	BLASTX
NCBI GI	g4406759
BLAST score	246
E value	8.0e-21
Match length	94
% identity	50
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177715
Seq. ID	jC-atXP89C244P21T7075d1
Method	BLASTX
NCBI GI	g2281629
BLAST score	110
E value	8.0e-75
Match length	141
% identity	98
NCBI Description	(AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana]

Seq. No.	177716
Seq. ID	jC-atXP89C244P6T7043d1
Method	BLASTN
NCBI GI	g3449320
BLAST score	378
E value	0.0e+00
Match length	476
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	177717
Seq. ID	jC-atXP89C245C12T7079d1
Method	BLASTX
NCBI GI	g1172872
BLAST score	123
E value	3.0e-60
Match length	159
% identity	76
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	177718
Seq. ID	jC-atXP89C245C13T7087d1
Method	BLASTX
NCBI GI	g4680498
BLAST score	281
E value	7.0e-25
Match length	142
% identity	36
NCBI Description	(AF119222) TIA-1 related protein [Oryza sativa]

Seq. No.	177719
Seq. ID	jC-atXP89C245D1T7024d1
Method	BLASTX
NCBI GI	g417103
BLAST score	629
E value	1.0e-65
Match length	130
% identity	98
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	177720
Seq. ID	jC-atXP89C245D8T7048d1
Method	BLASTX
NCBI GI	g2129726
BLAST score	291
E value	4.0e-53
Match length	114
% identity	100
NCBI Description	RNA polymerase II third largest chain RPB35.5A - Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No.	177721
Seq. ID	jC-atXP89C245F3T7088d1
Method	BLASTX
NCBI GI	g3176714
BLAST score	271
E value	2.0e-29
Match length	84
% identity	82
NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No.	177722
Seq. ID	jC-atXP89CG2015d1
Method	BLASTN
NCBI GI	g4589428
BLAST score	37
E value	3.0e-11
Match length	251
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	177723
Seq. ID	jC-atXP89CG6A8T7092d1
Method	BLASTN

NCBI GI	g4159709
BLAST score	71
E value	2.0e-31
Match length	336
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	177724
Seq. ID	jC-atXP89CG6B3T7005d1
Method	BLASTX
NCBI GI	g2791278
BLAST score	354
E value	2.0e-33
Match length	152
% identity	46
NCBI Description	(Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No.	177725
Seq. ID	jC-atXP89CG6B6T7021d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	177726
Seq. ID	jC-atXP89CG6B9T7037d1
Method	BLASTX
NCBI GI	g4099090
BLAST score	218
E value	5.0e-20
Match length	121
% identity	45
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	177727
Seq. ID	jC-atXP89CG6C3T7053d1
Method	BLASTX
NCBI GI	g1170373
BLAST score	480
E value	3.0e-48
Match length	109
% identity	88
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177728
Seq. ID	jC-atXP89CG6C9T7085d1
Method	BLASTN
NCBI GI	g2924651
BLAST score	260
E value	1.0e-144

Match length	471
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	177729
Seq. ID	jC-atXP89CG6D6T7014d1
Method	BLASTN
NCBI GI	g984051
BLAST score	52
E value	4.0e-20
Match length	98
% identity	94
NCBI Description	A.thaliana mRNA for thioglucoside glucohydrolase

Seq. No.	177730
Seq. ID	jC-atXP89CG6D9T7030d1
Method	BLASTN
NCBI GI	g2341023
BLAST score	62
E value	4.0e-26
Match length	210
% identity	82
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177731
Seq. ID	jC-atXP89CH5A1T7007d1
Method	BLASTX
NCBI GI	g419760
BLAST score	148
E value	2.0e-09
Match length	73
% identity	52
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	177732
Seq. ID	jC-atXP89CH5A5T7039d1
Method	BLASTN
NCBI GI	g4263642
BLAST score	131
E value	2.0e-67
Match length	233
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T13H18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177733
Seq. ID	jC-atXP8C92G8T7d1
Method	BLASTN
NCBI GI	g3150396
BLAST score	111
E value	9.0e-56
Match length	167
% identity	92

NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177734
Seq. ID	jC-atXP8C92K1T7d1
Method	BLASTX
NCBI GI	g4651204
BLAST score	181
E value	3.0e-13
Match length	52
% identity	54
NCBI Description	(AB026262) ring finger protein [Cicer arietinum]

Seq. No.	177735
Seq. ID	jC-atXP8C92M10T7d1
Method	BLASTN
NCBI GI	g4220637
BLAST score	51
E value	1.0e-19
Match length	83
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	177736
Seq. ID	jC-atXP8C92M9T7d1
Method	BLASTX
NCBI GI	g4107101
BLAST score	589
E value	5.0e-61
Match length	116
% identity	99
NCBI Description	(AB015142) AHP2 [Arabidopsis thaliana] >gi_4156241_dbj_BAA37110_ (AB012568) ATHP1 [Arabidopsis thaliana]

Seq. No.	177737
Seq. ID	jC-atXP8C92M9T7s1
Method	BLASTX
NCBI GI	g4107101
BLAST score	779
E value	3.0e-83
Match length	156
% identity	99
NCBI Description	(AB015142) AHP2 [Arabidopsis thaliana] >gi_4156241_dbj_BAA37110_ (AB012568) ATHP1 [Arabidopsis thaliana]

Seq. No.	177738
Seq. ID	jC-atXP8C92N8T7s1
Method	BLASTN
NCBI GI	g3790580
BLAST score	166
E value	2.0e-88
Match length	286
% identity	90
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHB1a mRNA,

complete cds

Seq. No.	177739
Seq. ID	jC-atXP90C242O3T7s2
Method	BLASTX
NCBI GI	g2062169
BLAST score	437
E value	3.0e-43
Match length	122
% identity	49
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	177740
Seq. ID	jC-atXP90C245F14T7s2
Method	BLASTN
NCBI GI	g3420042
BLAST score	380
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177741
Seq. ID	jC-atXP90C245I22T7s2
Method	BLASTN
NCBI GI	g2689438
BLAST score	50
E value	4.0e-19
Match length	234
% identity	82
NCBI Description	Arabidopsis thaliana BAC F24O1 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177742
Seq. ID	jC-atXP90C245M2T7s2
Method	BLASTX
NCBI GI	g510876
BLAST score	414
E value	1.0e-40
Match length	98
% identity	83
NCBI Description	(X80051) NADP dependent malic enzyme [Phaseolus vulgaris]

Seq. No.	177743
Seq. ID	jC-atXP90C245N10T7s2
Method	BLASTN
NCBI GI	g3046853
BLAST score	150
E value	4.0e-79
Match length	198
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No. 177744

Seq. ID	jC-atXP90C245O22T7d2
Method	BLASTN
NCBI GI	g4163996
BLAST score	98
E value	7.0e-48
Match length	146
% identity	89
NCBI Description	Arabidopsis thaliana alpha-xylosidase precursor (XYL1) mRNA, partial cds

Seq. No.	177745
Seq. ID	jC-atXP90C246E12T7s2
Method	BLASTN
NCBI GI	g4115370
BLAST score	44
E value	2.0e-15
Match length	120
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177746
Seq. ID	jC-atXP90C246F18T7d2
Method	BLASTX
NCBI GI	g3123296
BLAST score	219
E value	6.0e-18
Match length	43
% identity	100
NCBI Description	CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED >gi_598067 (L34546) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	177747
Seq. ID	jC-atXP90C246G20T7s2
Method	BLASTN
NCBI GI	g2160155
BLAST score	136
E value	2.0e-70
Match length	275
% identity	90
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177748
Seq. ID	jC-atXP91C246I24T7d1
Method	BLASTN
NCBI GI	g3152602
BLAST score	90
E value	3.0e-43
Match length	202
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177749
Seq. ID	jC-atXP91C246J6T7b1
Method	BLASTX

NCBI GI	g2191138
BLAST score	726
E value	7.0e-77
Match length	145
% identity	100
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	177750
Seq. ID	jC-atXP91C247C14T7b1
Method	BLASTX
NCBI GI	g4539456
BLAST score	1259
E value	1.0e-139
Match length	231
% identity	98
NCBI Description	(AL049500) osmotin precursor [Arabidopsis thaliana]

Seq. No.	177751
Seq. ID	jC-atXP91C247G15T7b1
Method	BLASTX
NCBI GI	g1170034
BLAST score	605
E value	6.0e-82
Match length	161
% identity	96
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	177752
Seq. ID	jC-atXP91CG6H1T7b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	419
E value	7.0e-41
Match length	166
% identity	54
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	177753
Seq. ID	jC-atXP91CH1C10T7b1
Method	BLASTN
NCBI GI	g3283989
BLAST score	50
E value	1.0e-18
Match length	50
% identity	100
NCBI Description	Cloning vector pCMVTAG2b, complete sequence

Seq. No.	177754
Seq. ID	jC-atXP91CH1C12T7b1
Method	BLASTX

NCBI GI	g1169598
BLAST score	317
E value	5.0e-29
Match length	149
% identity	46
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	177755
Seq. ID	jC-atXP91CH1C8T7b1
Method	BLASTN
NCBI GI	g4582428
BLAST score	75
E value	1.0e-33
Match length	238
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	177756
Seq. ID	jC-atXP91CH1E3T7b1
Method	BLASTN
NCBI GI	g3492855
BLAST score	250
E value	1.0e-138
Match length	645
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	177757
Seq. ID	jC-atXP92C246M18T7081d1
Method	BLASTX
NCBI GI	g3928099
BLAST score	110
E value	7.0e-14
Match length	171
% identity	17
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	177758
Seq. ID	jC-atXP92C246N21T7004d1
Method	BLASTX
NCBI GI	g1732570
BLAST score	773
E value	2.0e-82
Match length	151
% identity	97
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	177759
Seq. ID	jC-atXP92C249A17T7075d1
Method	BLASTX
NCBI GI	g119975
BLAST score	607
E value	6.0e-63

Match length	148
% identity	84
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	177760
Seq. ID	jC-atXP92C249B14T7013d1
Method	BLASTX
NCBI GI	g3819710
BLAST score	937
E value	1.0e-101
Match length	183
% identity	94
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	177761
Seq. ID	jC-atXP92C249C3T7037d1
Method	BLASTX
NCBI GI	g1934726
BLAST score	900
E value	2.0e-97
Match length	179
% identity	99
NCBI Description	(U95034) germin-like protein [Arabidopsis thaliana]

Seq. No.	177762
Seq. ID	jC-atXP92C249D20T7085d1
Method	BLASTX
NCBI GI	g4335764
BLAST score	80
E value	3.4e-01
Match length	53
% identity	23
NCBI Description	(AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No.	177763
Seq. ID	jC-atXP92CG3023d1
Method	BLASTX
NCBI GI	g4455223
BLAST score	202
E value	2.0e-15
Match length	99
% identity	48
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	177764
Seq. ID	jC-atXP92CH3G10T7086d1
Method	BLASTX
NCBI GI	g3913379
BLAST score	876
E value	2.0e-94

Match length	166
% identity	97
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	177765
Seq. ID	jC-atXP92CH3G12T7094d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	34
E value	3.0e-09
Match length	42
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	177766
Seq. ID	jC-atXP92CH3H8T7047d1
Method	BLASTX
NCBI GI	g642134
BLAST score	718
E value	6.0e-76
Match length	137
% identity	100
NCBI Description	(D45355) protein kinase [Arabidopsis thaliana] >gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3 [Arabidopsis thaliana]

Seq. No.	177767
Seq. ID	jC-atXP92CH4A3T7087d1
Method	BLASTX
NCBI GI	g3212869
BLAST score	168
E value	2.0e-11
Match length	132
% identity	28
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	177768
Seq. ID	jC-atXP92CH4A5T7095d1
Method	BLASTX
NCBI GI	g642134
BLAST score	106
E value	4.0e-41
Match length	134
% identity	77
NCBI Description	(D45355) protein kinase [Arabidopsis thaliana] >gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3 [Arabidopsis thaliana]

Seq. No.	177769
Seq. ID	jC-atXP92CH4B2T7048d1
Method	BLASTX
NCBI GI	g2191138
BLAST score	292
E value	1.0e-31
Match length	138

% identity	61
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	177770
Seq. ID	jC-atXP94CG11A10T7061d1
Method	BLASTN
NCBI GI	g4589440
BLAST score	76
E value	2.0e-34
Match length	428
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	177771
Seq. ID	jC-atXP94CG11A11T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	59
E value	2.0e-24
Match length	75
% identity	95
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177772
Seq. ID	jC-atXP94CG11A2T7b1
Method	BLASTX
NCBI GI	g3834307
BLAST score	147
E value	2.0e-09
Match length	40
% identity	70
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	177773
Seq. ID	jC-atXP94CG11A9T7053d1
Method	BLASTN
NCBI GI	g3413510
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Spinacia oleracea mRNA (nuclear-encoded) for chloroplast glucose-6-phosphate isomerase

Seq. No.	177774
Seq. ID	jC-atXP94CG11B4T7006d1
Method	BLASTX
NCBI GI	g4539327
BLAST score	195
E value	8.0e-15
Match length	52
% identity	73

NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]
Seq. No.	177775
Seq. ID	jC-atXP94CG11B5T7014d1
Method	BLASTX
NCBI GI	g3023516
BLAST score	433
E value	7.0e-77
Match length	155
% identity	95
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR (DXP SYNTHASE) >gi_1399261 (U27099) DEF [Arabidopsis thaliana]
Seq. No.	177776
Seq. ID	jC-atXP94CG11C10T7039d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	42
E value	4.0e-14
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase
Seq. No.	177777
Seq. ID	jC-atXP94CG11C4T7b1
Method	BLASTN
NCBI GI	g1890232
BLAST score	48
E value	6.0e-18
Match length	60
% identity	95
NCBI Description	T.evansi mRNA, clone Q16R1
Seq. No.	177778
Seq. ID	jC-atXP94CG11C6T7b1
Method	BLASTN
NCBI GI	g499300
BLAST score	153
E value	1.0e-80
Match length	257
% identity	90
NCBI Description	A.thaliana mRNA for ABI1 protein
Seq. No.	177779
Seq. ID	jC-atXP94CG11D3T7063d1
Method	BLASTN
NCBI GI	g1070003
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222
Seq. No.	177780

Seq. ID	jC-atXP94CG11D4T7071d1
Method	BLASTX
NCBI GI	g2407790
BLAST score	209
E value	2.0e-16
Match length	94
% identity	54
NCBI Description	(AF019910) grr1 [Glycine max]

Seq. No.	177781
Seq. ID	jC-atXP94CG11D7T7087d1
Method	BLASTX
NCBI GI	g1175013
BLAST score	126
E value	2.0e-36
Match length	149
% identity	60
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	177782
Seq. ID	jC-atXP94CG11D8T7095d1
Method	BLASTN
NCBI GI	g4159704
BLAST score	107
E value	4.0e-53
Match length	275
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	177783
Seq. ID	jC-atXP94CG11D8T7b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	71
E value	1.0e-31
Match length	187
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	177784
Seq. ID	jC-atXP94CG11E2T7032d1
Method	BLASTX
NCBI GI	g99752
BLAST score	429
E value	3.0e-42
Match length	145
% identity	67
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	177785
Seq. ID	jC-atXP94CG11E5T7048d1

Method	BLASTX
NCBI GI	g1488521
BLAST score	331
E value	1.0e-30
Match length	67
% identity	100
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	177786
Seq. ID	jC-atXP94CG11E7T7064d1
Method	BLASTN
NCBI GI	g4662609
BLAST score	46
E value	1.0e-16
Match length	174
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	177787
Seq. ID	jC-atXP94CG11E7T7b1
Method	BLASTN
NCBI GI	g4662609
BLAST score	153
E value	1.0e-80
Match length	262
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	177788
Seq. ID	jC-atXP94CG12A6T7088d1
Method	BLASTX
NCBI GI	g2129559
BLAST score	79
E value	2.0e-49
Match length	133
% identity	81
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	177789
Seq. ID	jC-atXP94CH4F10T7051d1
Method	BLASTN
NCBI GI	g3702729
BLAST score	194
E value	1.0e-105
Match length	409
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	177790

Seq. ID	jC-atXP94CH4F10T7b1
Method	BLASTN
NCBI GI	g3894179
BLAST score	111
E value	2.0e-55
Match length	255
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177791
Seq. ID	jC-atXP94CH4G2T7075d1
Method	BLASTN
NCBI GI	g4519188
BLAST score	71
E value	1.0e-31
Match length	174
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	177792
Seq. ID	jC-atXP94CH4G5T7004d1
Method	BLASTN
NCBI GI	g3449323
BLAST score	97
E value	5.0e-47
Match length	251
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	177793
Seq. ID	jC-atXP94CH4G9T7b1
Method	BLASTX
NCBI GI	g2384671
BLAST score	446
E value	2.0e-44
Match length	91
% identity	98
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	177794
Seq. ID	jC-atXP94CH4H10T7076d1
Method	BLASTN
NCBI GI	g4580454
BLAST score	298
E value	1.0e-167
Match length	419
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	177795
Seq. ID	jC-atXP94CH4H10T7b1
Method	BLASTN

NCBI GI	g4512690
BLAST score	37
E value	2.0e-11
Match length	113
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	177796
Seq. ID	jC-atXP94CH4H1T7044d1
Method	BLASTX
NCBI GI	g1173187
BLAST score	425
E value	9.0e-42
Match length	115
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	177797
Seq. ID	jC-atXP94CH4H1T7b1
Method	BLASTX
NCBI GI	g267073
BLAST score	368
E value	2.0e-35
Match length	72
% identity	94
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	177798
Seq. ID	jC-atXP94CH4H5T7052d1
Method	BLASTX
NCBI GI	g3980385
BLAST score	65
E value	2.0e-12
Match length	125
% identity	45
NCBI Description	(AC004561) putative 18 kDa class I heat shock protein [Arabidopsis thaliana]

Seq. No.	177799
Seq. ID	jC-atXP94CH5E12T7041d1
Method	BLASTN
NCBI GI	g2271484
BLAST score	49
E value	2.0e-18
Match length	153
% identity	85
NCBI Description	Arabidopsis thaliana arginine decarboxylase (spe2) mRNA, complete cds

Seq. No.	177800

Seq. ID	jC-atXP94CH5E7T7b1
Method	BLASTN
NCBI GI	g2804255
BLAST score	36
E value	9.0e-11
Match length	44
% identity	95
NCBI Description	Oryctolagus cuniculus mRNA for interferon gamma, complete cds

Seq. No.	177801
Seq. ID	jC-atXP94CH5F1T7049d1
Method	BLASTN
NCBI GI	g1070003
BLAST score	39
E value	7.0e-13
Match length	47
% identity	96
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	177802
Seq. ID	jC-atXP94CH5F3T7065d1
Method	BLASTN
NCBI GI	g4027862
BLAST score	159
E value	5.0e-84
Match length	440
% identity	85
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177803
Seq. ID	jC-atXP94CH5F5T7b1
Method	BLASTN
NCBI GI	g3986093
BLAST score	44
E value	1.0e-15
Match length	60
% identity	95
NCBI Description	Chalinochromis brichardi DNA, microsatellite region

Seq. No.	177804
Seq. ID	jC-atXP94CH5F8T7b1
Method	BLASTN
NCBI GI	g3269280
BLAST score	102
E value	4.0e-50
Match length	270
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	177805
Seq. ID	jC-atXP94CH5G4T7b1
Method	BLASTN

NCBI GI	g2522426
BLAST score	41
E value	9.0e-14
Match length	57
% identity	93
NCBI Description	Cloning vector pWSK29, complete sequence

Seq. No.	177806
Seq. ID	jC-atXP94CH5G7T7026d1
Method	BLASTN
NCBI GI	g4454587
BLAST score	119
E value	4.0e-60
Match length	482
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	177807
Seq. ID	jC-atXP94CH5G8T7034d1
Method	BLASTN
NCBI GI	g1297184
BLAST score	367
E value	0.0e+00
Match length	465
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	177808
Seq. ID	jC-atXP94CH5H1T7b1
Method	BLASTN
NCBI GI	g2352027
BLAST score	44
E value	1.0e-15
Match length	56
% identity	95
NCBI Description	Cloning vector pRS402 with ADE2 marker, complete sequence

Seq. No.	177809
Seq. ID	jC-atXP94CH5H2T7050d1
Method	BLASTN
NCBI GI	g2668397
BLAST score	43
E value	9.0e-15
Match length	51
% identity	96
NCBI Description	Mus musculus mGLT-1 mRNA, complete cds

Seq. No.	177810
Seq. ID	jC-atXP94CH5H9T7074d1
Method	BLASTN
NCBI GI	g4580744
BLAST score	124
E value	4.0e-63

Match length	348
% identity	84
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	177811
Seq. ID	jC-atXP95CG11E10T7093b1
Method	BLASTN
NCBI GI	g4585890
BLAST score	93
E value	1.0e-44
Match length	311
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	177812
Seq. ID	jC-atXP95CG11E10T7093d1
Method	BLASTN
NCBI GI	g4585890
BLAST score	94
E value	3.0e-45
Match length	202
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	177813
Seq. ID	jC-atXP95CG11E11T7006d1
Method	BLASTN
NCBI GI	g2980787
BLAST score	90
E value	5.0e-43
Match length	207
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	177814
Seq. ID	jC-atXP95CG11F10T7062b1
Method	BLASTX
NCBI GI	g3461848
BLAST score	358
E value	6.0e-34
Match length	117
% identity	64
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	177815
Seq. ID	jC-atXP95CG11F12T7078d1
Method	BLASTX
NCBI GI	g3643607
BLAST score	338
E value	1.0e-31
Match length	80
% identity	78
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	177816
Seq. ID	jC-atXP95CG11F4T7030d1
Method	BLASTX
NCBI GI	g1170373
BLAST score	468
E value	8.0e-47
Match length	142
% identity	72
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	177817
Seq. ID	jC-atXP95CG11F7T7046b1
Method	BLASTN
NCBI GI	g4519193
BLAST score	103
E value	5.0e-51
Match length	119
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	177818
Seq. ID	jC-atXP95CG11F7T7046d1
Method	BLASTN
NCBI GI	g4519193
BLAST score	69
E value	2.0e-30
Match length	144
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	177819
Seq. ID	jC-atXP95CG11G10T7047b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	41
E value	1.0e-13
Match length	69
% identity	90
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177820
Seq. ID	jC-atXP95CG11G4T7015b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	61
E value	1.0e-25
Match length	73
% identity	96
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	177821

Seq. ID	jC-atXP95CG11G6T7031d1
Method	BLASTN
NCBI GI	g3702739
BLAST score	98
E value	1.0e-47
Match length	174
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	177822
Seq. ID	jC-atXP95CG11H12T7095d1
Method	BLASTX
NCBI GI	g113026
BLAST score	720
E value	2.0e-76
Match length	152
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	177823
Seq. ID	jC-atXP95CG12B1T7009b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	51
E value	1.0e-19
Match length	74
% identity	93
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177824
Seq. ID	jC-atXP95CG12B2T7017d1
Method	BLASTN
NCBI GI	g4220633
BLAST score	75
E value	6.0e-34
Match length	238
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	177825
Seq. ID	jC-atXP95CG12B4T7033d1
Method	BLASTN
NCBI GI	g4589418
BLAST score	178
E value	2.0e-95
Match length	290
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	177826
Seq. ID	jC-atXP95CG12B8T7049b1
Method	BLASTN
NCBI GI	g2264316
BLAST score	47
E value	3.0e-17
Match length	107
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	177827
Seq. ID	jC-atXP95CG12B9T7057d1
Method	BLASTN
NCBI GI	g2264316
BLAST score	69
E value	2.0e-30
Match length	257
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	177828
Seq. ID	jC-atXP95CG12C1T7081d1
Method	BLASTN
NCBI GI	g3241920
BLAST score	87
E value	5.0e-41
Match length	368
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	177829
Seq. ID	jC-atXP95CG12C4T7010d1
Method	BLASTX
NCBI GI	g4455329
BLAST score	100
E value	6.0e-19
Match length	88
% identity	61
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	177830
Seq. ID	jC-atXP95CG12C5T7018b1
Method	BLASTN
NCBI GI	g3892595
BLAST score	37
E value	1.0e-11
Match length	67
% identity	91
NCBI Description	Mus musculus mRNA for pheromone receptor

Seq. No.	177831
Seq. ID	jC-atXP95CG12C6T7026d1

Method	BLASTN
NCBI GI	g4159704
BLAST score	70
E value	7.0e-31
Match length	283
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	177832
Seq. ID	jC-atXP95CG12D10T7027d1
Method	BLASTX
NCBI GI	g2129639
BLAST score	230
E value	6.0e-19
Match length	83
% identity	61
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	177833
Seq. ID	jC-atXP95CG12D6T7090b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	199
E value	2.0e-15
Match length	129
% identity	41
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	177834
Seq. ID	jC-atXP95CG12D6T7090d1
Method	BLASTN
NCBI GI	g4760411
BLAST score	110
E value	9.0e-55
Match length	257
% identity	86
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	177835
Seq. ID	jC-atXP95CG12E5T7083b1
Method	BLASTN
NCBI GI	g3335331
BLAST score	82
E value	4.0e-38
Match length	166
% identity	87
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177836
Seq. ID	jC-atXP95CG12F1T7020d1
Method	BLASTX

NCBI GI	g4589123
BLAST score	118
E value	2.0e-12
Match length	86
% identity	48
NCBI Description	(AF126374) At14a protein [Arabidopsis thaliana]

Seq. No.	177837
Seq. ID	jC-atXP95CG12F5T7044d1
Method	BLASTX
NCBI GI	g2244750
BLAST score	688
E value	1.0e-72
Match length	142
% identity	90
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	177838
Seq. ID	jC-atXP95CG12F6T7052d1
Method	BLASTX
NCBI GI	g1707364
BLAST score	374
E value	8.0e-36
Match length	131
% identity	65
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	177839
Seq. ID	jC-atXP95CG12G12T7069d1
Method	BLASTX
NCBI GI	g3702323
BLAST score	151
E value	1.0e-09
Match length	51
% identity	61
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	177840
Seq. ID	jC-atXP95CG12G2T7005d1
Method	BLASTN
NCBI GI	g2980787
BLAST score	171
E value	3.0e-91
Match length	423
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	177841
Seq. ID	jC-atXP95CG12G5T7021b1
Method	BLASTN
NCBI GI	g4538990
BLAST score	93
E value	1.0e-44
Match length	201

% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	177842
Seq. ID	jC-atXP95CG12G5T7021d1
Method	BLASTN
NCBI GI	g4538990
BLAST score	72
E value	2.0e-32
Match length	115
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	177843
Seq. ID	jC-atXP95CG12G9T7045d1
Method	BLASTN
NCBI GI	g2244950
BLAST score	132
E value	6.0e-68
Match length	328
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177844
Seq. ID	jC-atXP95CH2A10T7072b1
Method	BLASTN
NCBI GI	g2244901
BLAST score	90
E value	6.0e-43
Match length	261
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	177845
Seq. ID	jC-atXP95CH2A5T7048b1
Method	BLASTX
NCBI GI	g2102691
BLAST score	119
E value	1.0e-13
Match length	70
% identity	64
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	177846
Seq. ID	jC-atXP95CH2A9T7064b1
Method	BLASTN
NCBI GI	g1161509
BLAST score	237
E value	1.0e-130
Match length	394
% identity	92
NCBI Description	A.thaliana mRNA for shaggy-like kinase dzeta

Seq. No.	177847
Seq. ID	jC-atXP95CH2A9T7064d1
Method	BLASTN
NCBI GI	g3201608
BLAST score	154
E value	5.0e-81
Match length	314
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177848
Seq. ID	jC-atXP95CH2B6T7096d1
Method	BLASTX
NCBI GI	g1351840
BLAST score	250
E value	2.0e-28
Match length	144
% identity	53
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_1084319_pir__S53505 isocitrate lyase - cucumber >gi_1052578_emb_CAA84632_ (Z35499) isocitrate lyase [Cucumis sativus]

Seq. No.	177849
Seq. ID	jC-atXP96C248A23T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	9.0e-20
Match length	55
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177850
Seq. ID	jC-atXP96C248A5T7b1
Method	BLASTX
NCBI GI	g1336084
BLAST score	732
E value	9.0e-78
Match length	141
% identity	99
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	177851
Seq. ID	jC-atXP96C248B18T7b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	177852
Seq. ID	jC-atXP96C248C18T7b1
Method	BLASTN
NCBI GI	g984923
BLAST score	45
E value	7.0e-16
Match length	61
% identity	47
NCBI Description	Plasmid pBSL97 cloning vector, complete sequence

Seq. No.	177853
Seq. ID	jC-atXP96C248D4T7b1
Method	BLASTN
NCBI GI	g4558521
BLAST score	37
E value	4.0e-11
Match length	146
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	177854
Seq. ID	jC-atXP96C248D9T7b1
Method	BLASTN
NCBI GI	g4325323
BLAST score	72
E value	5.0e-32
Match length	286
% identity	84
NCBI Description	Arabidopsis thaliana lysyl-tRNA synthetase mRNA, complete cds

Seq. No.	177855
Seq. ID	jC-atXP96C248H22T7b1
Method	BLASTX
NCBI GI	g3080415
BLAST score	623
E value	7.0e-65
Match length	147
% identity	75
NCBI Description	(AL022604) cysteine proteinase-like protein [Arabidopsis thaliana]

Seq. No.	177856
Seq. ID	jC-atXP96C249E9T7b1
Method	BLASTX
NCBI GI	g417204
BLAST score	376
E value	6.0e-36
Match length	175
% identity	45
NCBI Description	ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_322067_pir__S17070 adenylate kinase (EC 2.7.4.3) - Micrococcus luteus >gi_44436_emb_CAA35568_ (X17524) Adk protein [Micrococcus luteus]

Seq. No.	177857

Seq. ID	jC-atXP96C249G10T7b1
Method	BLASTX
NCBI GI	g231995
BLAST score	186
E value	9.0e-14
Match length	80
% identity	47
NCBI Description	DEHYDRIN RAB18 >gi_282880_pir__S28021 rab18 protein - Arabidopsis thaliana >gi_16451_emb_CAA48178_ (X68042) RAB18 [Arabidopsis thaliana]

Seq. No.	177858
Seq. ID	jC-atXP96C249G4T7b1
Method	BLASTX
NCBI GI	g3928543
BLAST score	849
E value	2.0e-91
Match length	178
% identity	89
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	177859
Seq. ID	jC-atXP96C249H18T7b1
Method	BLASTX
NCBI GI	g3738328
BLAST score	418
E value	6.0e-41
Match length	138
% identity	59
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	177860
Seq. ID	jC-atXP96C249H4T7b1
Method	BLASTX
NCBI GI	g166570
BLAST score	218
E value	1.0e-17
Match length	115
% identity	45
NCBI Description	(L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No.	177861
Seq. ID	jC-atXP96C249I5T7b1
Method	BLASTX
NCBI GI	g135626
BLAST score	565
E value	4.0e-58
Match length	114
% identity	62
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID-1 (TATA-BOX FACTOR 1) (TATA SEQUENCE-BINDING PROTEIN 1) (TBP-1) >gi_99763_pir__S10946 transcription initiation factor IID (clone At-2) - Arabidopsis thaliana >gi_1943466_pdb_1VOK_A Chain A, Arabidopsis Thaliana Tbp (Dimer) >gi_1943467_pdb_1VOK_B Chain B, Arabidopsis Thaliana Tbp

	(Dimer) >gi_1943469_pdb_1VOL_B Chain B, Tfiib (Human Core Domain)TBP (A.THALIANA)TATA ELEMENT Ternary Complex >gi_16548_emb_CAA38743_ (X54996) transcription initiation factor II [Arabidopsis thaliana] >gi_227074_prf__1613452B transcription initiation factor TFIID-2 [Arabidopsis thaliana]
Seq. No.	177862
Seq. ID	jC-atXP96C249J2T7b1
Method	BLASTN
NCBI GI	g3873174
BLAST score	441
E value	0.0e+00
Match length	587
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]
Seq. No.	177863
Seq. ID	jC-atXP96C249J3T7b1
Method	BLASTN
NCBI GI	g14140
BLAST score	67
E value	6.0e-29
Match length	87
% identity	94
NCBI Description	O.berteriana mitochondrial 18S rRNA & 5S rRNA genes
Seq. No.	177864
Seq. ID	jC-atXP96C250A5T7b1
Method	BLASTX
NCBI GI	g115385
BLAST score	654
E value	1.0e-68
Match length	125
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	177865
Seq. ID	jC-atXP96C250A8T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	7.0e-19
Match length	50
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	177866
Seq. ID	jC-atXP96C250C22T7b1
Method	BLASTN
NCBI GI	g1374771
BLAST score	510
E value	0.0e+00

Match length	553
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for diacylglycerol kinase, complete cds

Seq. No.	177867
Seq. ID	jC-atXP96C250D14T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	8.0e-22
Match length	55
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177868
Seq. ID	jC-atXP96C250D22T7b1
Method	BLASTX
NCBI GI	g499301
BLAST score	539
E value	5.0e-55
Match length	106
% identity	100
NCBI Description	(X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856) abscisic acid insensitive protein [Arabidopsis thaliana] >gi_4538937_emb_CAB39673.1_ (AL049483) protein phosphatase ABI1 [Arabidopsis thaliana]

Seq. No.	177869
Seq. ID	jC-atXP96CA2b1
Method	BLASTX
NCBI GI	g2117612
BLAST score	290
E value	5.0e-33
Match length	87
% identity	77
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	177870
Seq. ID	jC-atXP96CD5b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	177871
Seq. ID	jC-atXP96CH2B9T7b1
Method	BLASTX
NCBI GI	g3158370
BLAST score	345
E value	3.0e-32
Match length	99

% identity	74
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	177872
Seq. ID	jC-atXP96CH2C12T7b1
Method	BLASTX
NCBI GI	g4559332
BLAST score	239
E value	6.0e-20
Match length	70
% identity	71
NCBI Description	(AC007087) putative phosphoenolpyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	177873
Seq. ID	jC-atXP96CH2C4T7b1
Method	BLASTX
NCBI GI	g2104679
BLAST score	295
E value	2.0e-26
Match length	77
% identity	69
NCBI Description	(X97906) transcription factor [Vicia faba]

Seq. No.	177874
Seq. ID	jC-atXP96CH2D2T7b1
Method	BLASTN
NCBI GI	g4559319
BLAST score	135
E value	1.0e-69
Match length	235
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	177875
Seq. ID	jC-atXP96CH2D3T7b1
Method	BLASTX
NCBI GI	g122087
BLAST score	567
E value	3.0e-58
Match length	136
% identity	85
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	177876
Seq. ID	jC-atXP96CH2D5T7b1
Method	BLASTN
NCBI GI	g2160716
BLAST score	81

E value	3.0e-37
Match length	197
% identity	88
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	177877
Seq. ID	jC-atXP96CH2D6T7b1
Method	BLASTX
NCBI GI	g1729783
BLAST score	326
E value	4.0e-30
Match length	122
% identity	50
NCBI Description	(Y09798) colR [Pseudomonas fluorescens]

Seq. No.	177878
Seq. ID	jC-atXP98CH2E2T7b1
Method	BLASTX
NCBI GI	g2583125
BLAST score	735
E value	6.0e-78
Match length	153
% identity	87
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	177879
Seq. ID	jC-atXP98CH2E7T7051d1
Method	BLASTN
NCBI GI	g1070003
BLAST score	33
E value	1.0e-08
Match length	45
% identity	93
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	177880
Seq. ID	jC-atXP98CH2F1T7b1
Method	BLASTX
NCBI GI	g114330
BLAST score	316
E value	4.0e-40
Match length	137
% identity	67
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35) type 1, plasma membrane - Arabidopsis thaliana >gi_166746 (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]

Seq. No.	177881
Seq. ID	jC-atXP98CH2F4T7b1
Method	BLASTX
NCBI GI	g2827143
BLAST score	350

E value	7.0e-33
Match length	96
% identity	74
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	177882
Seq. ID	jC-atXP98CH2F5T7012d1
Method	BLASTX
NCBI GI	g2191165
BLAST score	327
E value	5.0e-30
Match length	106
% identity	57
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No.	177883
Seq. ID	jC-atXP98CH2F8T7b1
Method	BLASTX
NCBI GI	g2996650
BLAST score	140
E value	6.0e-08
Match length	336
% identity	7
NCBI Description	(AC004493) KIAA0324 [Homo sapiens]

Seq. No.	177884
Seq. ID	jC-atXP98CH2F9T7036d1
Method	BLASTN
NCBI GI	g2351073
BLAST score	155
E value	2.0e-81
Match length	315
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	177885
Seq. ID	jC-atXP98CH2G4T7068d1
Method	BLASTX
NCBI GI	g3415117
BLAST score	124
E value	7.0e-34
Match length	82
% identity	95
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	177886
Seq. ID	jC-atXP98CH2H11T7b1
Method	BLASTN
NCBI GI	g3264774
BLAST score	65
E value	8.0e-28
Match length	228
% identity	87
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete

sequence [Arabidopsis thaliana]

Seq. No.	177887
Seq. ID	jC-atXP98CH2H12T7006d1
Method	BLASTX
NCBI GI	g2980641
BLAST score	140
E value	1.0e-38
Match length	166
% identity	61
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	177888
Seq. ID	jC-atXP98CH2H8T7b1
Method	BLASTX
NCBI GI	g4314363
BLAST score	167
E value	2.0e-11
Match length	143
% identity	32
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177889
Seq. ID	jC-atXP98CH2H9T7077d1
Method	BLASTX
NCBI GI	g2498277
BLAST score	154
E value	1.0e-09
Match length	311
% identity	11
NCBI Description	CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II) >gi_2136733_pir__I46014 cylicin II - bovine >gi_757754_emb_CAA86753_ (Z46789) cylicin II [Bos taurus]

Seq. No.	177890
Seq. ID	jC-atXP98CH7B6T7033d1
Method	BLASTX
NCBI GI	g786117
BLAST score	125
E value	2.0e-06
Match length	278
% identity	2
NCBI Description	(L41834) nuclear protein [Ensis minor]

Seq. No.	177891
Seq. ID	jC-atXP98CH7C10T7081d1
Method	BLASTN
NCBI GI	g2264311
BLAST score	166
E value	4.0e-88
Match length	330
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	177892
Seq. ID	jC-atXP98CH7C4T7049d1

Method	BLASTN
NCBI GI	g166628
BLAST score	33
E value	1.0e-08
Match length	174
% identity	87
NCBI Description	A.thaliana plasma membrane H+-ATPase gene, complete cds

Seq. No.	177893
Seq. ID	jC-atXP98CH7C8T7b1
Method	BLASTX
NCBI GI	g3876863
BLAST score	175
E value	3.0e-12
Match length	127
% identity	31
NCBI Description	(Z81078) predicted using Genefinder; Similarity to Yeast E1-E2 ATPase (SW:YIE8_YEAST); cDNA EST EMBL:D34828 comes from this gene; cDNA EST EMBL:D35545 comes from this gene; cDNA EST EMBL:D35631 comes from this gene; cDNA EST EM... >gi_3880373_emb_CAA16284_ (AL021466) predicted using Genefinder; Similarity to Yeast E1-E2 ATPase (SW:YIE8_YEAST); cDNA EST EMBL:D34828 comes from this gene; cDNA EST EMBL:D35545 comes from this gene; cDNA EST EMBL:D35631 comes from this gene; cDNA EST

Seq. No.	177894
Seq. ID	jC-atXP98CH7D7T7042d1
Method	BLASTX
NCBI GI	g541858
BLAST score	529
E value	1.0e-53
Match length	134
% identity	75
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	177895
Seq. ID	jC-atXP98CH7E1T7b1
Method	BLASTN
NCBI GI	g3046856
BLAST score	197
E value	1.0e-106
Match length	341
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	177896
Seq. ID	jC-atXP98CH8A7T7b1
Method	BLASTX
NCBI GI	g542059
BLAST score	143
E value	1.0e-08
Match length	37

% identity	78
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_457744_emb_CAA54869_ (X77915) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	177897
Seq. ID	jC-atXP98CH8B3T7007d1
Method	BLASTX
NCBI GI	g2921158
BLAST score	376
E value	5.0e-52
Match length	222
% identity	47
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	177898
Seq. ID	jC-atXP98CH8C10T7095d1
Method	BLASTN
NCBI GI	g4159705
BLAST score	383
E value	0.0e+00
Match length	525
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	177899
Seq. ID	jC-atXP98CH8D3T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	41
E value	1.0e-13
Match length	69
% identity	90
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177900
Seq. ID	jC-atXP98CH8D6T7b1
Method	BLASTN
NCBI GI	g4028986
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	pGAII(+) SK positive selection cloning vector gltS gene

Seq. No.	177901
Seq. ID	jC-atXP98CH8E10T7080d1
Method	BLASTX
NCBI GI	g1495251
BLAST score	104
E value	1.0e-11
Match length	100
% identity	50
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	177902

Seq. ID	jC-atXP98CH8E10T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	48
E value	1.0e-17
Match length	84
% identity	89
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)

Seq. No.	177903
Seq. ID	jC-atXP98CH8E5T7b1
Method	BLASTX
NCBI GI	g2224911
BLAST score	285
E value	3.0e-25
Match length	140
% identity	46
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	177904
Seq. ID	jC-atXP98CH8F6T7096d1
Method	BLASTN
NCBI GI	g3985932
BLAST score	325
E value	0.0e+00
Match length	389
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	177905
Seq. ID	jC-atXP98CH8F6T7b1
Method	BLASTN
NCBI GI	g3985932
BLAST score	35
E value	7.0e-10
Match length	129
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	177906
Seq. ID	jC-atXP9C93F17T7s1
Method	BLASTN
NCBI GI	g3249094
BLAST score	361
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177907
Seq. ID	jC-atXP9C93G12T7s1
Method	BLASTN
NCBI GI	g2618602

BLAST score	72
E value	1.0e-32
Match length	156
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	177908
Seq. ID	jC-atXP9C93I12T7d1
Method	BLASTN
NCBI GI	g3212846
BLAST score	111
E value	7.0e-56
Match length	143
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177909
Seq. ID	jC-atXP9C93L24T7d1
Method	BLASTN
NCBI GI	g2351068
BLAST score	61
E value	4.0e-26
Match length	129
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	177910
Seq. ID	jC-atXP9C93L24T7s1
Method	BLASTN
NCBI GI	g2351068
BLAST score	80
E value	2.0e-37
Match length	136
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	177911
Seq. ID	jC-atXP9C93P15T7s1
Method	BLASTN
NCBI GI	g4589410
BLAST score	179
E value	3.0e-96
Match length	267
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	177912
Seq. ID	jC-atXP9C94C12T7s1
Method	BLASTN
NCBI GI	g4580744
BLAST score	126
E value	1.0e-64

Match length	250
% identity	88
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	177913
Seq. ID	jC-atXP9C94C22T7d1
Method	BLASTN
NCBI GI	g2341023
BLAST score	383
E value	0.0e+00
Match length	431
% identity	97
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	177914
Seq. ID	jC-atXP9C94I10T7s1
Method	BLASTN
NCBI GI	g460831
BLAST score	72
E value	9.0e-33
Match length	127
% identity	91
NCBI Description	A.thaliana ASK-alpha mRNA >gi_1769888_emb_X68525_ATASKA A.thaliana ASKalpha gene for serine/threonine protein kinase

Seq. No.	177915
Seq. ID	jC-atXP9C94J16T7d1
Method	BLASTX
NCBI GI	g3822403
BLAST score	145
E value	1.0e-09
Match length	35
% identity	77
NCBI Description	(AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No.	177916
Seq. ID	jC-atXU104f1
Method	BLASTX
NCBI GI	g3928084
BLAST score	345
E value	3.0e-32
Match length	166
% identity	48
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	177917
Seq. ID	jC-atXU313f1
Method	BLASTX
NCBI GI	g126737
BLAST score	626
E value	4.0e-82
Match length	160
% identity	90

NCBI Description	MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_65939_pir__DEZMMX malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) precursor, chloroplast - maize >gi_168528 (J05130) NADP-dependent malic enzyme (EC 1.1.1.40) [Zea mays]

Seq. No.	177918
Seq. ID	jC-atXU42f1
Method	BLASTX
NCBI GI	g3548810
BLAST score	168
E value	2.0e-11
Match length	156
% identity	30
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	177919
Seq. ID	jC-atXU42r1
Method	BLASTX
NCBI GI	g3548810
BLAST score	166
E value	4.0e-21
Match length	137
% identity	39
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	177920
Seq. ID	jC-atXU54f1
Method	BLASTN
NCBI GI	g2623247
BLAST score	35
E value	7.0e-10
Match length	79
% identity	86
NCBI Description	Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No.	177921
Seq. ID	jC-atXU65d1
Method	BLASTN
NCBI GI	g1333680
BLAST score	37
E value	5.0e-11
Match length	141
% identity	90
NCBI Description	Cloning vector pKF19k DNA, complete sequence

Seq. No.	177922
Seq. ID	jC-atXU84f1
Method	BLASTN
NCBI GI	g1419369
BLAST score	64
E value	3.0e-27
Match length	64
% identity	100

NCBI Description	Z.mays ZmABP3 mRNA for actin depolymerizing factor
Seq. No.	177923
Seq. ID	jC-atXU93a1
Method	BLASTN
NCBI GI	g432601
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain {5' region} [chickens, liver, Genomic, 607 nt]
Seq. No.	177924
Seq. ID	jC-atXU95f1
Method	BLASTN
NCBI GI	g209214
BLAST score	49
E value	3.0e-18
Match length	93
% identity	96
NCBI Description	pUC19 cloning vector
Seq. No.	177925
Seq. ID	jC-atXXX23022Q2E1F12XXb1
Method	BLASTN
NCBI GI	g4757662
BLAST score	89
E value	1.0e-42
Match length	201
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence
Seq. No.	177926
Seq. ID	jC-atXmonuni10Aa06a1
Method	BLASTN
NCBI GI	g4581103
BLAST score	167
E value	6.0e-89
Match length	354
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence
Seq. No.	177927
Seq. ID	jC-atXmonuni10Ab06a1
Method	BLASTN
NCBI GI	g2351066
BLAST score	139
E value	2.0e-72
Match length	230
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.	177928

Seq. ID	jC-atXmonuni10Ab11a1
Method	BLASTX
NCBI GI	g2911053
BLAST score	465
E value	1.0e-46
Match length	100
% identity	88
NCBI Description	(AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177929
Seq. ID	jC-atXmonuni10Ae01a1
Method	BLASTN
NCBI GI	g4415928
BLAST score	229
E value	1.0e-126
Match length	313
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177930
Seq. ID	jC-atXmonuni10Af04a1
Method	BLASTN
NCBI GI	g3766106
BLAST score	226
E value	1.0e-124
Match length	262
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177931
Seq. ID	jC-atXmonuni10Ag01a1
Method	BLASTN
NCBI GI	g3420042
BLAST score	69
E value	9.0e-31
Match length	179
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177932
Seq. ID	jC-atXmonuni10Ag08a1
Method	BLASTX
NCBI GI	g2842478
BLAST score	220
E value	5.0e-18
Match length	107
% identity	42
NCBI Description	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]

Seq. No.	177933
Seq. ID	jC-atXmonuni10Ag09a1
Method	BLASTN
NCBI GI	g2618604

BLAST score 117
E value 3.0e-59
Match length 199
% identity 94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No. 177934
Seq. ID jC-atXmonuni10Ba08b1
Method BLASTX
NCBI GI g1730777
BLAST score 187
E value 6.0e-14
Match length 142
% identity 33
NCBI Description HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION >gi_1078050_pir__S55151 probable membrane protein YNL132w - yeast (Saccharomyces cerevisiae) >gi_854505_emb_CAA86893_ (Z46843) orf16 [Saccharomyces cerevisiae] >gi_1302072_emb_CAA96014_ (Z71408) ORF YNL132w [Saccharomyces cerevisiae]

Seq. No. 177935
Seq. ID jC-atXmonuni10Bb04a1
Method BLASTX
NCBI GI g1495804
BLAST score 267
E value 2.0e-23
Match length 96
% identity 60
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 177936
Seq. ID jC-atXmonuni10Be01a1
Method BLASTX
NCBI GI g3342556
BLAST score 191
E value 1.0e-14
Match length 63
% identity
NCBI Description (AF077528) importin alpha [Arabidopsis thaliana]

Seq. No. 177937
Seq. ID jC-atXmonuni10Be04b1
Method BLASTX
NCBI GI g267082
BLAST score 664
E value 7.0e-70
Match length 123
% identity 100
NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No. 177938
Seq. ID jC-atXmonuni10Be09a1
Method BLASTX

NCBI GI	g4539335
BLAST score	228
E value	8.0e-19
Match length	83
% identity	47
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	177939
Seq. ID	jC-atXmonuni10Bf01a1
Method	BLASTN
NCBI GI	g4159705
BLAST score	127
E value	4.0e-65
Match length	297
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	177940
Seq. ID	jC-atXmonuni10Bf04a1
Method	BLASTX
NCBI GI	g4324470
BLAST score	157
E value	1.0e-10
Match length	103
% identity	41
NCBI Description	(AF105010) LAG1Ce-1 [Caenorhabditis elegans]

Seq. No.	177941
Seq. ID	jC-atXmonuni10Bg02a1
Method	BLASTN
NCBI GI	g4757402
BLAST score	203
E value	1.0e-110
Match length	370
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	177942
Seq. ID	jC-atXmonuni10Bg04a1
Method	BLASTX
NCBI GI	g4454032
BLAST score	166
E value	1.0e-11
Match length	65
% identity	60
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	177943
Seq. ID	jC-atXmonuni10Bg04b1
Method	BLASTX
NCBI GI	g4454032
BLAST score	165
E value	2.0e-11
Match length	62
% identity	61

NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	177944
Seq. ID	jC-atXmonuni10Bh06a1
Method	BLASTN
NCBI GI	g3702728
BLAST score	116
E value	1.0e-58
Match length	249
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	177945
Seq. ID	jC-atXmonuni10Da04a1
Method	BLASTN
NCBI GI	g4589451
BLAST score	293
E value	1.0e-164
Match length	324
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T32G24, complete sequence

Seq. No.	177946
Seq. ID	jC-atXmonuni10Dc06b1
Method	BLASTX
NCBI GI	g4206763
BLAST score	250
E value	2.0e-21
Match length	48
% identity	100
NCBI Description	(AF104328) cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana]

Seq. No.	177947
Seq. ID	jC-atXmonuni10Dc10a1
Method	BLASTN
NCBI GI	g4376087
BLAST score	101
E value	9.0e-50
Match length	237
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	177948
Seq. ID	jC-atXmonuni10Dc12a1
Method	BLASTN
NCBI GI	g2827644
BLAST score	68
E value	4.0e-30
Match length	184
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	177949
Seq. ID	jC-atXmonuni10Dd03a1
Method	BLASTN
NCBI GI	g4337186
BLAST score	136
E value	1.0e-70
Match length	196
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177950
Seq. ID	jC-atXmonuni10De03a1
Method	BLASTN
NCBI GI	g4519193
BLAST score	77
E value	2.0e-35
Match length	250
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	177951
Seq. ID	jC-atXmonuni10De06a1
Method	BLASTN
NCBI GI	g4589443
BLAST score	253
E value	1.0e-140
Match length	333
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	177952
Seq. ID	jC-atXmonuni10Df09a1
Method	BLASTN
NCBI GI	g2827538
BLAST score	108
E value	8.0e-54
Match length	160
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	177953
Seq. ID	jC-atXmonuni10Dg02a1
Method	BLASTN
NCBI GI	g2213606
BLAST score	143
E value	7.0e-75
Match length	203
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	177954
Seq. ID	jC-atXmonuni10Dg08b1

Method	BLASTN
NCBI GI	g4490717
BLAST score	33
E value	3.0e-09
Match length	45
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	177955
Seq. ID	jC-atXmonuni25Aa08a1
Method	BLASTN
NCBI GI	g2351069
BLAST score	48
E value	3.0e-18
Match length	116
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	177956
Seq. ID	jC-atXmonuni25Ab03b1
Method	BLASTX
NCBI GI	g3894172
BLAST score	245
E value	9.0e-21
Match length	100
% identity	44
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	177957
Seq. ID	jC-atXmonuni25Ac03a1
Method	BLASTN
NCBI GI	g3763944
BLAST score	100
E value	2.0e-49
Match length	116
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	177958
Seq. ID	jC-atXmonuni25Ac05a1
Method	BLASTN
NCBI GI	g3449327
BLAST score	108
E value	5.0e-54
Match length	164
% identity	71
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	177959
Seq. ID	jC-atXmonuni25Ad02a1
Method	BLASTN
NCBI GI	g4335744

BLAST score	230
E value	1.0e-126
Match length	250
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177960
Seq. ID	jC-atXmonuni25Ad02b1
Method	BLASTN
NCBI GI	g4335744
BLAST score	65
E value	2.0e-28
Match length	137
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177961
Seq. ID	jC-atXmonuni25Ad07a1
Method	BLASTN
NCBI GI	g3046850
BLAST score	43
E value	5.0e-15
Match length	59
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	177962
Seq. ID	jC-atXmonuni25Ae09a1
Method	BLASTN
NCBI GI	g3892698
BLAST score	374
E value	0.0e+00
Match length	374
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project)

Seq. No.	177963
Seq. ID	jC-atXmonuni25Af02b1
Method	BLASTX
NCBI GI	g2500497
BLAST score	314
E value	9.0e-29
Match length	72
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225.1_ (X98656) ribosomal protein S21 [Zea mays]

Seq. No.	177964
Seq. ID	jC-atXmonuni25Af04a1
Method	BLASTN
NCBI GI	g2924733
BLAST score	43
E value	6.0e-16

Match length	51
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	177965
Seq. ID	jC-atXmonuni25Ah03a1
Method	BLASTN
NCBI GI	g3600045
BLAST score	85
E value	2.0e-40
Match length	117
% identity	93
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	177966
Seq. ID	jC-atXmonuni25Ah12b1
Method	BLASTN
NCBI GI	g2262135
BLAST score	204
E value	1.0e-111
Match length	384
% identity	96
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	177967
Seq. ID	jC-atXmonuni25Bb03b1
Method	BLASTX
NCBI GI	g3913727
BLAST score	314
E value	7.0e-29
Match length	75
% identity	81
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_1174336_emb_CAA59012_ (X84230) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No.	177968
Seq. ID	jC-atXmonuni25Bc05b1
Method	BLASTX
NCBI GI	g1707019
BLAST score	495
E value	4.0e-50
Match length	129
% identity	78
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	177969
Seq. ID	jC-atXmonuni25Bc10b1
Method	BLASTN
NCBI GI	g2828184
BLAST score	172
E value	5.0e-92
Match length	221
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	177970
Seq. ID	jC-atXmonuni25Be04b1
Method	BLASTN
NCBI GI	g2924728
BLAST score	87
E value	2.0e-41
Match length	225
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	177971
Seq. ID	jC-atXmonuni25Cd01b1
Method	BLASTN
NCBI GI	g4580744
BLAST score	175
E value	5.0e-94
Match length	175
% identity	100
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	177972
Seq. ID	jC-atXmonuni25Cd04b1
Method	BLASTN
NCBI GI	g3128138
BLAST score	130
E value	4.0e-67
Match length	182
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	177973
Seq. ID	jC-atXmonuni25Ce04b1
Method	BLASTX
NCBI GI	g3980394
BLAST score	614
E value	4.0e-64
Match length	118
% identity	100
NCBI Description	(AC004561) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	177974
Seq. ID	jC-atXmonuni25Ce08a1
Method	BLASTN
NCBI GI	g4220643
BLAST score	368
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	177975

Seq. ID	jC-atXmonuni25Cf04b1
Method	BLASTN
NCBI GI	g3983124
BLAST score	90
E value	4.0e-43
Match length	210
% identity	90
NCBI Description	Arabidopsis thaliana phosphate/triose-phosphate translocator precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	177976
Seq. ID	jC-atXmonuni25Da06a1
Method	BLASTN
NCBI GI	g2264318
BLAST score	67
E value	9.0e-30
Match length	126
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	177977
Seq. ID	jC-atXmonuni25Da06b1
Method	BLASTN
NCBI GI	g2264306
BLAST score	175
E value	7.0e-94
Match length	250
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	177978
Seq. ID	jC-atXmonuni25Da11b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	322
E value	0.0e+00
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	177979
Seq. ID	jC-atXmonuni25Db03b1
Method	BLASTN
NCBI GI	g16472
BLAST score	200
E value	1.0e-109
Match length	70
% identity	47
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	177980
Seq. ID	jC-atXmonuni25Db04b1
Method	BLASTX

NCBI GI	g420233
BLAST score	198
E value	2.0e-15
Match length	113
% identity	42
NCBI Description	transcription factor R-kappa-B - mouse (fragment)

Seq. No.	177981
Seq. ID	jC-atXmonuni25Db06b1
Method	BLASTX
NCBI GI	g3892061
BLAST score	314
E value	3.0e-29
Match length	83
% identity	73
NCBI Description	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	177982
Seq. ID	jC-atXmonuni25Db07b1
Method	BLASTN
NCBI GI	g16473
BLAST score	243
E value	1.0e-134
Match length	282
% identity	66
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	177983
Seq. ID	jC-atXmonuni25Db09b1
Method	BLASTN
NCBI GI	g2435510
BLAST score	174
E value	4.0e-93
Match length	320
% identity	88
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	177984
Seq. ID	jC-atXmonuni25Db11b1
Method	BLASTN
NCBI GI	g4544381
BLAST score	275
E value	1.0e-153
Match length	282
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	177985
Seq. ID	jC-atXmonuni25Dc01b1
Method	BLASTN
NCBI GI	g806534
BLAST score	280
E value	1.0e-156
Match length	320
% identity	48

NCBI Description	A.thaliana DNA for Athila retroelement

Seq. No.	177986
Seq. ID	jC-atXmonuni25Dc02b1
Method	BLASTN
NCBI GI	g2914688
BLAST score	48
E value	4.0e-18
Match length	56
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	177987
Seq. ID	jC-atXmonuni25Dc04b1
Method	BLASTN
NCBI GI	g4678266
BLAST score	347
E value	0.0e+00
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	177988
Seq. ID	jC-atXmonuni25Dc08b1
Method	BLASTN
NCBI GI	g2894557
BLAST score	106
E value	2.0e-52
Match length	405
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	177989
Seq. ID	jC-atXmonuni25Dc09b1
Method	BLASTN
NCBI GI	g4455348
BLAST score	93
E value	6.0e-45
Match length	176
% identity	75
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	177990
Seq. ID	jC-atXmonuni25Dc10b1
Method	BLASTN
NCBI GI	g4699935
BLAST score	314
E value	1.0e-176
Match length	346
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC F14P14 genomic sequence, complete sequence

Seq. No.	177991
Seq. ID	jC-atXmonuni25Dc11a1
Method	BLASTN
NCBI GI	g4235150
BLAST score	198
E value	1.0e-107
Match length	461
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	177992
Seq. ID	jC-atXmonuni25Dc11b1
Method	BLASTX
NCBI GI	g1769897
BLAST score	603
E value	7.0e-63
Match length	123
% identity	97
NCBI Description	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No.	177993
Seq. ID	jC-atXmonuni25Dc12b1
Method	BLASTN
NCBI GI	g4589440
BLAST score	221
E value	1.0e-121
Match length	304
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	177994
Seq. ID	jC-atXmonuni25Dd01b1
Method	BLASTN
NCBI GI	g4587582
BLAST score	325
E value	0.0e+00
Match length	353
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	177995
Seq. ID	jC-atXmonuni25Dd02a1
Method	BLASTN
NCBI GI	g3702738
BLAST score	75
E value	4.0e-34
Match length	210
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	177996
Seq. ID	jC-atXmonuni25Dd05b1
Method	BLASTX

NCBI GI g4417285
BLAST score 182
E value 2.0e-13
Match length 90
% identity 54
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 177997
Seq. ID jC-atXmonuni25Dd06b1
Method BLASTX
NCBI GI g4263050
BLAST score 265
E value 2.0e-23
Match length 102
% identity 59
NCBI Description (AC005142) putative nodulin [Arabidopsis thaliana]

Seq. No. 177998
Seq. ID jC-atXmonuni25Dd11b1
Method BLASTX
NCBI GI g4587601
BLAST score 277
E value 5.0e-38
Match length 120
% identity 43
NCBI Description (AC006951) unknown protein [Arabidopsis thaliana]

Seq. No. 177999
Seq. ID jC-atXmonuni25Dd12b1
Method BLASTX
NCBI GI g3298537
BLAST score 219
E value 8.0e-18
Match length 93
% identity 55
NCBI Description (AC004681) hypothetical protein [Arabidopsis thaliana]

Seq. No. 178000
Seq. ID jC-atXmonuni25De01a1
Method BLASTX
NCBI GI g3128172
BLAST score 217
E value 1.0e-17
Match length 67
% identity 51
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 178001
Seq. ID jC-atXmonuni25De02b1
Method BLASTX
NCBI GI g3582779
BLAST score 85
E value 2.0e-11
Match length 62
% identity 32
NCBI Description (AF056282) peroxisomal targeting sequence 1 receptor [Nicotiana tabacum]

Seq. No.	178002
Seq. ID	jC-atXmonuni25De03b1
Method	BLASTN
NCBI GI	g4567259
BLAST score	218
E value	1.0e-119
Match length	226
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	178003
Seq. ID	jC-atXmonuni25De04b1
Method	BLASTN
NCBI GI	g4092471
BLAST score	198
E value	1.0e-107
Match length	293
% identity	94
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	178004
Seq. ID	jC-atXmonuni25De05b1
Method	BLASTN
NCBI GI	g4586019
BLAST score	112
E value	4.0e-56
Match length	334
% identity	32
NCBI Description	Arabidopsis thaliana chromosome II BAC T3P4 genomic sequence, complete sequence

Seq. No.	178005
Seq. ID	jC-atXmonuni25De09b1
Method	BLASTN
NCBI GI	g4734011
BLAST score	225
E value	1.0e-123
Match length	289
% identity	72
NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	178006
Seq. ID	jC-atXmonuni25De12b1
Method	BLASTN
NCBI GI	g4732167
BLAST score	207
E value	1.0e-112
Match length	455
% identity	54
NCBI Description	Arabidopsis thaliana BAC F28D6

Seq. No.	178007
Seq. ID	jC-atXmonuni25Df01b1

Method	BLASTX
NCBI GI	g2829893
BLAST score	212
E value	2.0e-36
Match length	127
% identity	68
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	178008
Seq. ID	jC-atXmonuni25Df02b1
Method	BLASTX
NCBI GI	g4510342
BLAST score	463
E value	2.0e-46
Match length	131
% identity	73
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	178009
Seq. ID	jC-atXmonuni25Df04b1
Method	BLASTX
NCBI GI	g4773908
BLAST score	532
E value	1.0e-54
Match length	104
% identity	93
NCBI Description	(AF147259) No definition line found [Arabidopsis thaliana]

Seq. No.	178010
Seq. ID	jC-atXmonuni25Df07b1
Method	BLASTN
NCBI GI	g2264316
BLAST score	240
E value	1.0e-132
Match length	294
% identity	69
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	178011
Seq. ID	jC-atXmonuni25Df12b1
Method	BLASTX
NCBI GI	g4309767
BLAST score	294
E value	5.0e-47
Match length	124
% identity	77
NCBI Description	(AC006217) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	178012
Seq. ID	jC-atXmonuni25Dg02b1
Method	BLASTX
NCBI GI	g70642
BLAST score	265
E value	2.0e-23

Match length	63
% identity	18
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	178013
Seq. ID	jC-atXmonuni25Dg11a1
Method	BLASTN
NCBI GI	g2505873
BLAST score	112
E value	3.0e-56
Match length	316
% identity	84
NCBI Description	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No.	178014
Seq. ID	jC-atXmonuni25Dg11b1
Method	BLASTN
NCBI GI	g4584531
BLAST score	402
E value	0.0e+00
Match length	474
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	178015
Seq. ID	jC-atXmonuni25Dh01b1
Method	BLASTN
NCBI GI	g4589438
BLAST score	273
E value	1.0e-152
Match length	285
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	178016
Seq. ID	jC-atXmonuni25Dh04b1
Method	BLASTN
NCBI GI	g4159703
BLAST score	157
E value	5.0e-83
Match length	181
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	178017
Seq. ID	jC-atXmonuni25Dh06b1
Method	BLASTX
NCBI GI	g2129741
BLAST score	368
E value	4.0e-50

Match length	137
% identity	73
NCBI Description	sterol-C5-desaturase - Arabidopsis thaliana >gi_1061038_emb_CAA62079_ (X90454) sterol-C5-desaturase [Arabidopsis thaliana]

Seq. No.	178018
Seq. ID	jC-atXmonuni25Dh07b1
Method	BLASTN
NCBI GI	g4580454
BLAST score	44
E value	2.0e-15
Match length	91
% identity	47
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	178019
Seq. ID	jC-atXmonuni25Dh08b1
Method	BLASTN
NCBI GI	g3281847
BLAST score	178
E value	2.0e-95
Match length	335
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	178020
Seq. ID	jC-atXmonuni25Dh12b1
Method	BLASTX
NCBI GI	g3021276
BLAST score	356
E value	7.0e-40
Match length	105
% identity	87
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	178021
Seq. ID	jC-atXmonuni26Aa02a1
Method	BLASTN
NCBI GI	g313151
BLAST score	205
E value	1.0e-111
Match length	249
% identity	96
NCBI Description	A.thaliana ribosomal protein S15 mRNA, complete CDS

Seq. No.	178022
Seq. ID	jC-atXmonuni26Aa08b1
Method	BLASTN
NCBI GI	g2833627
BLAST score	175
E value	6.0e-94
Match length	175
% identity	100

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	178023
Seq. ID	jC-atXmonuni26Aa11a1
Method	BLASTN
NCBI GI	g2245031
BLAST score	193
E value	1.0e-104
Match length	266
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	178024
Seq. ID	jC-atXmonuni26Ab09a1
Method	BLASTN
NCBI GI	g3702733
BLAST score	340
E value	0.0e+00
Match length	360
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana]

Seq. No.	178025
Seq. ID	jC-atXmonuni26Ab11a1
Method	BLASTX
NCBI GI	g3252805
BLAST score	321
E value	8.0e-30
Match length	68
% identity	93
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana] >gi_3650027 (AC005396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	178026
Seq. ID	jC-atXmonuni26Ac06a1
Method	BLASTX
NCBI GI	g2982247
BLAST score	152
E value	6.0e-10
Match length	48
% identity	56
NCBI Description	(AF051206) probable thioredoxin H [Picea mariana]

Seq. No.	178027
Seq. ID	jC-atXmonuni26Ad05a1
Method	BLASTN
NCBI GI	g3036791
BLAST score	220
E value	1.0e-120
Match length	324
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No.	178028
Seq. ID	jC-atXmonuni26Ad12a1
Method	BLASTX
NCBI GI	g3834319
BLAST score	405
E value	9.0e-40
Match length	85
% identity	99
NCBI Description	(AC005679) Similar to gi_2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	178029
Seq. ID	jC-atXmonuni26Ae06a1
Method	BLASTN
NCBI GI	g4589409
BLAST score	195
E value	1.0e-106
Match length	251
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	178030
Seq. ID	jC-atXmonuni26Ae07a1
Method	BLASTN
NCBI GI	g3449329
BLAST score	303
E value	1.0e-170
Match length	319
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	178031
Seq. ID	jC-atXmonuni26Ae09a1
Method	BLASTN
NCBI GI	g4567237
BLAST score	341
E value	0.0e+00
Match length	389
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	178032
Seq. ID	jC-atXmonuni26Af09a1
Method	BLASTN
NCBI GI	g3449321
BLAST score	231
E value	1.0e-127
Match length	268
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	178033
Seq. ID	jC-atXmonuni26Af12a1
Method	BLASTN
NCBI GI	g4753645
BLAST score	87
E value	9.0e-42
Match length	119
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	178034
Seq. ID	jC-atXmonuni26Ag08a1
Method	BLASTN
NCBI GI	g3873174
BLAST score	157
E value	4.0e-83
Match length	232
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	178035
Seq. ID	jC-atXmonuni26Bb03a1
Method	BLASTN
NCBI GI	g4159699
BLAST score	164
E value	4.0e-87
Match length	326
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence

Seq. No.	178036
Seq. ID	jC-atXmonuni26Ca12b1
Method	BLASTX
NCBI GI	g4097557
BLAST score	581
E value	3.0e-60
Match length	115
% identity	97
NCBI Description	(U64911) ATFP8 [Arabidopsis thaliana]

Seq. No.	178037
Seq. ID	jC-atXmonuni26Cc03a1
Method	BLASTN
NCBI GI	g3668073
BLAST score	261
E value	1.0e-145
Match length	450
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178038
Seq. ID	jC-atXmonuni26Cc12a1
Method	BLASTN

NCBI GI	g4539331
BLAST score	103
E value	5.0e-51
Match length	191
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	178039
Seq. ID	jC-atXmonuni26Cd01a1
Method	BLASTN
NCBI GI	g3242700
BLAST score	91
E value	8.0e-44
Match length	219
% identity	45
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178040
Seq. ID	jC-atXmonuni26Cd03a1
Method	BLASTN
NCBI GI	g4191760
BLAST score	151
E value	2.0e-79
Match length	382
% identity	81
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	178041
Seq. ID	jC-atXmonuni26Ce03a1
Method	BLASTN
NCBI GI	g2618724
BLAST score	43
E value	3.0e-15
Match length	107
% identity	85
NCBI Description	Arabidopsis thaliana early auxin-induced (IAA18) mRNA, partial cds

Seq. No.	178042
Seq. ID	jC-atXmonuni26Ce07a1
Method	BLASTN
NCBI GI	g4581161
BLAST score	174
E value	2.0e-93
Match length	182
% identity	78
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	178043
Seq. ID	jC-atXmonuni26Ce11a1
Method	BLASTN
NCBI GI	g2244901
BLAST score	206

E value	1.0e-112
Match length	250
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	178044
Seq. ID	jC-atXmonuni26Cf11a1
Method	BLASTN
NCBI GI	g3150006
BLAST score	86
E value	2.0e-40
Match length	86
% identity	40
NCBI Description	CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No.	178045
Seq. ID	jC-atXmonuni26Cg06a1
Method	BLASTX
NCBI GI	g399298
BLAST score	217
E value	2.0e-17
Match length	66
% identity	71
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]

Seq. No.	178046
Seq. ID	jC-atXmonuni26Da01a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	88
E value	2.0e-42
Match length	96
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	178047
Seq. ID	jC-atXmonuni26Da08b1
Method	BLASTX
NCBI GI	g3386546
BLAST score	285
E value	2.0e-25
Match length	92
% identity	71
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No.	178048
Seq. ID	jC-atXmonuni26Da09a1
Method	BLASTX
NCBI GI	g3548802
BLAST score	527

E value	8.0e-54
Match length	100
% identity	100
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	178049
Seq. ID	jC-atXmonuni26Db01a1
Method	BLASTN
NCBI GI	g3043414
BLAST score	110
E value	4.0e-55
Match length	209
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for At-hsc70-3 protein

Seq. No.	178050
Seq. ID	jC-atXmonuni26Db09a1
Method	BLASTX
NCBI GI	g1362093
BLAST score	157
E value	1.0e-10
Match length	54
% identity	57
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No.	178051
Seq. ID	jC-atXmonuni26Dc04b1
Method	BLASTN
NCBI GI	g2252823
BLAST score	128
E value	7.0e-66
Match length	144
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	178052
Seq. ID	jC-atXmonuni26Dc06a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	97
E value	2.0e-47
Match length	97
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	178053
Seq. ID	jC-atXmonuni26Dd08a1
Method	BLASTN
NCBI GI	g4106527
BLAST score	65
E value	2.0e-28
Match length	107
% identity	65

NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	178054
Seq. ID	jC-atXmonuni26Dh02b1
Method	BLASTN
NCBI GI	g3212846
BLAST score	112
E value	2.0e-56
Match length	177
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178055
Seq. ID	jC-atXmonuni27Aa11a1
Method	BLASTN
NCBI GI	g3402747
BLAST score	66
E value	3.0e-29
Match length	106
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)

Seq. No.	178056
Seq. ID	jC-atXmonuni27Ab03a1
Method	BLASTN
NCBI GI	g4159712
BLAST score	192
E value	1.0e-104
Match length	204
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	178057
Seq. ID	jC-atXmonuni27Ac03a1
Method	BLASTX
NCBI GI	g136682
BLAST score	188
E value	4.0e-14
Match length	82
% identity	50
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN THIOLESTERASE L3) >gi_108014_pir__A40085 ubiquitin carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human >gi_2914274_pdb_1UCH_ Deubiquitinating Enzyme Uch-L3 (Human) At 1.8 Angstrom Resolution >gi_340074 (M30496) ubiquitin carboxyl-terminal hydrolase [Homo sapiens]

Seq. No.	178058
Seq. ID	jC-atXmonuni27Ac12b1
Method	BLASTX
NCBI GI	g1946373
BLAST score	295
E value	6.0e-27
Match length	57

% identity	100
NCBI Description	(U93215) leader peptidase I isolog [Arabidopsis thaliana]

Seq. No.	178059
Seq. ID	jC-atXmonuni27Af03b1
Method	BLASTN
NCBI GI	g4220635
BLAST score	385
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	178060
Seq. ID	jC-atXmonuni27Ba08a1
Method	BLASTX
NCBI GI	g4567208
BLAST score	212
E value	7.0e-17
Match length	73
% identity	56
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	178061
Seq. ID	jC-atXmonuni27Be12a1
Method	BLASTN
NCBI GI	g3176694
BLAST score	188
E value	1.0e-101
Match length	344
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178062
Seq. ID	jC-atXmonuni27Bf01a1
Method	BLASTN
NCBI GI	g3402747
BLAST score	182
E value	5.0e-98
Match length	253
% identity	78
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)

Seq. No.	178063
Seq. ID	jC-atXmonuni27Bf06a1
Method	BLASTN
NCBI GI	g2335089
BLAST score	56
E value	7.0e-23
Match length	140
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178064
Seq. ID	jC-atXmonuni27Bf08a1
Method	BLASTN
NCBI GI	g4757678
BLAST score	94
E value	2.0e-45
Match length	297
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	178065
Seq. ID	jC-atXmonuni27Bh09b1
Method	BLASTN
NCBI GI	g433664
BLAST score	444
E value	0.0e+00
Match length	457
% identity	99
NCBI Description	A.thaliana for Sec61 beta-subunit homolog

Seq. No.	178066
Seq. ID	jC-atXmonuni27Cb01a1
Method	BLASTN
NCBI GI	g4406805
BLAST score	127
E value	2.0e-65
Match length	191
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	178067
Seq. ID	jC-atXmonuni27Cc12b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	292
E value	1.0e-163
Match length	452
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	178068
Seq. ID	jC-atXmonuni27Ce01a1
Method	BLASTN
NCBI GI	g4757678
BLAST score	50
E value	4.0e-19
Match length	211
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	178069
Seq. ID	jC-atXmonuni27Ce09b1
Method	BLASTX

NCBI GI	g1352458
BLAST score	704
E value	2.0e-74
Match length	138
% identity	100
NCBI Description	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD) >gi_2117507_pir__JC4999 IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana >gi_1100063 (L34684) IMP dehydrogenase [Arabidopsis thaliana]

Seq. No.	178070
Seq. ID	jC-atXmonuni27Ce11a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	266
E value	1.0e-148
Match length	274
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	178071
Seq. ID	jC-atXmonuni27Ce12b1
Method	BLASTX
NCBI GI	g2494610
BLAST score	409
E value	6.0e-40
Match length	167
% identity	57
NCBI Description	CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR >gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]

Seq. No.	178072
Seq. ID	jC-atXmonuni27Cf02b1
Method	BLASTX
NCBI GI	g4678364
BLAST score	314
E value	9.0e-29
Match length	120
% identity	56
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	178073
Seq. ID	jC-atXmonuni27Cf03b1
Method	BLASTX
NCBI GI	g4678923
BLAST score	230
E value	6.0e-19
Match length	86
% identity	53
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	178074
Seq. ID	jC-atXmonuni27Cf11b1
Method	BLASTX
NCBI GI	g4539383
BLAST score	705

E value	1.0e-74
Match length	167
% identity	86
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	178075
Seq. ID	jC-atXmonuni27Cg02a1
Method	BLASTX
NCBI GI	g3880434
BLAST score	303
E value	1.0e-27
Match length	94
% identity	61
NCBI Description	(Z66521) cDNA EST yk291d10.3 comes from this gene; cDNA EST yk291d10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	178076
Seq. ID	jC-atXmonuni27Ch04a1
Method	BLASTX
NCBI GI	g3702326
BLAST score	94
E value	1.0e-43
Match length	90
% identity	98
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	178077
Seq. ID	jC-atXmonuni27Ch05a1
Method	BLASTX
NCBI GI	g4585995
BLAST score	246
E value	5.0e-21
Match length	83
% identity	70
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	178078
Seq. ID	jC-atXmonuni27Da06b1
Method	BLASTN
NCBI GI	g2264312
BLAST score	60
E value	2.0e-25
Match length	140
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	178079
Seq. ID	ARABL1-01-Q1-B2-B7

Seq. No.	178080
Seq. ID	ARABL1-01-Q1-B2-E1

Seq. No.	178081
Seq. ID	ARABL1-01-Q1-E1-B7

Seq. No. 178082
Seq. ID ARABL1-01-Q1-E1-C3

Seq. No. 178083
Seq. ID ARABL1-01-Q1-E1-D11

Seq. No. 178084
Seq. ID ARABL1-019-Q1-B1-A6

Seq. No. 178085
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Seq. No. 178086
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Seq. No. 178087
Seq. ID ARABL1-020-Q1-B1-D4

Seq. No. 178088
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Seq. No. 178089
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Seq. No. 178110
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Seq. No. 178111
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Seq. No. 178112
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Seq. No. 178132
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Seq. No. 178249
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Seq. No. 178250
Seq. ID LIB146-029-Q1-K1-A2

Seq. No. 178251
Seq. ID LIB146-029-Q1-K1-E11

Seq. No. 178252
Seq. ID LIB146-029-Q1-K1-F10

Seq. No. 178253
Seq. ID LIB146-029-Q1-K1-F12

Seq. No. 178254
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Seq. No. 178255
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Seq. No. 178256
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Seq. No. 178257
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Seq. No. 178260
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Seq. No. 178263
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Seq. No. 178264
Seq. ID LIB22-004-Q1-E1-G3

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Gossypium hirsutum

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Match length 139
% identity 88
NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No. 189969
Contig ID 2_1.R1039

5'-most EST	LIB3197-038-Q1-M1-H6
Method	BLASTX
NCBI GI	g401322
BLAST score	3143
E value	0.0e+00
Match length	623
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi|167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	189970
Contig ID	2_2.R1039
5'-most EST	LIB3197-059-Q1-M1-H9
Method	BLASTX
NCBI GI	g3169287
BLAST score	3142
E value	0.0e+00
Match length	623
% identity	98
NCBI Description	(AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No.	189971
Contig ID	3_1.R1039
5'-most EST	uC-gsronu33B166a02b2
Method	BLASTN
NCBI GI	g435038
BLAST score	440
E value	0.0e+00
Match length	799
% identity	93
NCBI Description	Gossypium hirsutum proline-rich cell wall protein mRNA, complete cds

Seq. No.	189972
Contig ID	3_2.R1039
5'-most EST	g5044970
Method	BLASTX
NCBI GI	g451544
BLAST score	180
E value	8.0e-13
Match length	111
% identity	62
NCBI Description	(U04267) proline-rich cell wall protein [Gossypium barbadense]

Seq. No.	189973
Contig ID	3_3.R1039
5'-most EST	LIB3166-047-P1-K1-F8
Method	BLASTX
NCBI GI	g2558654
BLAST score	178
E value	1.0e-12
Match length	97
% identity	41
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	189974
Contig ID	4_1.R1039
5'-most EST	LIB3189-031-P1-K1-F11
Method	BLASTX
NCBI GI	g232024
BLAST score	825
E value	1.0e-119
Match length	210
% identity	100
NCBI Description	PROTEIN E6 >gi|421806|pir||A46130 fiber protein - upland cotton >gi|2129498|pir||S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi|167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi|1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	189975
Contig ID	4_2.R1039
5'-most EST	gb5046243
Method	BLASTX
NCBI GI	g2062167
BLAST score	1160
E value	1.0e-127
Match length	321
% identity	68
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	189976
Contig ID	4_3.R1039
5'-most EST	LIB3189-030-P1-K1-H6
Method	BLASTX
NCBI GI	g2129499
BLAST score	1082
E value	1.0e-118
Match length	235
% identity	88
NCBI Description	fiber protein E6 (clone CKE6-4A) - upland cotton >gi|1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No.	189977
Contig ID	4_4.R1039
5'-most EST	LIB3145-019-Q1-K1-E7
Method	BLASTX
NCBI GI	g2062167
BLAST score	566
E value	5.0e-62
Match length	155
% identity	79
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	189978
Contig ID	4_5.R1039
5'-most EST	LIB3147-031-Q1-K1-E9
Method	BLASTX
NCBI GI	g2062167

BLAST score	343
E value	3.0e-32
Match length	110
% identity	61
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	189979
Contig ID	4_7.R1039
5'-most EST	LIB3197-005-P1-M1-G4
Method	BLASTX
NCBI GI	g232024
BLAST score	381
E value	1.0e-36
Match length	101
% identity	85
NCBI Description	PROTEIN E6 >gi|421806|pir||A46130 fiber protein - upland cotton >gi|2129498|pir||S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi|167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi|1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	189980
Contig ID	5_1.R1039
5'-most EST	LIB3166-021-P1-K1-F10
Method	BLASTN
NCBI GI	g167327
BLAST score	595
E value	0.0e+00
Match length	595
% identity	100
NCBI Description	Gossypium hirsutum group 4 late embryogenesis-abundant protein (Lea14-A) mRNA, complete cds

Seq. No.	189981
Contig ID	6_1.R1039
5'-most EST	g167338
Method	BLASTX
NCBI GI	g126076
BLAST score	521
E value	8.0e-53
Match length	102
% identity	100
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN D-19 (LEA D-19) >gi|81551|pir||S19225 embryonic abundant protein D-19 - upland cotton >gi|18494|emb|CAA31593| (X13205) D-19 Lea protein [Gossypium hirsutum] >gi|167321 (M85261) putative desiccation protectant; putative [Gossypium hirsutum] >gi|167337 (M73752) Lea4-A [Gossypium hirsutum] >gi|167339 (M86754) Lea4-A108 protein [Gossypium hirsutum] >gi|167341 (M73751) Lea4-D D19 protein [Gossypium hirsutum] >gi|167343 (M86753) Lea4-D9 protein [Gossypium hirsutum] >gi|444335|prf||1906384A water stress-related protein [Gossypium hirsutum]

Seq. No.	189982
Contig ID	9_1.R1039

5'-most EST	uC-gsflnu33B061f02b1
Method	BLASTX
NCBI GI	g1170747
BLAST score	474
E value	2.0e-47
Match length	105
% identity	88
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi|167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	189983
Contig ID	9_3.R1039
5'-most EST	LIB3135-002-Q1-K1-A10
Method	BLASTX
NCBI GI	g1170747
BLAST score	293
E value	3.0e-45
Match length	101
% identity	97
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi|167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	189984
Contig ID	9_4.R1039
5'-most EST	LIB3048-015-Q1-L1-G11
Method	BLASTX
NCBI GI	g585550
BLAST score	297
E value	1.0e-26
Match length	70
% identity	79
NCBI Description	NADPH-CYTOCHROME P450 REDUCTASE (CPR) >gi|295448 (L07843) NADPH cytochrome P450 [Vigna radiata]

Seq. No.	189985
Contig ID	13_1.R1039
5'-most EST	LIB3196-056-P1-M1-B7
Method	BLASTX
NCBI GI	g3915742
BLAST score	2131
E value	0.0e+00
Match length	509
% identity	82
NCBI Description	LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi|167319 (M69188) legumin A [Gossypium hirsutum] >gi|444320|prf||1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum]

Seq. No.	189986
Contig ID	14_1.R1039
5'-most EST	g437326
Method	BLASTX
NCBI GI	g437327

BLAST score	1461
E value	1.0e-163
Match length	294
% identity	93
NCBI Description	(L04497) MYB A; putative [Gossypium hirsutum]

Seq. No.	189987
Contig ID	14_2.R1039
5'-most EST	uC-gsronu33B136f03b1
Method	BLASTX
NCBI GI	g437327
BLAST score	799
E value	6.0e-91
Match length	218
% identity	79
NCBI Description	(L04497) MYB A; putative [Gossypium hirsutum]

Seq. No.	189988
Contig ID	15_1.R1039
5'-most EST	LIB3196-057-P1-M1-F7
Method	BLASTX
NCBI GI	g266691
BLAST score	593
E value	3.0e-61
Match length	154
% identity	78
NCBI Description	OLEOSIN 16.4 KD >gi|167361 (L00934) 16.4 kDa oleosin [Gossypium hirsutum]

Seq. No.	189989
Contig ID	16_1.R1039
5'-most EST	g167362
Method	BLASTX
NCBI GI	g266690
BLAST score	655
E value	2.0e-68
Match length	168
% identity	78
NCBI Description	OLEOSIN 18.2 KD >gi|167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi|167365 (L00936) 18.2 kDa oleosin [Gossypium hirsutum]

Seq. No.	189990
Contig ID	17_1.R1039
5'-most EST	LIB3272-026-P1-K1-A7
Method	BLASTX
NCBI GI	g167367
BLAST score	1582
E value	1.0e-177
Match length	332
% identity	91
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]

Seq. No.	189991
Contig ID	17_2.R1039
5'-most EST	LIB3166-037-P1-K1-E7
Method	BLASTX

NCBI GI	g3822223
BLAST score	387
E value	2.0e-37
Match length	83
% identity	83
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	189992
Contig ID	17_5.R1039
5'-most EST	LIB3148-059-Q1-K1-G4
Method	BLASTN
NCBI GI	g167366
BLAST score	223
E value	1.0e-122
Match length	339
% identity	93
NCBI Description	Gossypium hirsutum peroxidase mRNA, complete cds

Seq. No.	189993
Contig ID	18_1.R1039
5'-most EST	LIB3196-045-P1-M1-C4
Method	BLASTX
NCBI GI	g126156
BLAST score	2096
E value	0.0e+00
Match length	516
% identity	81
NCBI Description	LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi|72288|pir||FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi|167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi|1171335 (U43727) legumin B [Gossypium hirsutum] >gi|225582|prf||1306412C storage protein C134 [Saguinus oedipus]

Seq. No.	189994
Contig ID	19_1.R1039
5'-most EST	LIB3196-036-P1-M1-B11
Method	BLASTX
NCBI GI	g137580
BLAST score	2027
E value	0.0e+00
Match length	589
% identity	70
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72) >gi|72286|pir||FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi|167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No.	189995
Contig ID	19_2.R1039
5'-most EST	LIB3196-050-P1-M1-H6
Method	BLASTX
NCBI GI	g125080
BLAST score	1053
E value	1.0e-120
Match length	233

% identity	97
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi|2144816|pir||KRHUE keratin, 50K type I cytoskeletal - human >gi|386848 (J00124) keratin [Homo sapiens] >gi|4504913|ref|NP_000517.1|pKRT14| keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	189996
Contig ID	19_3.R1039
5'-most EST	LIB3196-034-P1-M1-A1
Method	BLASTX
NCBI GI	g137578
BLAST score	798
E value	2.0e-85
Match length	236
% identity	65
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi|81545|pir||S06398 alpha-globulin type A precursor - upland cotton >gi|167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi|207906 (M18027) alpha globulin A [Artificial gene] >gi|226119|prf||1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	189997
Contig ID	19_4.R1039
5'-most EST	LIB3196-014-P1-M1-G4
Method	BLASTX
NCBI GI	g137578
BLAST score	1439
E value	1.0e-160
Match length	361
% identity	79
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi|81545|pir||S06398 alpha-globulin type A precursor - upland cotton >gi|167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi|207906 (M18027) alpha globulin A [Artificial gene] >gi|226119|prf||1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	189998
Contig ID	19_5.R1039
5'-most EST	LIB3196-024-P1-M1-D4
Method	BLASTX
NCBI GI	g1363944
BLAST score	1159
E value	1.0e-127
Match length	283
% identity	89
NCBI Description	type I keratin 16 - human >gi|1195531|bbs|172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens]

Seq. No.	189999
Contig ID	19_6.R1039
5'-most EST	LIB3196-014-P1-M1-E10
Method	BLASTX
NCBI GI	g280816

BLAST score	930
E value	1.0e-100
Match length	187
% identity	99
NCBI Description	keratin 13, type I, cytoskeletal, short form - human >gi|30377|emb|CAA36673| (X52426) cytokeratin 13 [Homo sapiens] >gi|3603253 (AF049259) keratin 13 [Homo sapiens] >gi|4504911|ref|NP_002265.1|pKRT13| keratin

Seq. No.	190000
Contig ID	19_9.R1039
5'-most EST	LIB3196-013-P1-M1-G1
Method	BLASTN
NCBI GI	g4504912
BLAST score	378
E value	0.0e+00
Match length	544
% identity	96
NCBI Description	Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) (KRT14) mRNA

Seq. No.	190001
Contig ID	19_11.R1039
5'-most EST	LIB3196-022-P1-M1-F4
Method	BLASTX
NCBI GI	g125080
BLAST score	557
E value	3.0e-91
Match length	234
% identity	80
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi|2144816|pir||KRHUE keratin, 50K type I cytoskeletal - human >gi|386848 (J00124) keratin [Homo sapiens] >gi|4504913|ref|NP_000517.1|pKRT14| keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No.	190002
Contig ID	19_14.R1039
5'-most EST	LIB3196-034-P1-M1-G9
Method	BLASTX
NCBI GI	g547751
BLAST score	835
E value	1.0e-89
Match length	177
% identity	94
NCBI Description	KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK 17) (39.1) (VERSION 1) >gi|422802|pir||S30433 keratin 17, cytoskeletal - human >gi|30379|emb|CAA79626| (Z19574) cytokeratin 17 [Homo sapiens] >gi|34075|emb|CAA44451| (X62571) keratin related product [Homo sapiens] >gi|4557701|ref|NP_000413.1|pKRT17| keratin

Seq. No.	190003
Contig ID	24_1.R1039
5'-most EST	LIB3135-047-Q1-K1-A4
Method	BLASTX
NCBI GI	g126075

BLAST score	335
E value	3.0e-31
Match length	143
% identity	50
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN D-113 (LEA D-113) >gi|81550|pir||S04044 embryonic abundant protein D-113 - upland cotton >gi|18492|emb|CAA31590| (X13202) D-113 Lea protein [Gossypium hirsutum] >gi|226553|prf||1601521C Lea D-113 gene [Saguinus oedipus]

Seq. No.	190004
Contig ID	25_1.R1039
5'-most EST	LIB3165-037-P1-K1-G2
Method	BLASTX
NCBI GI	g4468153
BLAST score	601
E value	1.0e-73
Match length	181
% identity	75
NCBI Description	(AJ132000) sucrose synthase [Craterostigma plantagineum]

Seq. No.	190005
Contig ID	26_1.R1039
5'-most EST	LIB3189-005-P1-K1-C8
Method	BLASTX
NCBI GI	g2244732
BLAST score	1465
E value	1.0e-163
Match length	265
% identity	100
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	190006
Contig ID	27_1.R1039
5'-most EST	uC-gsflmaxxa055d10b1
Method	BLASTX
NCBI GI	g1669387
BLAST score	1539
E value	0.0e+00
Match length	376
% identity	93
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	190007
Contig ID	27_2.R1039
5'-most EST	g5045598
Method	BLASTX
NCBI GI	g3420239
BLAST score	1647
E value	0.0e+00
Match length	373
% identity	90
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	190008
Contig ID	27_3.R1039
5'-most EST	uC-gsflnu33B132h09b1

Method	BLASTX
NCBI GI	g1168324
BLAST score	710
E value	6.0e-84
Match length	233
% identity	77
NCBI Description	ACTIN 3 >gi|2119318|pir||S58316 actin - garden pea >gi|940813|emb|CAA62028| (X90378) actin [Pisum sativum]

Seq. No.	190009
Contig ID	27_4.R1039
5'-most EST	LIB3189-045-P1-K1-D11
Method	BLASTX
NCBI GI	g3420239
BLAST score	771
E value	1.0e-158
Match length	301
% identity	93
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	190010
Contig ID	27_5.R1039
5'-most EST	uC-gsronu33B167f11b1
Method	BLASTX
NCBI GI	g2244734
BLAST score	589
E value	7.0e-61
Match length	115
% identity	98
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No.	190011
Contig ID	27_6.R1039
5'-most EST	LIB3147-017-Q1-K1-F7
Method	BLASTX
NCBI GI	g1351869
BLAST score	253
E value	3.0e-38
Match length	122
% identity	78
NCBI Description	ACTIN >gi|508701 (U10867) actin [Filobasidiella neoformans]

Seq. No.	190012
Contig ID	27_7.R1039
5'-most EST	LIB3165-033-P1-K1-A9
Method	BLASTX
NCBI GI	g131397
BLAST score	641
E value	8.0e-67
Match length	230
% identity	60
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi|81480|pir||S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi|755802|emb|CAA29056| (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia

oleracea] >gi|225597|prf||1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	190013
Contig ID	27_8.R1039
5'-most EST	LIB3272-003-P1-K1-C4
Method	BLASTX
NCBI GI	g461465
BLAST score	717
E value	5.0e-76
Match length	137
% identity	98
NCBI Description	ACTIN >gi|322751|pir||S31933 actin - common tobacco >gi|22609|emb|CAA45149| (X63603) actin [Nicotiana tabacum]

Seq. No.	190014
Contig ID	27_9.R1039
5'-most EST	LIB3120-010-Q1-K1-C1
Method	BLASTX
NCBI GI	g131397
BLAST score	359
E value	5.0e-34
Match length	151
% identity	56
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi|81480|pir||S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi|755802|emb|CAA29056| (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi|225597|prf||1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	190015
Contig ID	27_10.R1039
5'-most EST	LIB3165-011-P1-K1-G2
Method	BLASTX
NCBI GI	g1703129
BLAST score	679
E value	1.0e-71
Match length	127
% identity	99
NCBI Description	ACTIN 11 >gi|2129522|pir||S68109 actin 11 - Arabidopsis thaliana >gi|1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	190016
Contig ID	27_11.R1039
5'-most EST	uC-gsflnu33B029h12b1
Method	BLASTX
NCBI GI	g1703129
BLAST score	654
E value	1.0e-68
Match length	124
% identity	100
NCBI Description	ACTIN 11 >gi|2129522|pir||S68109 actin 11 - Arabidopsis thaliana >gi|1002533 (U27981) actin-11 [Arabidopsis

thaliana]

Seq. No.	190017
Contig ID	27_13.R1039
5'-most EST	g5049938
Method	BLASTX
NCBI GI	g3980383
BLAST score	360
E value	6.0e-34
Match length	83
% identity	78
NCBI Description	(AC004561) unknown protein [Arabidopsis thaliana]

Seq. No.	190018
Contig ID	27_14.R1039
5'-most EST	LIB3145-007-Q1-K1-A1
Method	BLASTX
NCBI GI	g3980383
BLAST score	354
E value	1.0e-33
Match length	76
% identity	83
NCBI Description	(AC004561) unknown protein [Arabidopsis thaliana]

Seq. No.	190019
Contig ID	27_15.R1039
5'-most EST	LIB3147-006-Q1-K1-H4
Method	BLASTN
NCBI GI	g2244733
BLAST score	161
E value	3.0e-85
Match length	358
% identity	86
NCBI Description	Cotton mRNA for actin, clone CF456, partial cds

Seq. No.	190020
Contig ID	27_16.R1039
5'-most EST	LIB3272-015-P1-K1-B9
Method	BLASTX
NCBI GI	g1703108
BLAST score	568
E value	1.0e-58
Match length	104
% identity	100
NCBI Description	ACTIN 2/7 >gi|2129525|pir||S71210 actin 2 - Arabidopsis thaliana >gi|2129528|pir||S68107 actin 7 - Arabidopsis thaliana >gi|1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi|1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	190021
Contig ID	27_17.R1039
5'-most EST	LIB3147-040-Q1-K1-G11
Method	BLASTX
NCBI GI	g3219769
BLAST score	338
E value	5.0e-51

Match length	137
% identity	83
NCBI Description	ACTIN 42 >gi|1498380 (U60488) actin [Solanum tuberosum]

Seq. No.	190022
Contig ID	27_18.R1039
5'-most EST	LIB3165-022-P1-K1-C4
Method	BLASTX
NCBI GI	g1666234
BLAST score	333
E value	4.0e-31
Match length	66
% identity	97
NCBI Description	(U76193) actin [Pisum sativum] >gi|1724143 (U81049) actin [Pisum sativum]

Seq. No.	190023
Contig ID	27_25.R1039
5'-most EST	LIB3149-055-Q1-K1-F4
Method	BLASTX
NCBI GI	g4139264
BLAST score	267
E value	4.0e-23
Match length	59
% identity	92
NCBI Description	(AF111812) actin [Brassica napus]

Seq. No.	190024
Contig ID	27_28.R1039
5'-most EST	LIB3165-001-Q1-K1-A3
Method	BLASTX
NCBI GI	g131397
BLAST score	314
E value	1.0e-28
Match length	126
% identity	57
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi|81480|pir||S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi|755802|emb|CAA29056| (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi|225597|prf||1307179B luminal protein 16kD [Spinacia oleracea]

Seq. No.	190025
Contig ID	27_31.R1039
5'-most EST	LIB3197-053-Q1-M1-C4
Method	BLASTX
NCBI GI	g2244734
BLAST score	284
E value	3.0e-25
Match length	57
% identity	95
NCBI Description	(D88414) actin [Gossypium hirsutum]

Seq. No. 190026

Contig ID	27_33.R1039
5'-most EST	LIB3147-010-Q1-K1-G12
Method	BLASTX
NCBI GI	g1168322
BLAST score	317
E value	2.0e-29
Match length	63
% identity	97
NCBI Description	ACTIN 71 >gi|21538|emb|CAA39279| (X55750) actin [Solanum tuberosum]

Seq. No.	190027
Contig ID	28_1.R1039
5'-most EST	LIB3197-005-P1-M1-H6
Method	BLASTX
NCBI GI	g2811278
BLAST score	1132
E value	1.0e-124
Match length	247
% identity	85
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	190028
Contig ID	28_2.R1039
5'-most EST	LIB3189-001-P1-K1-H6
Method	BLASTN
NCBI GI	g2244735
BLAST score	596
E value	0.0e+00
Match length	752
% identity	95
NCBI Description	Cotton mRNA for expansin, clone CF631, partial cds

Seq. No.	190029
Contig ID	29_1.R1039
5'-most EST	g2244737
Method	BLASTX
NCBI GI	g2244738
BLAST score	1351
E value	1.0e-150
Match length	266
% identity	100
NCBI Description	(D88416) endo-1,3-beta-glucanase [Gossypium hirsutum]

Seq. No.	190030
Contig ID	30_5.R1039
5'-most EST	LIB3147-032-Q1-K1-D4

Seq. No.	190031
Contig ID	30_6.R1039
5'-most EST	LIB3196-009-P1-M1-E4
Method	BLASTX
NCBI GI	g2196542
BLAST score	169
E value	5.0e-12
Match length	45
% identity	73

NCBI Description	(AF001894) glycine-rich protein [Oryza sativa]

Seq. No.	190032
Contig ID	30_7.R1039
5'-most EST	g5050302
Method	BLASTX
NCBI GI	g3342249
BLAST score	285
E value	1.0e-25
Match length	82
% identity	68
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi|3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	190033
Contig ID	30_8.R1039
5'-most EST	LIB3147-032-Q1-K1-G11
Method	BLASTX
NCBI GI	g232274
BLAST score	361
E value	6.0e-36
Match length	124
% identity	66
NCBI Description	17.6 KD CLASS II HEAT SHOCK PROTEIN >gi|71499|pir||HHMU17 heat shock protein 17.6-II - Arabidopsis thaliana >gi|16338|emb|CAA45039| (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]

Seq. No.	190034
Contig ID	30_9.R1039
5'-most EST	g5049426
Method	BLASTX
NCBI GI	g1168195
BLAST score	599
E value	5.0e-62
Match length	155
% identity	77
NCBI Description	14-3-3-LIKE PROTEIN >gi|478595|pir||S20580 protein kinase C inhibitor homolog - Hooker's evening primrose >gi|20062|emb|CAA44642| (X62838) protein kinase C inhibitor homologue [Oenothera elata subsp. hookeri]

Seq. No.	190035
Contig ID	30_10.R1039
5'-most EST	LIB3145-045-Q1-K1-C2
Method	BLASTX
NCBI GI	g1351988
BLAST score	710
E value	3.0e-75
Match length	158
% identity	84
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi|1084354|pir||S52387 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - wild cabbage >gi|669057|emb|CAA59138| (X84448) asparagine synthase (glutamine-hydrolysing) [Brassica oleracea]

Seq. No.	190036
Contig ID	30_11.R1039
5'-most EST	LIB3145-045-Q1-K1-D6
Method	BLASTN
NCBI GI	g3132674
BLAST score	138
E value	1.0e-71
Match length	454
% identity	83
NCBI Description	Elaeagnus umbellata asparagine synthetase (AS) mRNA, complete cds

Seq. No.	190037
Contig ID	30_12.R1039
5'-most EST	uC-gsflmaxxa048g06b1
Method	BLASTX
NCBI GI	g3355468
BLAST score	540
E value	3.0e-55
Match length	123
% identity	90
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	190038
Contig ID	30_13.R1039
5'-most EST	LIB3148-028-Q1-K1-G6

Seq. No.	190039
Contig ID	30_14.R1039
5'-most EST	LIB3197-034-Q1-M1-E10
Method	BLASTX
NCBI GI	g1916613
BLAST score	196
E value	9.0e-15
Match length	96
% identity	51
NCBI Description	(U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	190040
Contig ID	30_15.R1039
5'-most EST	LIB3272-030-P1-K1-C8
Method	BLASTX
NCBI GI	g2244740
BLAST score	403
E value	4.0e-39
Match length	92
% identity	82
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	190041
Contig ID	30_16.R1039
5'-most EST	uC-gsflmaxxa096f09b1
Method	BLASTX
NCBI GI	g1350707
BLAST score	217

E value	1.0e-17
Match length	52
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L29 >gi|539923|pir||JC2012 ribosomal protein 17K - mouse >gi|404766 (L08651) ribosomal protein [Mus musculus]

Seq. No.	190042
Contig ID	30_17.R1039
5'-most EST	LIB3120-008-Q1-K1-G9
Method	BLASTX
NCBI GI	g730463
BLAST score	315
E value	9.0e-29
Match length	105
% identity	58
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi|630323|pir||S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi|484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi|1420537|emb|CAA99454| (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	190043
Contig ID	30_18.R1039
5'-most EST	LIB3145-035-Q1-K1-E5
Method	BLASTX
NCBI GI	g3176668
BLAST score	460
E value	6.0e-46
Match length	102
% identity	84
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb|X62724 from Hordeum vulgare. ESTs gb|Z34728, gb|F19974, gb|T75677 and gb|Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	190044
Contig ID	30_19.R1039
5'-most EST	uC-gsronu33B058a04b1
Method	BLASTX
NCBI GI	g1350707
BLAST score	121
E value	2.0e-12
Match length	52
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L29 >gi|539923|pir||JC2012 ribosomal protein 17K - mouse >gi|404766 (L08651) ribosomal protein [Mus musculus]

Seq. No.	190045
Contig ID	30_20.R1039
5'-most EST	uC-gsflmaxxa005e05b1

Seq. No.	190046
Contig ID	30_21.R1039
5'-most EST	LIB3272-034-P1-K1-A4
Method	BLASTX

NCBI GI	g1813335
BLAST score	470
E value	8.0e-72
Match length	223
% identity	62
NCBI Description	(AB000703) phosphomannomutase [Schizosaccharomyces pombe]

Seq. No.	190047
Contig ID	30_22.R1039
5'-most EST	LIB3189-004-P1-K1-C4
Method	BLASTX
NCBI GI	g730526
BLAST score	397
E value	3.0e-38
Match length	194
% identity	35
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi|480787|pir||S37271 ribosomal protein L13 - Arabidopsis thaliana >gi|404166|emb|CAA53005| (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	190048
Contig ID	30_23.R1039
5'-most EST	LIB3147-005-Q1-K1-D12
Method	BLASTX
NCBI GI	g730450
BLAST score	608
E value	2.0e-72
Match length	181
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) >gi|480649|pir||S37134 cold-induced protein BnC24B - rape >gi|398922|emb|CAA80343| (Z22620) cold induced protein (BnC24B) [Brassica napus]

Seq. No.	190049
Contig ID	30_24.R1039
5'-most EST	LIB3272-052-P1-K1-D8
Method	BLASTX
NCBI GI	g730526
BLAST score	805
E value	4.0e-86
Match length	193
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi|480787|pir||S37271 ribosomal protein L13 - Arabidopsis thaliana >gi|404166|emb|CAA53005| (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	190050
Contig ID	30_25.R1039
5'-most EST	uC-gsflnu33B060e07b1
Method	BLASTX
NCBI GI	g2244740
BLAST score	1410
E value	1.0e-157
Match length	324

% identity	83
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	190051
Contig ID	30_26.R1039
5'-most EST	uC-gsronu33B015b08b1
Method	BLASTX
NCBI GI	g132964
BLAST score	212
E value	8.0e-17
Match length	52
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L29 (P23) >gi|71376|pir||R6RT43 ribosomal protein RL43 - rat >gi|57145|emb|CAA43146| (X60744) ribosomal protein [Rattus norvegicus] >gi|312208|emb|CAA48344| (X68283) rat ribosomal protein L29 [Rattus norvegicus]

Seq. No.	190052
Contig ID	30_27.R1039
5'-most EST	LIB3048-054-Q1-L1-A3
Method	BLASTX
NCBI GI	g1086252
BLAST score	839
E value	8.0e-90
Match length	305
% identity	55
NCBI Description	sucrose cleavage protein - Potato >gi|707001|bbs|157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	190053
Contig ID	30_28.R1039
5'-most EST	g3326440
Method	BLASTX
NCBI GI	g3386615
BLAST score	161
E value	2.0e-10
Match length	40
% identity	72
NCBI Description	(AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No.	190054
Contig ID	30_29.R1039
5'-most EST	LIB3189-040-P1-K1-H10
Method	BLASTN
NCBI GI	g2687433
BLAST score	81
E value	2.0e-37
Match length	117
% identity	92
NCBI Description	Tragopogon dubius large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	190055

Contig ID	30_30.R1039
5'-most EST	uC-gsflnu33B018f12b1
Method	BLASTX
NCBI GI	g730463
BLAST score	246
E value	1.0e-21
Match length	97
% identity	59
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi|630323|pir||S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi|484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi|1420537|emb|CAA99454| (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	190056
Contig ID	30_31.R1039
5'-most EST	LIB3048-022-Q1-L1-C8
Method	BLASTX
NCBI GI	g1305549
BLAST score	510
E value	1.0e-129
Match length	291
% identity	83
NCBI Description	(U55874) asparagine synthetase [Glycine max]

Seq. No.	190057
Contig ID	30_32.R1039
5'-most EST	g5050651

Seq. No.	190058
Contig ID	30_33.R1039
5'-most EST	LIB3147-034-Q1-K1-D12
Method	BLASTX
NCBI GI	g1168196
BLAST score	1058
E value	1.0e-115
Match length	256
% identity	85
NCBI Description	14-3-3-LIKE PROTEIN >gi|555974 (U15036) 14-3-3-like protein [Pisum sativum]

Seq. No.	190059
Contig ID	30_34.R1039
5'-most EST	LIB3149-013-Q1-K1-A4
Method	BLASTX
NCBI GI	g730463
BLAST score	178
E value	3.0e-25
Match length	105
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi|630323|pir||S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi|484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi|1420537|emb|CAA99454| (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	190060
Contig ID	30_35.R1039
5'-most EST	uC-gsronu33B111e05b1
Method	BLASTX
NCBI GI	g3355468
BLAST score	305
E value	4.0e-46
Match length	123
% identity	73
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	190061
Contig ID	30_36.R1039
5'-most EST	LIB3083-002-Q1-L1-H5
Method	BLASTX
NCBI GI	g3513727
BLAST score	842
E value	1.0e-135
Match length	339
% identity	54
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi|4539358|emb|CAB40052.1| (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	190062
Contig ID	30_37.R1039
5'-most EST	LIB3272-055-P1-K1-A11
Method	BLASTX
NCBI GI	g629483
BLAST score	187
E value	6.0e-18
Match length	118
% identity	47
NCBI Description	gene 1-Sc3 protein - European white birch >gi|534898|emb|CAA54696| (X77601) 1 Sc-3 [Betula pendula] >gi|1584322|prf||2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No.	190063
Contig ID	30_38.R1039
5'-most EST	uC-gsronu33B164f02b2
Method	BLASTX
NCBI GI	g2414158
BLAST score	211
E value	2.0e-16
Match length	148
% identity	39
NCBI Description	(Z72436) major allergen Bet v 1 [Betula pendula]

Seq. No.	190064
Contig ID	30_39.R1039
5'-most EST	g5048902

Seq. No.	190065
Contig ID	30_40.R1039
5'-most EST	uC-gsronu33B016a12b1
Method	BLASTX
NCBI GI	g3821280
BLAST score	1123
E value	1.0e-154
Match length	327
% identity	77
NCBI Description	(AJ009952) asparagine synthetase type II [Phaseolus vulgaris]

Seq. No.	190066
Contig ID	30_41.R1039
5'-most EST	LIB3147-037-Q1-K2-E7
Method	BLASTX
NCBI GI	g730449
BLAST score	428
E value	8.0e-79
Match length	193
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi|480647|pir||S37132 ribosomal protein L13.A - rape >gi|398918|emb|CAA80341| (Z22618) cold induced protein (BnC24A) [Brassica napus]

Seq. No.	190067
Contig ID	30_42.R1039
5'-most EST	LIB3135-046-Q1-K1-F2
Method	BLASTX
NCBI GI	g629483
BLAST score	224
E value	6.0e-38
Match length	159
% identity	55
NCBI Description	gene 1-Sc3 protein - European white birch >gi|534898|emb|CAA54696| (X77601) 1 Sc-3 [Betula pendula] >gi|1584322|prf||2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No.	190068
Contig ID	30_43.R1039
5'-most EST	uC-gsflnu33B005d09b1
Method	BLASTX
NCBI GI	g2267567
BLAST score	266
E value	1.0e-29
Match length	81
% identity	80
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi|2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	190069
Contig ID	30_44.R1039
5'-most EST	LIB3120-026-Q1-K1-B2
Method	BLASTX

NCBI GI	g1781348
BLAST score	837
E value	1.0e-151
Match length	349
% identity	82
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	190070
Contig ID	30_45.R1039
5'-most EST	LIB3189-017-P1-K1-A1
Method	BLASTN
NCBI GI	g2687434
BLAST score	452
E value	0.0e+00
Match length	786
% identity	91
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	190071
Contig ID	30_46.R1039
5'-most EST	uC-gsflnu33B022f03b1
Method	BLASTX
NCBI GI	g1928981
BLAST score	781
E value	2.0e-83
Match length	188
% identity	86
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No.	190072
Contig ID	30_47.R1039
5'-most EST	uC-gsronu33B145b03b1
Method	BLASTX
NCBI GI	g3901018
BLAST score	91
E value	9.0e-11
Match length	128
% identity	51
NCBI Description	(AJ130889) stress and pathogenesis-related protein [Fagus sylvatica]

Seq. No.	190073
Contig ID	30_48.R1039
5'-most EST	g5050645
Method	BLASTX
NCBI GI	g1545805
BLAST score	359
E value	3.0e-33
Match length	246
% identity	46
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	190074
Contig ID	32_1.R1039

5'-most EST	LIB3272-007-P1-K1-D8
Method	BLASTX
NCBI GI	g1345674
BLAST score	2691
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	CATALASE ISOZYME 1 >gi|99598|pir||S10770 catalase (EC 1.11.1.6) - upland cotton >gi|18484|emb|CAA36380| (X52135) catalase subunit 1 (AA 1-492) [Gossypium hirsutum]

Seq. No.	190075
Contig ID	32_2.R1039
5'-most EST	LIB3166-005-P1-K1-A8
Method	BLASTX
NCBI GI	g1345674
BLAST score	530
E value	1.0e-113
Match length	241
% identity	87
NCBI Description	CATALASE ISOZYME 1 >gi|99598|pir||S10770 catalase (EC 1.11.1.6) - upland cotton >gi|18484|emb|CAA36380| (X52135) catalase subunit 1 (AA 1-492) [Gossypium hirsutum]

Seq. No.	190076
Contig ID	33_1.R1039
5'-most EST	g18485
Method	BLASTX
NCBI GI	g113029
BLAST score	2875
E value	0.0e+00
Match length	576
% identity	95
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi|68209|pir||WZCNIU isocitrate lyase (EC 4.1.3.1) - upland cotton >gi|18486|emb|CAA36381| (X52136) isocitrate lyase (AA 1-576) [Gossypium hirsutum]

Seq. No.	190077
Contig ID	34_1.R1039
5'-most EST	LIB3165-007-P1-K1-H12
Method	BLASTX
NCBI GI	g231688
BLAST score	2684
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi|99599|pir||S17493 catalase (EC 1.11.1.6) - upland cotton >gi|18488|emb|CAA39998| (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	190078
Contig ID	34_3.R1039
5'-most EST	LIB3165-021-P1-K1-A11
Method	BLASTX
NCBI GI	g231688
BLAST score	298

E value	5.0e-27
Match length	57
% identity	100
NCBI Description	CATALASE ISOZYME 2 >gi|99599|pir||S17493 catalase (EC 1.11.1.6) - upland cotton >gi|18488|emb|CAA39998| (X56675) subunit 2 of cotton catalase [Gossypium hirsutum]

Seq. No.	190079
Contig ID	36_1.R1039
5'-most EST	g18506
Method	BLASTX
NCBI GI	g126770
BLAST score	3014
E value	0.0e+00
Match length	567
% identity	100
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi|68218|pir||SYCNMU malate synthase (EC 4.1.3.2) - upland cotton >gi|18507|emb|CAA36546| (X52305) malate synthase (AA 1-567) [Gossypium hirsutum]

Seq. No.	190080
Contig ID	37_1.R1039
5'-most EST	LIB3196-021-P1-M1-G7
Method	BLASTX
NCBI GI	g2578033
BLAST score	2081
E value	0.0e+00
Match length	385
% identity	98
NCBI Description	(X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	190081
Contig ID	38_1.R1039
5'-most EST	LIB3147-003-Q1-K1-G8
Method	BLASTX
NCBI GI	g1173209
BLAST score	737
E value	3.0e-78
Match length	145
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi|541835|pir||S41193 ribosomal protein S16 protein - upland cotton >gi|439654|emb|CAA53567| (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No.	190082
Contig ID	38_2.R1039
5'-most EST	LIB3196-041-P1-M1-B3
Method	BLASTX
NCBI GI	g1702983
BLAST score	351
E value	8.0e-33
Match length	110
% identity	59
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi|99855|pir||S11850 hypothetical protein - garden strawberry

>gi|22573|emb|CAA36676| (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi|927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No.	190083
Contig ID	38_3.R1039
5'-most EST	uC-gsflmaxxa097b09b1
Method	BLASTX
NCBI GI	g1173209
BLAST score	470
E value	2.0e-66
Match length	143
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi|541835|pir||S41193 ribosomal protein S16 protein - upland cotton >gi|439654|emb|CAA53567| (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No.	190084
Contig ID	38_4.R1039
5'-most EST	uC-gsflnu33B078d05b1
Method	BLASTX
NCBI GI	g1173209
BLAST score	559
E value	1.0e-57
Match length	118
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi|541835|pir||S41193 ribosomal protein S16 protein - upland cotton >gi|439654|emb|CAA53567| (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No.	190085
Contig ID	38_7.R1039
5'-most EST	LIB3083-105-Q1-L1-D10
Method	BLASTX
NCBI GI	g2995990
BLAST score	168
E value	4.0e-14
Match length	116
% identity	48
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi|2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	190086
Contig ID	39_1.R1039
5'-most EST	LIB3196-044-P1-M1-G2
Method	BLASTN
NCBI GI	g407800
BLAST score	414
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	G.hirsutum mRNA for ribosomal protein 41, large subunit (RL41)

Seq. No.	190087
Contig ID	40_1.R1039
5'-most EST	g5045577
Method	BLASTX
NCBI GI	g1173256
BLAST score	1214
E value	1.0e-134
Match length	256
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein S4 - upland cotton >gi|488739|emb|CAA55882| (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	190088
Contig ID	40_2.R1039
5'-most EST	g5048270
Method	BLASTX
NCBI GI	g1173256
BLAST score	1141
E value	1.0e-125
Match length	256
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein S4 - upland cotton >gi|488739|emb|CAA55882| (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	190089
Contig ID	40_3.R1039
5'-most EST	LIB3196-006-P1-M1-C4
Method	BLASTX
NCBI GI	g1173256
BLAST score	967
E value	1.0e-105
Match length	206
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein S4 - upland cotton >gi|488739|emb|CAA55882| (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	190090
Contig ID	40_5.R1039
5'-most EST	LIB3146-047-Q1-K1-A12
Method	BLASTX
NCBI GI	g1173256
BLAST score	381
E value	1.0e-36
Match length	97
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein S4 - upland cotton >gi|488739|emb|CAA55882| (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	190091

Contig ID	40_6.R1039
5'-most EST	uC-gsronu33B058c06b1
Method	BLASTX
NCBI GI	g1173256
BLAST score	529
E value	4.0e-54
Match length	101
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein S4 - upland cotton >gi|488739|emb|CAA55882| (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No.	190092
Contig ID	41_1.R1039
5'-most EST	LIB3147-005-Q1-K1-G12
Method	BLASTX
NCBI GI	g3915031
BLAST score	2050
E value	0.0e+00
Match length	396
% identity	99
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi|1217628|emb|CAA65232| (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	190093
Contig ID	41_2.R1039
5'-most EST	LIB3146-047-Q1-K1-B3
Method	BLASTX
NCBI GI	g3915031
BLAST score	1220
E value	1.0e-134
Match length	271
% identity	85
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi|1217628|emb|CAA65232| (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	190094
Contig ID	41_4.R1039
5'-most EST	LIB3083-063-Q1-L1-B9
Method	BLASTX
NCBI GI	g3915031
BLAST score	661
E value	2.0e-77
Match length	177
% identity	84
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi|1217628|emb|CAA65232| (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]

Seq. No.	190095
Contig ID	41_5.R1039

5'-most EST	LIB3148-015-Q1-K1-H7
Method	BLASTN
NCBI GI	g1217627
BLAST score	112
E value	4.0e-56
Match length	314
% identity	94
NCBI Description	G.hinsutum mRNA for stearoyl-acyl-carrier protein desaturase

Seq. No.	190096
Contig ID	42_1.R1039
5'-most EST	g459197
Method	BLASTX
NCBI GI	g2493129
BLAST score	2501
E value	0.0e+00
Match length	488
% identity	100
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi|459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	190097
Contig ID	42_2.R1039
5'-most EST	LIB3197-047-Q1-M1-B7
Method	BLASTX
NCBI GI	g2493129
BLAST score	2432
E value	0.0e+00
Match length	488
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi|459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]

Seq. No.	190098
Contig ID	42_3.R1039
5'-most EST	LIB3272-005-P1-K1-B12

Seq. No.	190099
Contig ID	44_1.R1039
5'-most EST	LIB3120-027-Q1-K1-H3
Method	BLASTX
NCBI GI	g755150
BLAST score	581
E value	9.0e-60
Match length	165
% identity	75
NCBI Description	(U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum]

Seq. No.	190100
Contig ID	44_2.R1039
5'-most EST	g5046127
Method	BLASTX
NCBI GI	g2493146

BLAST score	580
E value	1.0e-59
Match length	165
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi|755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi|4519415|dbj|BAA75542.1| (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No.	190101
Contig ID	44_3.R1039
5'-most EST	LIB3135-049-Q1-K1-H10
Method	BLASTX
NCBI GI	g2493144
BLAST score	580
E value	8.0e-60
Match length	165
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi|2118221|pir||S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi|926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	190102
Contig ID	46_1.R1039
5'-most EST	g606941
Method	BLASTX
NCBI GI	g606942
BLAST score	1075
E value	1.0e-117
Match length	263
% identity	83
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	190103
Contig ID	46_2.R1039
5'-most EST	LIB3083-108-Q1-L1-H3
Method	BLASTX
NCBI GI	g606942
BLAST score	803
E value	7.0e-86
Match length	189
% identity	85
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	190104
Contig ID	47_1.R1039
5'-most EST	g5047961
Method	BLASTX
NCBI GI	g2829204
BLAST score	597
E value	8.0e-62
Match length	120
% identity	94
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No.	190105
Contig ID	47_2.R1039
5'-most EST	g4877644
Method	BLASTX
NCBI GI	g2497743
BLAST score	177
E value	2.0e-12
Match length	57
% identity	61
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi|999315|bbs|166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	190106
Contig ID	47_3.R1039
5'-most EST	LIB3083-006-Q1-L1-D6
Method	BLASTX
NCBI GI	g2129770
BLAST score	1196
E value	1.0e-131
Match length	285
% identity	73
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi|1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi|2154611|dbj|BAA20290| (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	190107
Contig ID	47_4.R1039
5'-most EST	g5045918
Method	BLASTX
NCBI GI	g2497743
BLAST score	204
E value	6.0e-32
Match length	90
% identity	83
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi|999315|bbs|166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	190108
Contig ID	47_5.R1039
5'-most EST	g5050907
Method	BLASTX
NCBI GI	g2154609
BLAST score	229
E value	1.0e-18
Match length	79
% identity	57
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi|4522010|gb|AAD21783.1| (AC007069) endoxyloglucan transferase [Arabidopsis

thaliana]

Seq. No.	190109
Contig ID	47_6.R1039
5'-most EST	g5044715
Method	BLASTX
NCBI GI	g2829204
BLAST score	174
E value	1.0e-12
Match length	35
% identity	91
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	190110
Contig ID	47_7.R1039
5'-most EST	g5049418
Method	BLASTX
NCBI GI	g2497743
BLAST score	172
E value	3.0e-12
Match length	34
% identity	94
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi|999315|bbs|166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	190111
Contig ID	47_8.R1039
5'-most EST	uC-gsflnu33B023a05b1
Method	BLASTX
NCBI GI	g2129770
BLAST score	246
E value	6.0e-21
Match length	70
% identity	66
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi|1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi|2154611|dbj|BAA20290| (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	190112
Contig ID	47_10.R1039
5'-most EST	g5047567
Method	BLASTX
NCBI GI	g2497742
BLAST score	189
E value	2.0e-14
Match length	35
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi|995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	190113

Contig ID	47_12.R1039
5'-most EST	g5050623
Method	BLASTX
NCBI GI	g2829204
BLAST score	189
E value	2.0e-14
Match length	35
% identity	100
NCBI Description	(AF044204) lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	190114
Contig ID	47_13.R1039
5'-most EST	LIB3189-048-P1-K1-F4
Method	BLASTX
NCBI GI	g4510347
BLAST score	221
E value	5.0e-18
Match length	77
% identity	60
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190115
Contig ID	47_14.R1039
5'-most EST	g5046732
Method	BLASTX
NCBI GI	g2497743
BLAST score	383
E value	3.0e-37
Match length	81
% identity	90
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi|999315|bbs|166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	190116
Contig ID	47_15.R1039
5'-most EST	LIB3083-094-Q1-L1-E4
Method	BLASTX
NCBI GI	g2497743
BLAST score	145
E value	5.0e-09
Match length	50
% identity	64
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) >gi|999315|bbs|166991 (S78173) LTP=lipid transfer protein [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa] [Gossypium hirsutum]

Seq. No.	190117
Contig ID	48_1.R1039
5'-most EST	LIB3147-022-Q1-K1-H5
Method	BLASTX
NCBI GI	g1469930
BLAST score	651
E value	5.0e-68

Match length 136
% identity 96
NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]

Seq. No. 190118
Contig ID 49_1.R1039
5'-most EST LIB3147-051-Q1-K1-C9
Method BLASTX
NCBI GI g3687235
BLAST score 309
E value 8.0e-46
Match length 199
% identity 56
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No. 190119
Contig ID 49_2.R1039
5'-most EST LIB3166-049-P1-K1-A7
Method BLASTX
NCBI GI g1220196
BLAST score 1911
E value 0.0e+00
Match length 379
% identity 96
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 190120
Contig ID 49_6.R1039
5'-most EST LIB3146-025-Q1-K1-E6
Method BLASTX
NCBI GI g1220196
BLAST score 538
E value 7.0e-55
Match length 137
% identity 78
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 190121
Contig ID 51_1.R1039
5'-most EST g1297364
Method BLASTX
NCBI GI g1263291
BLAST score 810
E value 1.0e-86
Match length 153
% identity 100
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 190122
Contig ID 53_1.R1039
5'-most EST uC-gsflmaxxa091b02b1
Method BLASTX
NCBI GI g1439609
BLAST score 1179
E value 1.0e-130

Match length	248
% identity	94
NCBI Description	(U62778) delta-tonoplast intrinsic protein [Gossypium hirsutum]

Seq. No.	190123
Contig ID	54_1.R1039
5'-most EST	uC-gsflmaxxa098h07b1
Method	BLASTX
NCBI GI	g2500380
BLAST score	572
E value	6.0e-59
Match length	105
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi|2119128|pir||JC4923 ribosomal protein RL44 - upland cotton >gi|1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi|1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	190124
Contig ID	55_1.R1039
5'-most EST	uC-gsronu33B113f11b1
Method	BLASTX
NCBI GI	g2500380
BLAST score	572
E value	5.0e-59
Match length	105
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi|2119128|pir||JC4923 ribosomal protein RL44 - upland cotton >gi|1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi|1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	190125
Contig ID	55_2.R1039
5'-most EST	uC-gsflmaxxa028g08b1
Method	BLASTX
NCBI GI	g3193303
BLAST score	353
E value	5.0e-33
Match length	142
% identity	61
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	190126
Contig ID	55_3.R1039
5'-most EST	LIB3189-050-P1-K1-D2
Method	BLASTX
NCBI GI	g2500380
BLAST score	565
E value	3.0e-58
Match length	105

% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi|2119128|pir||JC4923 ribosomal protein RL44 - upland cotton >gi|1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi|1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	190127
Contig ID	57_1.R1039
5'-most EST	LIB3145-018-Q1-K1-H2
Method	BLASTX
NCBI GI	g3024386
BLAST score	2091
E value	0.0e+00
Match length	404
% identity	99
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi|2129500|pir||S52006 polygalacturonase - upland cotton >gi|606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No.	190128
Contig ID	58_1.R1039
5'-most EST	LIB3196-033-P1-M1-A11
Method	BLASTX
NCBI GI	g3334115
BLAST score	1868
E value	0.0e+00
Match length	381
% identity	95
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi|2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	190129
Contig ID	58_2.R1039
5'-most EST	LIB3197-047-Q1-M1-B12
Method	BLASTX
NCBI GI	g870726
BLAST score	1179
E value	0.0e+00
Match length	467
% identity	88
NCBI Description	(L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi|1582354|prf||2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No.	190130
Contig ID	58_3.R1039
5'-most EST	uC-gsflmaxxa088g03b1
Method	BLASTX
NCBI GI	g3334115
BLAST score	1523
E value	1.0e-170
Match length	366
% identity	81
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi|2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No.	190131
Contig ID	58_4.R1039
5'-most EST	g5047834
Method	BLASTX
NCBI GI	g870726
BLAST score	620
E value	2.0e-64
Match length	154
% identity	81
NCBI Description	(L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi|1582354|prf||2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No.	190132
Contig ID	58_5.R1039
5'-most EST	uC-gsf1nu33B127b07b1
Method	BLASTX
NCBI GI	g3320379
BLAST score	821
E value	9.0e-88
Match length	350
% identity	84
NCBI Description	(AF014375) putative JUN kinase activation domain binding protein [Medicago sativa]

Seq. No.	190133
Contig ID	58_6.R1039
5'-most EST	LIB3145-009-Q1-K1-F6
Method	BLASTX
NCBI GI	g1890116
BLAST score	1400
E value	1.0e-155
Match length	316
% identity	85
NCBI Description	(U89839) ADP/ATP translocator [Lycopersicon esculentum]

Seq. No.	190134
Contig ID	58_7.R1039
5'-most EST	LIB3189-005-P1-K1-E1
Method	BLASTX
NCBI GI	g870726
BLAST score	379
E value	2.0e-36
Match length	93
% identity	82
NCBI Description	(L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi|1582354|prf||2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No.	190135
Contig ID	59_1.R1039
5'-most EST	g2463665
Method	BLASTX

NCBI GI	g2463666
BLAST score	478
E value	4.0e-48
Match length	130
% identity	99
NCBI Description	(AF006490) adenine nucleotide translocator 2 [Gossypium hirsutum]

Seq. No.	190136
Contig ID	60_1.R1039
5'-most EST	g2266946
Method	BLASTX
NCBI GI	g2266947
BLAST score	4881
E value	0.0e+00
Match length	965
% identity	97
NCBI Description	(AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium hirsutum]

Seq. No.	190137
Contig ID	61_1.R1039
5'-most EST	LIB3120-020-Q1-K1-B3
Method	BLASTX
NCBI GI	g115577
BLAST score	969
E value	1.0e-112
Match length	235
% identity	85
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME (PEPCASE) >gi|348536|pir||S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560 >gi|169844 (M86661) phosphoenolpyruvate carboxylase [Saccharum sp.]

Seq. No.	190138
Contig ID	62_1.R1039
5'-most EST	LIB3197-055-Q1-M1-A7
Method	BLASTX
NCBI GI	g3334405
BLAST score	1026
E value	1.0e-112
Match length	237
% identity	89
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi|2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	190139
Contig ID	62_2.R1039
5'-most EST	LIB3272-021-P1-K1-E7
Method	BLASTX
NCBI GI	g3334405
BLAST score	598
E value	5.0e-62
Match length	159
% identity	79

NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi|2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]
Seq. No.	190140
Contig ID	63_1.R1039
5'-most EST	LIB3083-050-Q1-L1-B4
Method	BLASTX
NCBI GI	g1174592
BLAST score	1017
E value	1.0e-112
Match length	206
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi|2119270|pir||S60233 alpha-tubulin - garden pea >gi|525332 (U12589) alpha-tubulin [Pisum sativum]
Seq. No.	190141
Contig ID	63_2.R1039
5'-most EST	LIB3146-016-Q1-K1-G5
Method	BLASTX
NCBI GI	g606648
BLAST score	260
E value	4.0e-34
Match length	85
% identity	79
NCBI Description	(U09612) alpha tubulin [Leishmania donovani]
Seq. No.	190142
Contig ID	64_1.R1039
5'-most EST	g5048690
Method	BLASTX
NCBI GI	g2118231
BLAST score	1318
E value	1.0e-157
Match length	410
% identity	71
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis thaliana >gi|765354|bbs|157347 (S74033) plasma membrane H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis thaliana]
Seq. No.	190143
Contig ID	64_2.R1039
5'-most EST	LIB3197-035-Q1-M1-A11
Method	BLASTX
NCBI GI	g2118231
BLAST score	876
E value	2.0e-94
Match length	219
% identity	79
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis thaliana >gi|765354|bbs|157347 (S74033) plasma membrane H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis thaliana]

Seq. No.	190144
Contig ID	66_1.R1039
5'-most EST	uC-gsflmaxxa069f01b1
Method	BLASTX
NCBI GI	g2662341
BLAST score	994
E value	0.0e+00
Match length	434
% identity	92
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi|2662345|dbj|BAA23659| (D63582) EF-1 alpha [Oryza sativa] >gi|2662347|dbj|BAA23660| (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	190145
Contig ID	66_2.R1039
5'-most EST	LIB3145-026-Q1-K1-A2
Method	BLASTX
NCBI GI	g1076627
BLAST score	2461
E value	0.0e+00
Match length	532
% identity	91
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi|790479|emb|CAA58701| (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	190146
Contig ID	66_4.R1039
5'-most EST	LIB3166-054-P1-K1-H4
Method	BLASTX
NCBI GI	g3319882
BLAST score	813
E value	1.0e-115
Match length	240
% identity	90
NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	190147
Contig ID	66_5.R1039
5'-most EST	LIB3272-027-P1-K1-D2
Method	BLASTX
NCBI GI	g1169476
BLAST score	997
E value	1.0e-134
Match length	305
% identity	80
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi|439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	190148
Contig ID	66_6.R1039
5'-most EST	LIB3166-018-P1-K1-D10
Method	BLASTX

NCBI GI	g3869088
BLAST score	904
E value	8.0e-98
Match length	173
% identity	99
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	190149
Contig ID	66_7.R1039
5'-most EST	g5048691
Method	BLASTX
NCBI GI	g2662343
BLAST score	628
E value	2.0e-65
Match length	126
% identity	96
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	190150
Contig ID	66_8.R1039
5'-most EST	g5050829
Method	BLASTX
NCBI GI	g3122071
BLAST score	600
E value	3.0e-62
Match length	118
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi|2130148|pir||S66339 translation elongation factor eEF-1 alpha chain - maize >gi|1321656|dbj|BAA08249| (D45408) alpha subunit of tlanslation elongation factor 1 [Zea mays]

Seq. No.	190151
Contig ID	66_9.R1039
5'-most EST	g5045038
Method	BLASTX
NCBI GI	g3319882
BLAST score	560
E value	2.0e-57
Match length	110
% identity	98
NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	190152
Contig ID	66_10.R1039
5'-most EST	LIB3083-101-Q1-L1-F6
Method	BLASTX
NCBI GI	g1199806
BLAST score	111
E value	6.0e-12
Match length	71
% identity	65
NCBI Description	(X95663) elongation factor 1 alpha [Brugia pahangi]

Seq. No.	190153
Contig ID	66_11.R1039

5'-most EST	LIB3165-020-P1-K1-C8
Method	BLASTX
NCBI GI	g2662343
BLAST score	684
E value	4.0e-72
Match length	131
% identity	100
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	190154
Contig ID	66_12.R1039
5'-most EST	uC-gsronu33B138d10b1
Method	BLASTX
NCBI GI	g2129949
BLAST score	477
E value	5.0e-48
Match length	95
% identity	98
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP5) - common tobacco

Seq. No.	190155
Contig ID	66_14.R1039
5'-most EST	LIB3197-037-Q1-M1-H2
Method	BLASTX
NCBI GI	g3869088
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	190156
Contig ID	66_15.R1039
5'-most EST	LIB3135-039-Q1-K1-H10
Method	BLASTX
NCBI GI	g485742
BLAST score	663
E value	1.0e-69
Match length	150
% identity	91
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]

Seq. No.	190157
Contig ID	66_19.R1039
5'-most EST	LIB3145-009-Q1-K1-D7
Method	BLASTN
NCBI GI	g644491
BLAST score	46
E value	1.0e-16
Match length	93
% identity	87
NCBI Description	Corn mRNA for elongation factor 1A

Seq. No.	190158
Contig ID	66_21.R1039
5'-most EST	LIB3147-032-Q1-K1-F11

Method	BLASTX
NCBI GI	g2662343
BLAST score	295
E value	2.0e-26
Match length	64
% identity	86
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	190159
Contig ID	66_24.R1039
5'-most EST	LIB3120-043-P1-K1-H7
Method	BLASTX
NCBI GI	g3319882
BLAST score	192
E value	2.0e-27
Match length	86
% identity	74
NCBI Description	(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No.	190160
Contig ID	66_34.R1039
5'-most EST	LIB3083-053-Q1-L1-F3
Method	BLASTX
NCBI GI	g1076627
BLAST score	307
E value	6.0e-28
Match length	113
% identity	58
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi|790479|emb|CAA58701| (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	190161
Contig ID	67_1.R1039
5'-most EST	uC-gsronu33B179b08b1
Method	BLASTX
NCBI GI	g417103
BLAST score	679
E value	3.0e-71
Match length	136
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa]

>gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	190162
Contig ID	67_2.R1039
5'-most EST	LIB3149-063-Q1-K1-A7
Method	BLASTX
NCBI GI	g417103
BLAST score	673
E value	2.0e-70
Match length	136
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa] >gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	190163
Contig ID	67_3.R1039
5'-most EST	uC-gsronu33B007b06b1
Method	BLASTX
NCBI GI	g417103
BLAST score	290
E value	2.0e-33
Match length	99
% identity	81
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana

tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa] >gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	190164
Contig ID	68_1.R1039
5'-most EST	LIB3147-055-Q1-K1-A6
Method	BLASTX
NCBI GI	g4580384
BLAST score	450
E value	2.0e-44
Match length	92
% identity	99
NCBI Description	(AC007184) putative histone H2B [Arabidopsis thaliana]

Seq. No.	190165
Contig ID	68_2.R1039
5'-most EST	g5047313
Method	BLASTX
NCBI GI	g4580384
BLAST score	457
E value	3.0e-45
Match length	114
% identity	83
NCBI Description	(AC007184) putative histone H2B [Arabidopsis thaliana]

Seq. No.	190166
Contig ID	68_3.R1039
5'-most EST	uC-gsflnu33B144a07b1
Method	BLASTX
NCBI GI	g2558962
BLAST score	452
E value	9.0e-45
Match length	92
% identity	100
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	190167
Contig ID	68_4.R1039
5'-most EST	LIB3147-013-Q1-K1-C9
Method	BLASTX
NCBI GI	g2558962
BLAST score	432
E value	2.0e-42
Match length	92
% identity	97
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	190168
Contig ID	69_1.R1039
5'-most EST	LIB3189-024-P1-K1-G7
Method	BLASTX
NCBI GI	g543841
BLAST score	929
E value	1.0e-100

Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|322518|pir||S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi|166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi|2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	190169
Contig ID	69_2.R1039
5'-most EST	g2921331
Method	BLASTX
NCBI GI	g2921332
BLAST score	1055
E value	1.0e-115
Match length	198
% identity	100
NCBI Description	(AF034130) MYB-like DNA-binding domain protein [Gossypium hirsutum]

Seq. No.	190170
Contig ID	69_3.R1039
5'-most EST	uC-gsronu33B104g07b1
Method	BLASTX
NCBI GI	g1351974
BLAST score	816
E value	7.0e-92
Match length	181
% identity	96
NCBI Description	ADP-RIBOSYLATION FACTOR >gi|1076788|pir||S49325 ADP-ribosylation factor - maize >gi|1076789|pir||S53486 ADP-ribosylation factor - maize >gi|556686|emb|CAA56351| (X80042) ADP-ribosylation factor [Zea mays]

Seq. No.	190171
Contig ID	73_1.R1039
5'-most EST	g2921339
Method	BLASTX
NCBI GI	g2921340
BLAST score	1226
E value	1.0e-135
Match length	226
% identity	100
NCBI Description	(AF034134) MYB-like DNA-binding domain protein [Gossypium hirsutum]

Seq. No.	190172
Contig ID	74_1.R1039
5'-most EST	g5046643
Method	BLASTX
NCBI GI	g4104242
BLAST score	1964
E value	0.0e+00
Match length	410
% identity	92
NCBI Description	(AF034266) palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]

Seq. No.	190173
Contig ID	74_2.R1039
5'-most EST	LIB3146-024-Q1-K1-E3
Method	BLASTX
NCBI GI	g4104242
BLAST score	722
E value	2.0e-76
Match length	182
% identity	77
NCBI Description	(AF034266) palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]

Seq. No.	190174
Contig ID	75_1.R1039
5'-most EST	LIB3272-042-P1-K1-F10
Method	BLASTX
NCBI GI	g3334147
BLAST score	1473
E value	1.0e-164
Match length	324
% identity	84
NCBI Description	ENDOCHITINASE 1 PRECURSOR >gi|1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No.	190175
Contig ID	79_1.R1039
5'-most EST	LIB3197-056-Q1-M1-G5
Method	BLASTX
NCBI GI	g806310
BLAST score	191
E value	7.0e-14
Match length	270
% identity	13
NCBI Description	(J02746) proline-rich protein [Glycine max]

Seq. No.	190176
Contig ID	79_2.R1039
5'-most EST	LIB3149-038-Q1-K1-D1
Method	BLASTX
NCBI GI	g3024126
BLAST score	1935
E value	0.0e+00
Match length	390
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi|1655576|emb|CAA95856| (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]

Seq. No.	190177
Contig ID	79_3.R1039
5'-most EST	g5050839
Method	BLASTX
NCBI GI	g231536
BLAST score	906
E value	1.0e-154

Match length	348
% identity	79
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi|99683|pir||S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi|16394|emb|CAA45040| (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi|4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	190178
Contig ID	79_6.R1039
5'-most EST	uC-gsronu33B149a04b1
Method	BLASTX
NCBI GI	g1170937
BLAST score	474
E value	2.0e-57
Match length	144
% identity	76
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi|450549|emb|CAA81481| (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	190179
Contig ID	79_8.R1039
5'-most EST	LIB3083-068-Q1-L1-F11
Method	BLASTX
NCBI GI	g1483563
BLAST score	741
E value	4.0e-95
Match length	196
% identity	86
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	190180
Contig ID	79_10.R1039
5'-most EST	uC-gsronu33B117d08b1
Method	BLASTX
NCBI GI	g4376203
BLAST score	361
E value	5.0e-34
Match length	267
% identity	34
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No.	190181
Contig ID	79_13.R1039
5'-most EST	uC-gsflmaxxa048e12b1
Method	BLASTX
NCBI GI	g127041
BLAST score	283
E value	3.0e-25
Match length	53
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi|81647|pir||JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi|166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	190182
Contig ID	79_17.R1039
5'-most EST	LIB3189-042-P1-K1-F9
Method	BLASTN
NCBI GI	g2829205
BLAST score	271
E value	1.0e-151
Match length	500
% identity	30
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	190183
Contig ID	82_1.R1039
5'-most EST	LIB3197-019-Q1-M1-G4
Method	BLASTX
NCBI GI	g464775
BLAST score	817
E value	2.0e-87
Match length	197
% identity	82
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi|542013|pir||S39492 superoxide dismutase - Para rubber tree >gi|348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	190184
Contig ID	82_2.R1039
5'-most EST	g5048190
Method	BLASTX
NCBI GI	g464775
BLAST score	517
E value	1.0e-102
Match length	203
% identity	89
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi|542013|pir||S39492 superoxide dismutase - Para rubber tree >gi|348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	190185
Contig ID	83_1.R1039
5'-most EST	LIB3189-023-P1-K1-H5
Method	BLASTX
NCBI GI	g3135693
BLAST score	819
E value	1.0e-87
Match length	160
% identity	97
NCBI Description	(AF064201) glutathione S-transferase [Gossypium hirsutum]

Seq. No.	190186
Contig ID	83_4.R1039
5'-most EST	LIB3165-001-Q1-K1-D6

Method	BLASTX
NCBI GI	g2213595
BLAST score	360
E value	4.0e-34
Match length	113
% identity	62
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	190187
Contig ID	84_1.R1039
5'-most EST	g3135694
Method	BLASTN
NCBI GI	g3135694
BLAST score	389
E value	0.0e+00
Match length	397
% identity	99
NCBI Description	Gossypium hirsutum vacuolar proton ATPase 16 kDa proteolipid subunit (VATPase) mRNA, partial cds

Seq. No.	190188
Contig ID	86_1.R1039
5'-most EST	LIB3272-040-P1-K1-D4
Method	BLASTX
NCBI GI	g2506090
BLAST score	367
E value	1.0e-49
Match length	180
% identity	58
NCBI Description	PROBABLE 26S PROTEASE SUBUNIT SUG2 (PROTEASOME CAP SUBUNIT) >gi|2133163|pir||S67156 SUG2 protein - yeast (Saccharomyces cerevisiae) >gi|1420585|emb|CAA99481| (Z75167) ORF YOR259c [Saccharomyces cerevisiae] >gi|1931623 (U93262) proteasome cap subunit [Saccharomyces cerevisiae]

Seq. No.	190189
Contig ID	87_1.R1039
5'-most EST	g3264827
Method	BLASTX
NCBI GI	g3264828
BLAST score	1684
E value	0.0e+00
Match length	331
% identity	98
NCBI Description	(AF072404) cotton fiber expressed protein 1 [Gossypium hirsutum]

Seq. No.	190190
Contig ID	91_1.R1039
5'-most EST	g4588011
Method	BLASTX
NCBI GI	g4206209
BLAST score	3589
E value	0.0e+00
Match length	1710
% identity	46
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis

thaliana] >gi|4263042|gb|AAD15311| (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	190191
Contig ID	93_1.R1039
5'-most EST	LIB3272-005-P1-K1-E12
Method	BLASTX
NCBI GI	g4545231
BLAST score	1089
E value	1.0e-119
Match length	207
% identity	100
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	190192
Contig ID	94_1.R1039
5'-most EST	LIB3166-019-P1-K1-H12
Method	BLASTX
NCBI GI	g4545262
BLAST score	215
E value	5.0e-17
Match length	48
% identity	85
NCBI Description	(AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No.	190193
Contig ID	95_1.R1039
5'-most EST	LIB3197-041-Q1-M1-C9
Method	BLASTX
NCBI GI	g464734
BLAST score	2338
E value	0.0e+00
Match length	485
% identity	92
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi|481237|pir||S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi|407412|emb|CAA81527| (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]

Seq. No.	190194
Contig ID	95_3.R1039
5'-most EST	g5047183
Method	BLASTX
NCBI GI	g992706
BLAST score	707
E value	3.0e-74
Match length	151
% identity	83
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	190195
Contig ID	95_4.R1039
5'-most EST	g5044463
Method	BLASTX

NCBI GI	g2160322
BLAST score	524
E value	4.0e-53
Match length	103
% identity	94
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	190196
Contig ID	95_5.R1039
5'-most EST	LIB3189-045-P1-K1-G9
Method	BLASTX
NCBI GI	g2815246
BLAST score	218
E value	2.0e-17
Match length	55
% identity	71
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	190197
Contig ID	95_6.R1039
5'-most EST	g5044467
Method	BLASTX
NCBI GI	g992706
BLAST score	656
E value	1.0e-69
Match length	152
% identity	84
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	190198
Contig ID	95_7.R1039
5'-most EST	LIB3197-015-P1-M1-D4
Method	BLASTX
NCBI GI	g1724102
BLAST score	514
E value	2.0e-52
Match length	117
% identity	84
NCBI Description	(U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No.	190199
Contig ID	95_8.R1039
5'-most EST	LIB3166-016-P1-K1-A6
Method	BLASTX
NCBI GI	g2815246
BLAST score	225
E value	3.0e-18
Match length	55
% identity	73
NCBI Description	(X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No.	190200
Contig ID	95_9.R1039
5'-most EST	LIB3147-055-Q1-K1-F5
Method	BLASTX

NCBI GI	g2160322
BLAST score	595
E value	2.0e-61
Match length	135
% identity	82
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	190201
Contig ID	95_10.R1039
5'-most EST	LIB3135-031-Q1-K1-H6
Method	BLASTX
NCBI GI	g2244750
BLAST score	584
E value	8.0e-77
Match length	169
% identity	80
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi|3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	190202
Contig ID	95_11.R1039
5'-most EST	LIB3189-007-P1-K1-B11
Method	BLASTX
NCBI GI	g1710838
BLAST score	305
E value	2.0e-27
Match length	63
% identity	90
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi|535584 (L36119) adenosylhomocysteinase [Medicago sativa]

Seq. No.	190203
Contig ID	95_13.R1039
5'-most EST	LIB3148-044-Q1-K1-B9
Method	BLASTX
NCBI GI	g992706
BLAST score	604
E value	8.0e-70
Match length	151
% identity	78
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	190204
Contig ID	95_14.R1039
5'-most EST	g5049988
Method	BLASTX
NCBI GI	g992706
BLAST score	325
E value	2.0e-60
Match length	150
% identity	74
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]

Seq. No.	190205

Contig ID 95_15.R1039
5'-most EST g5046216
Method BLASTX
NCBI GI g992706
BLAST score 516
E value 3.0e-52
Match length 138
% identity 69
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 190206
Contig ID 95_16.R1039
5'-most EST uC-gsflnu33B100g04b1
Method BLASTX
NCBI GI g2624417
BLAST score 252
E value 1.0e-30
Match length 119
% identity 61
NCBI Description (AJ002959) Ubiquitin carrier protein [Zea mays]

Seq. No. 190207
Contig ID 95_17.R1039
5'-most EST uC-gsflnu33B140b07b1

Seq. No. 190208
Contig ID 95_18.R1039
5'-most EST uC-gsflmaxxa015a01b1
Method BLASTX
NCBI GI g1724102
BLAST score 160
E value 1.0e-10
Match length 52
% identity 62
NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]

Seq. No. 190209
Contig ID 96_1.R1039
5'-most EST LIB3120-053-P1-K1-H6
Method BLASTX
NCBI GI g1354515
BLAST score 1063
E value 1.0e-116
Match length 309
% identity 67
NCBI Description (U55837) carbonic anhydrase [Populus tremula x Populus tremuloides]

Seq. No. 190210
Contig ID 96_2.R1039
5'-most EST LIB3120-023-Q1-K1-A5
Method BLASTX
NCBI GI g1705761
BLAST score 201
E value 4.0e-15
Match length 204

% identity	32
NCBI Description	CHALCONE--FLAVONONE ISOMERASE >gi|499036|emb|CAA53577| (X75963) chalcone isomerase [Vitis vinifera]
Seq. No.	190211
Contig ID	96_3.R1039
5'-most EST	LIB3120-032-Q1-K1-A5
Method	BLASTX
NCBI GI	g4512653
BLAST score	987
E value	1.0e-107
Match length	229
% identity	83
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.	190212
Contig ID	96_4.R1039
5'-most EST	uC-gsflmaxxa048d05b1
Method	BLASTN
NCBI GI	g4309683
BLAST score	56
E value	3.0e-22
Match length	339
% identity	85
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	190213
Contig ID	96_6.R1039
5'-most EST	LIB3146-037-P1-K1-F9
Method	BLASTX
NCBI GI	g4337178
BLAST score	742
E value	1.0e-78
Match length	151
% identity	89
NCBI Description	(AC006416) T31J12.5 [Arabidopsis thaliana]
Seq. No.	190214
Contig ID	98_1.R1039
5'-most EST	g5081778
Method	BLASTX
NCBI GI	g2827143
BLAST score	3303
E value	0.0e+00
Match length	701
% identity	87
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	190215
Contig ID	99_1.R1039
5'-most EST	LIB3272-009-P1-K1-D9
Method	BLASTX
NCBI GI	g2564237
BLAST score	2037
E value	0.0e+00

Match length	383
% identity	96
NCBI Description	(Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	190216
Contig ID	100_1.R1039
5'-most EST	LIB3189-005-P1-K1-B1
Method	BLASTX
NCBI GI	g3334113
BLAST score	466
E value	2.0e-46
Match length	89
% identity	100
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi|1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	190217
Contig ID	100_2.R1039
5'-most EST	LIB3120-006-Q1-K1-B2
Method	BLASTX
NCBI GI	g3334113
BLAST score	333
E value	6.0e-31
Match length	89
% identity	74
NCBI Description	ACYL-COA-BINDING PROTEIN (ACBP) >gi|1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No.	190218
Contig ID	100_3.R1039
5'-most EST	uC-gsronu33B001h05b1
Method	BLASTN
NCBI GI	g1006830
BLAST score	207
E value	1.0e-112
Match length	207
% identity	100
NCBI Description	Gossypium hirsutum acyl-CoA-binding protein mRNA, complete cds

Seq. No.	190219
Contig ID	101_1.R1039
5'-most EST	g5049903
Method	BLASTX
NCBI GI	g1019946
BLAST score	1359
E value	1.0e-151
Match length	288
% identity	91
NCBI Description	(U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No.	190220
Contig ID	102_1.R1039
5'-most EST	LIB3083-095-Q1-L1-B7
Method	BLASTX
NCBI GI	g1706956
BLAST score	4896

E value 0.0e+00
Match length 974
% identity 95
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 190221
Contig ID 103_1.R1039
5'-most EST LIB3083-059-Q1-L1-A7
Method BLASTX
NCBI GI g3511285
BLAST score 3587
E value 0.0e+00
Match length 866
% identity 79
NCBI Description (AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No. 190222
Contig ID 104_1.R1039
5'-most EST LIB3272-015-P1-K1-F10
Method BLASTX
NCBI GI g3493172
BLAST score 1555
E value 1.0e-174
Match length 316
% identity 97
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. No. 190223
Contig ID 105_1.R1039
5'-most EST uC-gsflmaxxa026d11b1
Method BLASTX
NCBI GI g1843527
BLAST score 1441
E value 1.0e-160
Match length 314
% identity 91
NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 190224
Contig ID 105_2.R1039
5'-most EST g3326071
Method BLASTX
NCBI GI g1843527
BLAST score 732
E value 1.0e-77
Match length 186
% identity 47
NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 190225
Contig ID 105_3.R1039
5'-most EST LIB3149-015-Q1-K1-F5
Method BLASTX
NCBI GI g2266994
BLAST score 463
E value 3.0e-46

Match length	153
% identity	58
NCBI Description	(U77413) O-linked GlcNAc transferase [Homo sapiens] >gi|4505499|ref|NP_003596.1|pOGT| O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase)

Seq. No.	190226
Contig ID	105_4.R1039
5'-most EST	LIB3147-051-Q1-K1-E2
Method	BLASTX
NCBI GI	g1843527
BLAST score	426
E value	1.0e-41
Match length	100
% identity	43
NCBI Description	(U73747) annexin [Gossypium hirsutum]

Seq. No.	190227
Contig ID	107_1.R1039
5'-most EST	uC-gsflmaxxa057d08b1
Method	BLASTX
NCBI GI	g3287834
BLAST score	2792
E value	0.0e+00
Match length	538
% identity	99
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE SYNTHASE) >gi|2147016|pir||S68366 (+)-delta-cadinene synthase isozyme XC14 - Gossypium arboreum >gi|1045314 (U23205) (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]

Seq. No.	190228
Contig ID	109_1.R1039
5'-most EST	g1087110
Method	BLASTX
NCBI GI	g2500197
BLAST score	932
E value	1.0e-101
Match length	196
% identity	93
NCBI Description	RAC-LIKE GTP BINDING PROTEIN RAC13 >gi|1361976|pir||S57325 GTP-binding protein Rac 13 - upland cotton >gi|1087111|bbs|170156 (S79308) 21.8 kda GTP-binding protein=Rac13 [Gossypium hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, Peptide, 196 aa] [Gossypium hirsutum]

Seq. No.	190229
Contig ID	111_1.R1039
5'-most EST	g4098125
Method	BLASTX
NCBI GI	g3915873
BLAST score	3721
E value	0.0e+00
Match length	805
% identity	87

NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi|2606081 (AF030231) sucrose synthase [Glycine max]

Seq. No.	190230
Contig ID	111_2.R1039
5'-most EST	uC-gsronu33B110a04b1
Method	BLASTX
NCBI GI	g4098129
BLAST score	480
E value	4.0e-48
Match length	101
% identity	89
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	190231
Contig ID	111_3.R1039
5'-most EST	LIB3189-008-P1-K1-H8
Method	BLASTX
NCBI GI	g4098129
BLAST score	1213
E value	1.0e-134
Match length	261
% identity	88
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	190232
Contig ID	111_7.R1039
5'-most EST	LIB3166-017-P1-K1-D12
Method	BLASTX
NCBI GI	g4098128
BLAST score	514
E value	2.0e-52
Match length	104
% identity	97
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

Seq. No.	190233
Contig ID	113_1.R1039
5'-most EST	LIB3196-046-P1-M1-D10
Method	BLASTX
NCBI GI	g4090257
BLAST score	464
E value	3.0e-46
Match length	91
% identity	97
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	190234
Contig ID	113_2.R1039
5'-most EST	LIB3147-019-Q1-K1-D12
Method	BLASTX
NCBI GI	g4090257
BLAST score	460
E value	6.0e-46
Match length	91
% identity	96

NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	190235
Contig ID	113_3.R1039
5'-most EST	LIB3148-055-Q1-K1-H8
Method	BLASTX
NCBI GI	g4090257
BLAST score	453
E value	4.0e-45
Match length	91
% identity	93
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	190236
Contig ID	115_1.R1039
5'-most EST	LIB3165-037-P1-K1-A4
Method	BLASTX
NCBI GI	g4158221
BLAST score	1535
E value	1.0e-171
Match length	336
% identity	82
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	190237
Contig ID	115_2.R1039
5'-most EST	uC-gsflnu33B055h12b1
Method	BLASTX
NCBI GI	g4158221
BLAST score	1722
E value	0.0e+00
Match length	363
% identity	85
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	190238
Contig ID	115_4.R1039
5'-most EST	LIB3166-020-P1-K1-E1
Method	BLASTX
NCBI GI	g560504
BLAST score	938
E value	1.0e-101
Match length	217
% identity	88
NCBI Description	(Z29593) guanine nucleotide regulatory protein [Vicia faba] >gi|1098296|prf||2115367D small GTP-binding protein [Vicia faba]

Seq. No.	190239
Contig ID	115_5.R1039
5'-most EST	LIB3147-037-Q1-K1-C8
Method	BLASTX
NCBI GI	g4158232
BLAST score	702
E value	8.0e-92
Match length	186
% identity	91

NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	190240
Contig ID	115_6.R1039
5'-most EST	g5047803
Method	BLASTX
NCBI GI	g1895084
BLAST score	244
E value	4.0e-22
Match length	94
% identity	67
NCBI Description	(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No.	190241
Contig ID	115_7.R1039
5'-most EST	g3325997
Method	BLASTX
NCBI GI	g3646373
BLAST score	1093
E value	1.0e-120
Match length	219
% identity	90
NCBI Description	(AJ011078) RGP1 protein [Oryza sativa]

Seq. No.	190242
Contig ID	115_11.R1039
5'-most EST	LIB3149-020-Q1-K1-C12
Method	BLASTX
NCBI GI	g3860319
BLAST score	764
E value	3.0e-81
Match length	168
% identity	89
NCBI Description	(AJ012686) nucleolar protein [Cicer arietinum]

Seq. No.	190243
Contig ID	117_1.R1039
5'-most EST	LIB3120-054-P1-K1-C1
Method	BLASTX
NCBI GI	g464849
BLAST score	2170
E value	0.0e+00
Match length	432
% identity	96
NCBI Description	TUBULIN ALPHA CHAIN >gi|486847|pir||S36232 tubulin alpha chain - almond >gi|20413|emb|CAA47635| (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	190244
Contig ID	117_2.R1039
5'-most EST	LIB3197-012-P1-M1-C6
Method	BLASTX
NCBI GI	g2088651
BLAST score	582
E value	1.0e-59
Match length	425

% identity	35
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	190245
Contig ID	117_4.R1039
5'-most EST	LIB3197-055-Q1-M1-H10
Method	BLASTX
NCBI GI	g267069
BLAST score	867
E value	2.0e-93
Match length	184
% identity	90
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi|320183|pir||JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi|166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi|166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	190246
Contig ID	117_5.R1039
5'-most EST	LIB3165-017-P1-K1-F1
Method	BLASTX
NCBI GI	g2864610
BLAST score	351
E value	4.0e-33
Match length	128
% identity	42
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi|4049336|emb|CAA22561| (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	190247
Contig ID	117_10.R1039
5'-most EST	LIB3083-010-Q1-L1-B1
Method	BLASTX
NCBI GI	g1174592
BLAST score	228
E value	6.0e-35
Match length	88
% identity	86
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi|2119270|pir||S60233 alpha-tubulin - garden pea >gi|525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	190248
Contig ID	120_1.R1039
5'-most EST	LIB3145-024-Q1-K1-C6
Method	BLASTX
NCBI GI	g3334157
BLAST score	772
E value	3.0e-82
Match length	170
% identity	86
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi|1220142|emb|CAA59468| (X85185) cyclophilin [Catharanthus roseus]

Seq. No.	190249
Contig ID	120_2.R1039
5'-most EST	LIB3189-016-P1-K1-A7
Method	BLASTX
NCBI GI	g464849
BLAST score	2169
E value	0.0e+00
Match length	432
% identity	95
NCBI Description	TUBULIN ALPHA CHAIN >gi|486847|pir||S36232 tubulin alpha chain - almond >gi|20413|emb|CAA47635| (X67162) alpha-tubulin [Prunus dulcis]

Seq. No.	190250
Contig ID	120_3.R1039
5'-most EST	uC-gsflmaxxa058c04b1
Method	BLASTX
NCBI GI	g267069
BLAST score	724
E value	9.0e-77
Match length	140
% identity	96
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi|320183|pir||JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi|166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi|166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	190251
Contig ID	120_4.R1039
5'-most EST	uC-gsronu33B144a10b1
Method	BLASTX
NCBI GI	g3334157
BLAST score	714
E value	1.0e-75
Match length	158
% identity	86
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi|1220142|emb|CAA59468| (X85185) cyclophilin [Catharanthus roseus]

Seq. No.	190252
Contig ID	120_6.R1039
5'-most EST	LIB3083-086-Q1-L1-A9

Seq. No.	190253
Contig ID	120_7.R1039
5'-most EST	LIB3166-028-P1-K1-H6

Seq. No.	190254
Contig ID	120_11.R1039
5'-most EST	LIB3083-014-Q1-L1-A4
Method	BLASTX
NCBI GI	g2459445
BLAST score	283
E value	2.0e-25

Match length	72
% identity	37
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	190255
Contig ID	121_1.R1039
5'-most EST	LIB3272-058-P1-K1-H3
Method	BLASTX
NCBI GI	g135406
BLAST score	2055
E value	0.0e+00
Match length	430
% identity	90
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi|99768|pir||A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi|166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi|166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	190256
Contig ID	121_2.R1039
5'-most EST	LIB3197-028-Q1-M1-A12
Method	BLASTX
NCBI GI	g464846
BLAST score	724
E value	1.0e-76
Match length	162
% identity	83
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi|322880|pir||S28983 tubulin alpha-6 chain - maize >gi|22158|emb|CAA44863| (X63178) alpha-tubulin #6 [Zea mays]

Seq. No.	190257
Contig ID	121_3.R1039
5'-most EST	LIB3147-011-Q1-K1-F4
Method	BLASTX
NCBI GI	g1477428
BLAST score	728
E value	5.0e-77
Match length	137
% identity	98
NCBI Description	(X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No.	190258
Contig ID	121_5.R1039
5'-most EST	LIB3147-041-Q1-K1-A5
Method	BLASTX
NCBI GI	g464847
BLAST score	411
E value	9.0e-40
Match length	82
% identity	95
NCBI Description	TUBULIN ALPHA CHAIN >gi|397913|emb|CAA80497| (Z22877) tubulin [Euglena gracilis]

Seq. No.	190259
Contig ID	122_1.R1039

5'-most EST	g5442427
Method	BLASTN
NCBI GI	g1885382
BLAST score	113
E value	1.0e-55
Match length	1226
% identity	82
NCBI Description	Arabidopsis thaliana phospholipase D (PLDbeta) mRNA, complete cds

Seq. No.	190260
Contig ID	124_1.R1039
5'-most EST	uC-gsflnu33B083f11b1
Method	BLASTX
NCBI GI	g2500194
BLAST score	884
E value	3.0e-95
Match length	174
% identity	97
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC5 >gi|1293668 (U52350) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	190261
Contig ID	125_1.R1039
5'-most EST	LIB3048-001-Q1-L1-A1

Seq. No.	190262
Contig ID	126_1.R1039
5'-most EST	LIB3120-030-Q1-K1-C4
Method	BLASTX
NCBI GI	g4263711
BLAST score	630
E value	2.0e-65
Match length	165
% identity	72
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	190263
Contig ID	127_1.R1039
5'-most EST	LIB3189-048-P1-K1-D4
Method	BLASTX
NCBI GI	g2811025
BLAST score	1881
E value	0.0e+00
Match length	493
% identity	70
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi|1944181|dbj|BAA19607| (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No.	190264
Contig ID	128_1.R1039
5'-most EST	LIB3048-001-Q1-L1-A3
Method	BLASTX
NCBI GI	g2129597
BLAST score	1113
E value	1.0e-122

Match length	225
% identity	93
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi|1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi|1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	190265
Contig ID	128_2.R1039
5'-most EST	g5047605
Method	BLASTX
NCBI GI	g2129597
BLAST score	1112
E value	1.0e-122
Match length	238
% identity	86
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi|1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi|1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	190266
Contig ID	129_1.R1039
5'-most EST	LIB3135-026-Q1-K1-F11
Method	BLASTN
NCBI GI	g3402695
BLAST score	36
E value	1.0e-10
Match length	136
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	190267
Contig ID	130_1.R1039
5'-most EST	LIB3197-037-Q1-M1-B3
Method	BLASTX
NCBI GI	g2558512
BLAST score	149
E value	2.0e-09
Match length	92
% identity	45
NCBI Description	(AJ002020) proton pump interactor [Arabidopsis thaliana]

Seq. No.	190268
Contig ID	131_1.R1039
5'-most EST	LIB3048-001-Q1-L1-A6
Method	BLASTX
NCBI GI	g2129496
BLAST score	1389
E value	1.0e-156
Match length	285
% identity	98
NCBI Description	acetolactate synthase (EC 4.1.3.18) precursor (clone A19) - upland cotton

Seq. No. 190269

Contig ID 132_1.R1039
5'-most EST LIB3048-047-Q1-L1-B3

Seq. No. 190270
Contig ID 133_1.R1039
5'-most EST LIB3197-015-P1-M1-A3
Method BLASTX
NCBI GI g1747296
BLAST score 813
E value 4.0e-87
Match length 211
% identity 76
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi|3298476|dbj|BAA31524| (AB012766) ovp2 [Oryza sativa]

Seq. No. 190271
Contig ID 134_1.R1039
5'-most EST LIB3048-041-Q1-L1-D8

Seq. No. 190272
Contig ID 135_1.R1039
5'-most EST g5049074
Method BLASTX
NCBI GI g3402693
BLAST score 350
E value 6.0e-33
Match length 141
% identity 55
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 190273
Contig ID 135_2.R1039
5'-most EST LIB3189-050-P1-K1-A4
Method BLASTN
NCBI GI g20163
BLAST score 73
E value 2.0e-32
Match length 406
% identity 83
NCBI Description O.sativa Rrl5 mRNA for 5S ribosomal RNA

Seq. No. 190274
Contig ID 136_1.R1039
5'-most EST LIB3145-053-Q1-K1-A5
Method BLASTX
NCBI GI g4519507
BLAST score 583
E value 2.0e-68
Match length 160
% identity 84
NCBI Description (D88434) protein abundantly expressed during apple fruit development [Malus domestica]

Seq. No. 190275
Contig ID 137_1.R1039
5'-most EST g3325988
Method BLASTX

NCBI GI g3292829
BLAST score 216
E value 4.0e-24
Match length 110
% identity 57
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 190276
Contig ID 138_1.R1039
5'-most EST LIB3048-001-Q1-L1-B2
Method BLASTX
NCBI GI g3128174
BLAST score 275
E value 2.0e-24
Match length 79
% identity 73
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 190277
Contig ID 139_1.R1039
5'-most EST LIB3048-033-Q1-L1-G4

Seq. No. 190278
Contig ID 140_1.R1039
5'-most EST LIB3048-001-Q1-L1-B4
Method BLASTX
NCBI GI g1572819
BLAST score 240
E value 4.0e-20
Match length 107
% identity 47
NCBI Description (U70855) similar to the RAS gene family [Caenorhabditis elegans]

Seq. No. 190279
Contig ID 141_1.R1039
5'-most EST LIB3048-003-Q1-L1-F6
Method BLASTX
NCBI GI g3775989
BLAST score 285
E value 2.0e-25
Match length 71
% identity 76
NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No. 190280
Contig ID 142_1.R1039
5'-most EST LIB3197-020-Q1-M1-F4
Method BLASTX
NCBI GI g729470
BLAST score 1582
E value 1.0e-177
Match length 351
% identity 85
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi|542089|pir||JQ2272 formate dehydrogenase (EC 1.2.1.2)

precursor, mitochondrial - potato >gi|297798|emb|CAA79702|
(Z21493) mitochondrial formate dehydrogenase precursor
[Solanum tuberosum]

Seq. No.	190281
Contig ID	143_1.R1039
5'-most EST	LIB3149-042-Q1-K1-H3
Method	BLASTX
NCBI GI	g1754522
BLAST score	251
E value	2.0e-21
Match length	107
% identity	47
NCBI Description	(D89984) ornithine decarboxylase [Nicotiana tabacum]

Seq. No.	190282
Contig ID	144_1.R1039
5'-most EST	g5049396
Method	BLASTX
NCBI GI	g3876865
BLAST score	243
E value	4.0e-20
Match length	173
% identity	35
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	190283
Contig ID	145_1.R1039
5'-most EST	LIB3048-001-Q1-L1-B9

Seq. No.	190284
Contig ID	147_1.R1039
5'-most EST	LIB3048-007-Q1-L1-E2
Method	BLASTX
NCBI GI	g3335351
BLAST score	482
E value	1.0e-48
Match length	135
% identity	11
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb|D83257 from A. thaliana. ESTs gb|T41629 and gb|AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	190285
Contig ID	148_1.R1039
5'-most EST	g5048681
Method	BLASTX
NCBI GI	g2632109
BLAST score	574
E value	3.0e-63
Match length	215
% identity	61
NCBI Description	(AJ000508) phospholipid glutathione peroxidase [Pisum sativum]

Seq. No.	190286
Contig ID	148_2.R1039
5'-most EST	LIB3145-024-Q1-K1-D12

Seq. No.	190287
Contig ID	148_3.R1039
5'-most EST	LIB3048-001-Q1-L1-C12
Method	BLASTX
NCBI GI	g1708062
BLAST score	170
E value	8.0e-12
Match length	96
% identity	40
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG PRECURSOR >gi|2129599|pir||S71250 glutathione peroxidase - Arabidopsis thaliana >gi|1061036|emb|CAA61965| (X89866) glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	190288
Contig ID	150_1.R1039
5'-most EST	LIB3166-028-P1-K1-A6
Method	BLASTX
NCBI GI	g2443890
BLAST score	580
E value	1.0e-59
Match length	156
% identity	72
NCBI Description	(AC002294) similar to NAM (gp|X92205|1321924) and CUC2 (gp|AB002560|1944132) proteins [Arabidopsis thaliana]

Seq. No.	190289
Contig ID	150_2.R1039
5'-most EST	LIB3048-038-Q1-L1-G5
Method	BLASTX
NCBI GI	g2443890
BLAST score	484
E value	1.0e-48
Match length	122
% identity	74
NCBI Description	(AC002294) similar to NAM (gp|X92205|1321924) and CUC2 (gp|AB002560|1944132) proteins [Arabidopsis thaliana]

Seq. No.	190290
Contig ID	151_1.R1039
5'-most EST	LIB3166-008-P1-K1-C5
Method	BLASTX
NCBI GI	g2833386
BLAST score	870
E value	9.0e-94
Match length	199
% identity	87
NCBI Description	RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi|2129493|pir||S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi|1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea]

>gi|3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi|1587969|prf||2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No.	190291
Contig ID	151_2.R1039
5'-most EST	LIB3120-020-Q1-K1-G8
Method	BLASTX
NCBI GI	g4102703
BLAST score	395
E value	3.0e-38
Match length	117
% identity	72
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	190292
Contig ID	153_1.R1039
5'-most EST	LIB3048-018-Q1-L1-A8
Method	BLASTX
NCBI GI	g4539335
BLAST score	304
E value	9.0e-28
Match length	133
% identity	43
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	190293
Contig ID	154_1.R1039
5'-most EST	g3325788
Method	BLASTX
NCBI GI	g2443329
BLAST score	541
E value	3.0e-55
Match length	189
% identity	59
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	190294
Contig ID	155_1.R1039
5'-most EST	LIB3048-001-Q1-L1-H1
Method	BLASTN
NCBI GI	g3869074
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	190295
Contig ID	156_1.R1039
5'-most EST	g5047444
Method	BLASTX
NCBI GI	g2978452
BLAST score	167
E value	4.0e-21

Match length	80
% identity	58
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	190296
Contig ID	156_2.R1039
5'-most EST	uC-gsflmaxxa039d02b1
Method	BLASTN
NCBI GI	g4159706
BLAST score	36
E value	2.0e-10
Match length	96
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]

Seq. No.	190297
Contig ID	157_1.R1039
5'-most EST	LIB3048-033-Q1-L1-H2
Method	BLASTX
NCBI GI	g3426048
BLAST score	448
E value	2.0e-44
Match length	157
% identity	76
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	190298
Contig ID	158_1.R1039
5'-most EST	LIB3048-011-Q1-L1-D2
Method	BLASTX
NCBI GI	g606942
BLAST score	421
E value	3.0e-41
Match length	152
% identity	58
NCBI Description	(U13760) unknown [Gossypium hirsutum]

Seq. No.	190299
Contig ID	162_1.R1039
5'-most EST	LIB3048-045-Q1-L1-D9
Method	BLASTX
NCBI GI	g4454052
BLAST score	144
E value	6.0e-09
Match length	89
% identity	42
NCBI Description	(AL035394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190300
Contig ID	167_1.R1039
5'-most EST	LIB3083-070-Q1-L1-A9
Method	BLASTX
NCBI GI	g1370166
BLAST score	996
E value	1.0e-108

Match length	203
% identity	95
NCBI Description	(Z73932) RAB1C [Lotus japonicus]

Seq. No.	190301
Contig ID	168_1.R1039
5'-most EST	LIB3048-009-Q1-L1-D4
Method	BLASTX
NCBI GI	g3033377
BLAST score	209
E value	9.0e-17
Match length	106
% identity	42
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	190302
Contig ID	169_1.R1039
5'-most EST	LIB3145-016-Q1-K1-E7
Method	BLASTX
NCBI GI	g4539315
BLAST score	452
E value	1.0e-44
Match length	196
% identity	49
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	190303
Contig ID	170_1.R1039
5'-most EST	uC-gsronu33B055b07b1
Method	BLASTX
NCBI GI	g1107526
BLAST score	684
E value	6.0e-72
Match length	173
% identity	75
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]

Seq. No.	190304
Contig ID	173_1.R1039
5'-most EST	LIB3083-078-Q1-L1-C10
Method	BLASTX
NCBI GI	g1172874
BLAST score	767
E value	2.0e-81
Match length	260
% identity	62
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi|479589|pir||S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi|391608|dbj|BAA01546| (D10703) rd22 [Arabidopsis thaliana] >gi|447134|prf||1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	190305
Contig ID	173_2.R1039
5'-most EST	LIB3197-008-P1-M1-F5

Method	BLASTX
NCBI GI	g1255951
BLAST score	935
E value	1.0e-101
Match length	200
% identity	82
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	190306
Contig ID	173_3.R1039
5'-most EST	g5047853
Method	BLASTX
NCBI GI	g1172874
BLAST score	204
E value	1.0e-15
Match length	172
% identity	33
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi|479589|pir||S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi|391608|dbj|BAA01546| (D10703) rd22 [Arabidopsis thaliana] >gi|447134|prf||1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	190307
Contig ID	175_1.R1039
5'-most EST	g3326814

Seq. No.	190308
Contig ID	176_1.R1039
5'-most EST	LIB3135-040-Q1-K1-F2
Method	BLASTX
NCBI GI	g548774
BLAST score	920
E value	2.0e-99
Match length	241
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi|542158|pir||S38360 ribosomal protein L7a - rice >gi|303855|dbj|BAA02156| (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	190309
Contig ID	176_3.R1039
5'-most EST	LIB3145-015-Q1-K1-B1
Method	BLASTX
NCBI GI	g548774
BLAST score	284
E value	2.0e-25
Match length	73
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi|542158|pir||S38360 ribosomal protein L7a - rice >gi|303855|dbj|BAA02156| (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	190310
Contig ID	176_5.R1039
5'-most EST	LIB3146-053-Q1-K1-C6
Method	BLASTX

NCBI GI	g548774
BLAST score	387
E value	2.0e-37
Match length	100
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi|542158|pir||S38360 ribosomal protein L7a - rice >gi|303855|dbj|BAA02156| (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	190311
Contig ID	177_1.R1039
5'-most EST	uC-gsflnu33B130g09b1
Method	BLASTX
NCBI GI	g3549691
BLAST score	887
E value	1.0e-95
Match length	209
% identity	74
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	190312
Contig ID	177_2.R1039
5'-most EST	LIB3135-062-Q1-K1-H11

Seq. No.	190313
Contig ID	177_4.R1039
5'-most EST	LIB3135-036-Q1-K1-G4
Method	BLASTX
NCBI GI	g3549691
BLAST score	442
E value	1.0e-43
Match length	104
% identity	72
NCBI Description	(AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No.	190314
Contig ID	178_1.R1039
5'-most EST	LIB3165-017-P1-K1-A2
Method	BLASTX
NCBI GI	g2576361
BLAST score	545
E value	6.0e-56
Match length	113
% identity	84
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	190315
Contig ID	179_1.R1039
5'-most EST	g3325929
Method	BLASTX
NCBI GI	g3242705
BLAST score	840
E value	4.0e-90
Match length	178
% identity	87
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase

[Arabidopsis thaliana]

Seq. No.	190316
Contig ID	179_2.R1039
5'-most EST	LIB3048-045-Q1-L1-B11
Method	BLASTX
NCBI GI	g3242705
BLAST score	367
E value	4.0e-35
Match length	83
% identity	78
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	190317
Contig ID	182_1.R1039
5'-most EST	LIB3048-001-Q1-L1-G10

Seq. No.	190318
Contig ID	183_1.R1039
5'-most EST	LIB3048-006-Q1-L1-F9

Seq. No.	190319
Contig ID	185_1.R1039
5'-most EST	LIB3048-001-Q1-L1-G2

Seq. No.	190320
Contig ID	187_1.R1039
5'-most EST	uC-gsflnu33B005f07b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	233
E value	4.0e-19
Match length	150
% identity	39
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	190321
Contig ID	188_1.R1039
5'-most EST	LIB3120-015-Q1-K1-A7
Method	BLASTX
NCBI GI	g2739046
BLAST score	281
E value	1.0e-41
Match length	146
% identity	61
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	190322
Contig ID	189_1.R1039
5'-most EST	LIB3048-014-Q1-L1-C10
Method	BLASTX
NCBI GI	g4325324
BLAST score	658
E value	3.0e-69
Match length	133

% identity	92
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	190323
Contig ID	196_1.R1039
5'-most EST	LIB3048-025-Q1-L1-E10
Method	BLASTX
NCBI GI	g4115371
BLAST score	304
E value	2.0e-27
Match length	186
% identity	42
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	190324
Contig ID	197_1.R1039
5'-most EST	LIB3048-001-Q1-L1-H3

Seq. No.	190325
Contig ID	198_1.R1039
5'-most EST	LIB3048-006-Q1-L1-C11

Seq. No.	190326
Contig ID	200_1.R1039
5'-most EST	LIB3048-004-Q1-L1-F11
Method	BLASTX
NCBI GI	g4538913
BLAST score	336
E value	2.0e-31
Match length	79
% identity	81
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	190327
Contig ID	201_1.R1039
5'-most EST	LIB3048-036-Q1-L1-G5
Method	BLASTN
NCBI GI	g4159706
BLAST score	88
E value	9.0e-42
Match length	293
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]

Seq. No.	190328
Contig ID	204_1.R1039
5'-most EST	g5045792
Method	BLASTX
NCBI GI	g3478700
BLAST score	1111
E value	1.0e-121
Match length	354
% identity	62
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	190329
Contig ID	204_2.R1039
5'-most EST	LIB3083-015-Q1-L2-A5
Method	BLASTX
NCBI GI	g2262170
BLAST score	536
E value	9.0e-55
Match length	187
% identity	58
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	190330
Contig ID	204_3.R1039
5'-most EST	uC-gsronu33B078h11b1
Method	BLASTX
NCBI GI	g549986
BLAST score	340
E value	8.0e-32
Match length	81
% identity	83
NCBI Description	(U13149) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	190331
Contig ID	204_4.R1039
5'-most EST	LIB3197-025-Q1-M1-C6
Method	BLASTX
NCBI GI	g2262170
BLAST score	183
E value	2.0e-13
Match length	62
% identity	58
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	190332
Contig ID	204_5.R1039
5'-most EST	LIB3165-019-P1-K1-D2
Method	BLASTX
NCBI GI	g2262170
BLAST score	246
E value	8.0e-21
Match length	136
% identity	42
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	190333
Contig ID	204_6.R1039
5'-most EST	LIB3165-007-P1-K1-E12

Seq. No.	190334
Contig ID	205_2.R1039
5'-most EST	LIB3166-002-Q1-K1-H6
Method	BLASTX
NCBI GI	g3955021

BLAST score 758
E value 1.0e-80
Match length 220
% identity 71
NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No. 190335
Contig ID 206_1.R1039
5'-most EST LIB3048-017-Q1-L1-B11

Seq. No. 190336
Contig ID 208_1.R1039
5'-most EST LIB3135-043-P1-K1-E3
Method BLASTX
NCBI GI g1402912
BLAST score 1159
E value 1.0e-127
Match length 307
% identity 72
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 190337
Contig ID 209_1.R1039
5'-most EST LIB3120-023-Q1-K1-C1
Method BLASTX
NCBI GI g2501850
BLAST score 2127
E value 0.0e+00
Match length 428
% identity 93
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No. 190338
Contig ID 209_2.R1039
5'-most EST uC-gsflnu33B108g05b1
Method BLASTX
NCBI GI g417148
BLAST score 588
E value 1.0e-60
Match length 221
% identity 53
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi|99912|pir||A33654 heat shock protein 26A - soybean >gi|169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No. 190339
Contig ID 209_3.R1039
5'-most EST LIB3272-022-P1-K1-F5
Method BLASTX
NCBI GI g3980393
BLAST score 384
E value 4.0e-37
Match length 110
% identity 63
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	190340
Contig ID	210_1.R1039
5'-most EST	LIB3048-052-Q1-L1-F11
Method	BLASTX
NCBI GI	g1001135
BLAST score	192
E value	2.0e-14
Match length	76
% identity	68
NCBI Description	(D64001) acetolactate synthase [Synechocystis sp.]

Seq. No.	190341
Contig ID	211_1.R1039
5'-most EST	LIB3189-040-P1-K1-B10
Method	BLASTX
NCBI GI	g480450
BLAST score	789
E value	2.0e-84
Match length	195
% identity	81
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi|402552|emb|CAA49506| (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	190342
Contig ID	212_1.R1039
5'-most EST	LIB3272-010-P1-K1-G8
Method	BLASTX
NCBI GI	g1173253
BLAST score	918
E value	3.0e-99
Match length	230
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi|543317|pir||S41170 ribosomal protein S3 - mouse >gi|57728|emb|CAA35916| (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi|439522|emb|CAA54167| (X76772) ribosomal protein S3 [Mus musculus]

Seq. No.	190343
Contig ID	213_1.R1039
5'-most EST	LIB3048-002-Q1-L1-A9
Method	BLASTX
NCBI GI	g2642158
BLAST score	1292
E value	1.0e-143
Match length	323
% identity	74
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190344
Contig ID	214_1.R1039
5'-most EST	LIB3147-024-Q1-K1-C3
Method	BLASTX
NCBI GI	g3641837
BLAST score	1148

E value	1.0e-126
Match length	312
% identity	74
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	190345
Contig ID	215_1.R1039
5'-most EST	g3326193

Seq. No.	190346
Contig ID	215_2.R1039
5'-most EST	g3325940

Seq. No.	190347
Contig ID	217_1.R1039
5'-most EST	LIB3048-029-Q1-L1-E4
Method	BLASTX
NCBI GI	g1709358
BLAST score	255
E value	9.0e-27
Match length	132
% identity	50
NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi|629638|pir||S48859 nucleoside triphosphatase - garden pea >gi|2129890|pir||S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi|563612|emb|CAA83655| (Z32743) nucleoside triphosphatase [Pisum sativum] >gi|4519173|dbj|BAA75506.1| (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	190348
Contig ID	218_1.R1039
5'-most EST	uC-gsflnu33B071f03b1
Method	BLASTX
NCBI GI	g232024
BLAST score	609
E value	7.0e-63
Match length	266
% identity	52
NCBI Description	PROTEIN E6 >gi|421806|pir||A46130 fiber protein - upland cotton >gi|2129498|pir||S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi|167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi|1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No.	190349
Contig ID	220_1.R1039
5'-most EST	LIB3048-003-Q1-L1-A5
Method	BLASTX
NCBI GI	g4115379
BLAST score	164
E value	2.0e-11
Match length	87
% identity	51
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No. 190350
Contig ID 221_1.R1039
5'-most EST LIB3197-041-Q1-M1-B11

Seq. No. 190351
Contig ID 221_2.R1039
5'-most EST LIB3048-024-Q1-L1-A1

Seq. No. 190352
Contig ID 222_1.R1039
5'-most EST LIB3048-042-Q1-L1-E2
Method BLASTX
NCBI GI g3218396
BLAST score 370
E value 6.0e-35
Match length 194
% identity 42
NCBI Description (AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 190353
Contig ID 223_1.R1039
5'-most EST LIB3048-014-Q1-L1-E9
Method BLASTX
NCBI GI g3024756
BLAST score 230
E value 5.0e-19
Match length 136
% identity 35
NCBI Description TYPE II DNA TOPOISOMERASE VI SUBUNIT B
>gi|1926403|emb|CAA71604| (Y10582) type II DNA
topoisomerase subunit B [Sulfolobus shibatae]

Seq. No. 190354
Contig ID 224_1.R1039
5'-most EST LIB3048-012-Q1-L1-B8

Seq. No. 190355
Contig ID 225_1.R1039
5'-most EST g3326156

Seq. No. 190356
Contig ID 225_2.R1039
5'-most EST uC-gsflnu33B036d05b1

Seq. No. 190357
Contig ID 225_3.R1039
5'-most EST uC-gsflnu33B142c02b1

Seq. No. 190358
Contig ID 226_1.R1039
5'-most EST LIB3048-010-Q1-L1-G6

Seq. No. 190359
Contig ID 226_2.R1039
5'-most EST LIB3148-011-Q1-K1-E3

Seq. No.	190360
Contig ID	227_1.R1039
5'-most EST	LIB3197-011-P1-M1-A11
Method	BLASTX
NCBI GI	g4455208
BLAST score	1506
E value	1.0e-172
Match length	394
% identity	76
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	190361
Contig ID	227_2.R1039
5'-most EST	LIB3165-047-Q1-K1-F4
Method	BLASTX
NCBI GI	g4455208
BLAST score	513
E value	5.0e-52
Match length	142
% identity	73
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	190362
Contig ID	227_3.R1039
5'-most EST	LIB3145-048-Q1-K1-A5
Method	BLASTX
NCBI GI	g4249382
BLAST score	2046
E value	0.0e+00
Match length	520
% identity	78
NCBI Description	(AC005966) Strong similarity to gi|3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb|AC004481. [Arabidopsis thaliana]

Seq. No.	190363
Contig ID	227_4.R1039
5'-most EST	LIB3165-045-Q1-K1-H12
Method	BLASTX
NCBI GI	g4249382
BLAST score	686
E value	4.0e-72
Match length	186
% identity	73
NCBI Description	(AC005966) Strong similarity to gi|3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb|AC004481. [Arabidopsis thaliana]

Seq. No.	190364
Contig ID	227_6.R1039
5'-most EST	LIB3120-019-Q1-K1-A2
Method	BLASTX
NCBI GI	g4455208
BLAST score	450
E value	2.0e-44
Match length	150

% identity	62
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	190365
Contig ID	228_1.R1039
5'-most EST	LIB3048-002-Q1-L1-C5
Seq. No.	190366
Contig ID	229_1.R1039
5'-most EST	LIB3048-026-Q1-L1-H11
Seq. No.	190367
Contig ID	230_1.R1039
5'-most EST	LIB3145-050-Q1-K1-B5
Method	BLASTX
NCBI GI	g1335862
BLAST score	759
E value	1.0e-155
Match length	303
% identity	91
NCBI Description	(U42608) clathrin heavy chain [Glycine max]
Seq. No.	190368
Contig ID	230_2.R1039
5'-most EST	LIB3048-039-Q1-L1-F3
Method	BLASTX
NCBI GI	g1335862
BLAST score	462
E value	4.0e-46
Match length	127
% identity	72
NCBI Description	(U42608) clathrin heavy chain [Glycine max]
Seq. No.	190369
Contig ID	231_1.R1039
5'-most EST	LIB3048-037-Q1-L1-B8
Method	BLASTX
NCBI GI	g633110
BLAST score	671
E value	9.0e-71
Match length	137
% identity	95
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]
Seq. No.	190370
Contig ID	232_1.R1039
5'-most EST	g3325903
Seq. No.	190371
Contig ID	232_2.R1039
5'-most EST	LIB3135-034-Q1-K1-F7
Method	BLASTX
NCBI GI	g4091008
BLAST score	292
E value	3.0e-26
Match length	108
% identity	56

NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 190372
Contig ID 234_1.R1039
5'-most EST uC-gsflnu33B066a04b1
Method BLASTX
NCBI GI g3212866
BLAST score 204
E value 6.0e-16
Match length 135
% identity 33
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 190373
Contig ID 235_1.R1039
5'-most EST LIB3048-025-Q1-L1-H4

Seq. No. 190374
Contig ID 236_1.R1039
5'-most EST LIB3048-030-Q1-L1-F11

Seq. No. 190375
Contig ID 238_1.R1039
5'-most EST LIB3165-013-P1-K1-G3
Method BLASTX
NCBI GI g1350680
BLAST score 1335
E value 1.0e-148
Match length 331
% identity 77
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 190376
Contig ID 238_2.R1039
5'-most EST uC-gsflnu33B138b11b1
Method BLASTX
NCBI GI g1350680
BLAST score 428
E value 6.0e-42
Match length 122
% identity 73
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 190377
Contig ID 238_3.R1039
5'-most EST g5044542
Method BLASTX
NCBI GI g1350680
BLAST score 815
E value 3.0e-87
Match length 200
% identity 78
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 190378
Contig ID 238_4.R1039
5'-most EST LIB3166-030-P1-K1-E7

Method	BLASTX
NCBI GI	g1350680
BLAST score	535
E value	1.0e-54
Match length	125
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	190379
Contig ID	238_5.R1039
5'-most EST	LIB3147-054-Q1-K1-D12
Method	BLASTX
NCBI GI	g1350680
BLAST score	246
E value	7.0e-21
Match length	74
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	190380
Contig ID	244_1.R1039
5'-most EST	LIB3048-019-Q1-L1-B4
Method	BLASTX
NCBI GI	g544250
BLAST score	550
E value	1.0e-56
Match length	135
% identity	77
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi|541860|pir||A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	190381
Contig ID	245_1.R1039
5'-most EST	LIB3048-053-Q1-L1-A9
Method	BLASTX
NCBI GI	g2062167
BLAST score	205
E value	5.0e-34
Match length	116
% identity	64
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	190382
Contig ID	247_1.R1039
5'-most EST	LIB3048-011-Q1-L1-B8
Method	BLASTN
NCBI GI	g4388705
BLAST score	39
E value	2.0e-12
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	190383

Contig ID	248_1.R1039
5'-most EST	LIB3048-047-Q1-L1-D3

Seq. No.	190384
Contig ID	249_1.R1039
5'-most EST	LIB3147-033-Q1-K1-C2
Method	BLASTX
NCBI GI	g1350983
BLAST score	552
E value	1.0e-112
Match length	235
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No.	190385
Contig ID	249_2.R1039
5'-most EST	LIB3165-013-P1-K1-H4
Method	BLASTX
NCBI GI	g1856971
BLAST score	396
E value	2.0e-39
Match length	96
% identity	89
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	190386
Contig ID	249_3.R1039
5'-most EST	LIB3135-053-Q1-K1-D8
Method	BLASTX
NCBI GI	g2661422
BLAST score	273
E value	5.0e-24
Match length	66
% identity	83
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|3096936|emb|CAA18846.1| (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	190387
Contig ID	249_4.R1039
5'-most EST	LIB3189-043-P1-K1-A12
Method	BLASTX
NCBI GI	g1856971
BLAST score	537
E value	7.0e-55
Match length	137
% identity	78
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	190388
Contig ID	249_7.R1039
5'-most EST	LIB3083-057-Q1-L1-A12

Method	BLASTX
NCBI GI	g1350983
BLAST score	285
E value	1.0e-25
Match length	72
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

Seq. No.	190389
Contig ID	250_1.R1039
5'-most EST	LIB3147-032-Q1-K1-A5
Method	BLASTX
NCBI GI	g3152576
BLAST score	734
E value	1.0e-77
Match length	257
% identity	55
NCBI Description	(AC002986) Similar to liver-specific transport protein gb|L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	190390
Contig ID	250_2.R1039
5'-most EST	LIB3048-027-Q1-L1-A11
Method	BLASTX
NCBI GI	g3152576
BLAST score	405
E value	1.0e-39
Match length	132
% identity	60
NCBI Description	(AC002986) Similar to liver-specific transport protein gb|L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	190391
Contig ID	251_2.R1039
5'-most EST	LIB3048-036-Q1-L1-H2
Method	BLASTX
NCBI GI	g629864
BLAST score	182
E value	2.0e-13
Match length	73
% identity	66
NCBI Description	histone H2B - garden asparagus >gi|563329|emb|CAA57778| (X82362) histone 2B [Asparagus officinalis]

Seq. No.	190392
Contig ID	252_1.R1039
5'-most EST	LIB3048-022-Q1-L1-F5

Seq. No.	190393
Contig ID	254_1.R1039
5'-most EST	LIB3048-002-Q1-L1-E9
Method	BLASTX
NCBI GI	g3047084
BLAST score	772
E value	1.0e-139
Match length	306
% identity	78

NCBI Description	(AF058914) similar to aminoacyl-tRNA synthetases [Arabidopsis thaliana]

Seq. No.	190394
Contig ID	255_1.R1039
5'-most EST	LIB3048-049-Q1-L1-B11

Seq. No.	190395
Contig ID	256_1.R1039
5'-most EST	LIB3048-048-Q1-L1-D5
Method	BLASTX
NCBI GI	g2191183
BLAST score	285
E value	1.0e-25
Match length	113
% identity	46
NCBI Description	(AF007271) similar to the ligand-gated ionic channels family [Arabidopsis thaliana]

Seq. No.	190396
Contig ID	259_1.R1039
5'-most EST	LIB3120-023-Q1-K1-D2
Method	BLASTX
NCBI GI	g1658197
BLAST score	1587
E value	1.0e-177
Match length	330
% identity	86
NCBI Description	(U74630) calreticulin [Ricinus communis] >gi|1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	190397
Contig ID	259_2.R1039
5'-most EST	LIB3272-004-P1-K1-F5
Method	BLASTX
NCBI GI	g465820
BLAST score	600
E value	4.0e-62
Match length	161
% identity	65
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi|280536|pir||S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi|3874819|emb|CAA79557| (Z19154) C40H1.6 [Caenorhabditis elegans]

Seq. No.	190398
Contig ID	259_3.R1039
5'-most EST	LIB3147-054-Q1-K1-C6
Method	BLASTX
NCBI GI	g465820
BLAST score	594
E value	3.0e-61
Match length	161
% identity	65
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi|280536|pir||S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi|3874819|emb|CAA79557| (Z19154)

C40H1.6 [Caenorhabditis elegans]

Seq. No.	190399
Contig ID	259_4.R1039
5'-most EST	LIB3135-031-Q1-K1-F8

Seq. No.	190400
Contig ID	259_5.R1039
5'-most EST	LIB3147-029-Q1-K1-C1
Method	BLASTX
NCBI GI	g4335864
BLAST score	546
E value	1.0e-55
Match length	130
% identity	75
NCBI Description	(AF052040) calreticulin [Berberis stolonifera]

Seq. No.	190401
Contig ID	259_7.R1039
5'-most EST	uC-gsflmaxxa098f09b1

Seq. No.	190402
Contig ID	260_1.R1039
5'-most EST	LIB3048-002-Q1-L1-F3
Method	BLASTX
NCBI GI	g2342728
BLAST score	217
E value	1.0e-17
Match length	88
% identity	43
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	190403
Contig ID	264_1.R1039
5'-most EST	LIB3048-020-Q1-L1-G12

Seq. No.	190404
Contig ID	266_1.R1039
5'-most EST	LIB3048-029-Q1-L1-F4

Seq. No.	190405
Contig ID	267_1.R1039
5'-most EST	LIB3048-020-Q1-L1-A7
Method	BLASTX
NCBI GI	g4433048
BLAST score	393
E value	4.0e-38
Match length	123
% identity	62
NCBI Description	(D26578) DNA-binding protein [Daucus carota]

Seq. No.	190406
Contig ID	272_1.R1039
5'-most EST	LIB3048-023-Q1-L1-E4
Method	BLASTX
NCBI GI	g2462826

BLAST score	418
E value	4.0e-41
Match length	145
% identity	54
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	190407
Contig ID	273_1.R1039
5'-most EST	uC-gsronu33B005e02b1
Method	BLASTX
NCBI GI	g3603353
BLAST score	249
E value	5.0e-21
Match length	85
% identity	56
NCBI Description	(AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana]

Seq. No.	190408
Contig ID	274_1.R1039
5'-most EST	LIB3147-008-Q1-K1-F7
Method	BLASTX
NCBI GI	g4490317
BLAST score	291
E value	1.0e-25
Match length	140
% identity	42
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	190409
Contig ID	276_1.R1039
5'-most EST	LIB3048-012-Q1-L1-E2
Method	BLASTX
NCBI GI	g1698548
BLAST score	1099
E value	1.0e-120
Match length	239
% identity	85
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	190410
Contig ID	280_1.R1039
5'-most EST	LIB3048-002-Q1-L1-H12
Method	BLASTX
NCBI GI	g3123515
BLAST score	724
E value	1.0e-76
Match length	151
% identity	92
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	190411
Contig ID	281_1.R1039
5'-most EST	LIB3048-028-Q1-L1-H9
Method	BLASTX
NCBI GI	g3152605
BLAST score	156

E value	2.0e-10
Match length	82
% identity	44
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190412
Contig ID	282_1.R1039
5'-most EST	LIB3048-014-Q1-L1-F5
Method	BLASTX
NCBI GI	g1143322
BLAST score	973
E value	1.0e-106
Match length	211
% identity	84
NCBI Description	(U40979) alfa-carboxyltransferase precursor [Glycine max]

Seq. No.	190413
Contig ID	283_1.R1039
5'-most EST	LIB3048-021-Q1-L1-H4

Seq. No.	190414
Contig ID	284_1.R1039
5'-most EST	LIB3048-022-Q1-L1-A10
Method	BLASTX
NCBI GI	g3738298
BLAST score	444
E value	7.0e-48
Match length	233
% identity	47
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi|4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	190415
Contig ID	287_1.R1039
5'-most EST	LIB3048-007-Q1-L1-A8
Method	BLASTX
NCBI GI	g3914370
BLAST score	242
E value	2.0e-20
Match length	74
% identity	72
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi|419754|pir||S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis thaliana >gi|217845|dbj|BAA00575| (D00672) glycerol-3-phosphate acyltransferase [Arabidopsis thaliana] >gi|217847|dbj|BAA00576| (D00673) glycerol-3-phosphate acyltransferase precursor [Arabidopsis thaliana]

Seq. No.	190416
Contig ID	289_1.R1039
5'-most EST	LIB3048-046-Q1-L1-B8
Method	BLASTN
NCBI GI	g3738275
BLAST score	33
E value	1.0e-08

Match length 254
% identity 84
NCBI Description Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 190417
Contig ID 291_1.R1039
5'-most EST LIB3048-032-Q1-L1-B1
Method BLASTX
NCBI GI g1002796
BLAST score 514
E value 2.0e-52
Match length 119
% identity 76
NCBI Description (U33915) Cpm10 [Craterostigma plantagineum]

Seq. No. 190418
Contig ID 293_1.R1039
5'-most EST g5047969
Method BLASTX
NCBI GI g3152609
BLAST score 660
E value 4.0e-69
Match length 199
% identity 61
NCBI Description (AC004482) putative Su(var)3-9 protein [Arabidopsis thaliana]

Seq. No. 190419
Contig ID 294_1.R1039
5'-most EST LIB3048-003-Q1-L1-A3
Method BLASTX
NCBI GI g1352439
BLAST score 196
E value 4.0e-15
Match length 134
% identity 41
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi|1008881 (L47221) eukaryotic initiation factor 5 [Phaseolus vulgaris]

Seq. No. 190420
Contig ID 295_1.R1039
5'-most EST LIB3048-053-Q1-L1-A3

Seq. No. 190421
Contig ID 297_1.R1039
5'-most EST LIB3083-092-Q1-L1-D8
Method BLASTX
NCBI GI g4063751
BLAST score 866
E value 8.0e-93
Match length 569
% identity 34
NCBI Description (AC005851) putative white protein [Arabidopsis thaliana] >gi|4510409|gb|AAD21495.1| (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	190422
Contig ID	298_1.R1039
5'-most EST	LIB3189-041-P1-K1-A1
Method	BLASTX
NCBI GI	g3047082
BLAST score	1398
E value	1.0e-155
Match length	366
% identity	70
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	190423
Contig ID	299_1.R1039
5'-most EST	g5048520
Method	BLASTX
NCBI GI	g2597826
BLAST score	526
E value	3.0e-53
Match length	187
% identity	56
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	190424
Contig ID	299_2.R1039
5'-most EST	LIB3048-033-Q1-L1-F12
Method	BLASTX
NCBI GI	g2597826
BLAST score	177
E value	7.0e-13
Match length	57
% identity	56
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	190425
Contig ID	300_1.R1039
5'-most EST	LIB3135-032-Q1-K1-F9

Seq. No.	190426
Contig ID	302_1.R1039
5'-most EST	LIB3048-030-Q1-L1-G6

Seq. No.	190427
Contig ID	303_1.R1039
5'-most EST	LIB3197-041-Q1-M1-E1
Method	BLASTX
NCBI GI	g4432860
BLAST score	649
E value	7.0e-68
Match length	231
% identity	16
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	190428
Contig ID	304_1.R1039

5'-most EST	g3325584
Method	BLASTX
NCBI GI	g2181180
BLAST score	411
E value	8.0e-40
Match length	216
% identity	37
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	190429
Contig ID	304_3.R1039
5'-most EST	g3326373
Method	BLASTX
NCBI GI	g2181180
BLAST score	303
E value	4.0e-27
Match length	187
% identity	35
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	190430
Contig ID	305_1.R1039
5'-most EST	LIB3048-026-Q1-L1-D4
Method	BLASTX
NCBI GI	g4309698
BLAST score	617
E value	3.0e-64
Match length	177
% identity	73
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	190431
Contig ID	306_1.R1039
5'-most EST	LIB3048-030-Q1-L1-D8

Seq. No.	190432
Contig ID	308_1.R1039
5'-most EST	LIB3083-104-Q1-L1-C1
Method	BLASTX
NCBI GI	g765203
BLAST score	1147
E value	1.0e-126
Match length	278
% identity	78
NCBI Description	(S73865) linoleate:oxygen oxidoreductase, lipoxygenase, LOX {EC 1.13.11.12} [Solanum tuberosum, cv. Desiree, roots, Peptide, 857 aa] [Solanum tuberosum]

Seq. No.	190433
Contig ID	309_1.R1039
5'-most EST	LIB3145-006-Q1-K1-B1
Method	BLASTX
NCBI GI	g4193388
BLAST score	633
E value	7.0e-66
Match length	168

% identity	75
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	190434
Contig ID	309_2.R1039
5'-most EST	LIB3197-046-Q1-M1-A7
Method	BLASTX
NCBI GI	g3894387
BLAST score	353
E value	6.0e-33
Match length	242
% identity	4
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	190435
Contig ID	309_4.R1039
5'-most EST	LIB3272-047-P1-K1-H12
Method	BLASTX
NCBI GI	g4193388
BLAST score	156
E value	9.0e-11
Match length	46
% identity	85
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	190436
Contig ID	309_8.R1039
5'-most EST	LIB3189-023-P1-K1-A7
Method	BLASTX
NCBI GI	g4193388
BLAST score	298
E value	4.0e-27
Match length	70
% identity	81
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	190437
Contig ID	310_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A2
Method	BLASTX
NCBI GI	g730583
BLAST score	245
E value	8.0e-21
Match length	114
% identity	47
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi|551267|emb|CAA55047| (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	190438
Contig ID	313_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A1
Method	BLASTX
NCBI GI	g2281115

BLAST score	701
E value	3.0e-74
Match length	145
% identity	91
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	190439
Contig ID	316_2.R1039
5'-most EST	LIB3120-013-Q1-K1-D5

Seq. No.	190440
Contig ID	316_3.R1039
5'-most EST	LIB3048-003-Q1-L1-C6
Method	BLASTX
NCBI GI	g2444178
BLAST score	649
E value	5.0e-68
Match length	178
% identity	75
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	190441
Contig ID	317_1.R1039
5'-most EST	LIB3048-047-Q1-L1-E2
Method	BLASTX
NCBI GI	g4508068
BLAST score	229
E value	6.0e-19
Match length	135
% identity	45
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]

Seq. No.	190442
Contig ID	317_2.R1039
5'-most EST	LIB3145-021-Q1-K1-F1
Method	BLASTN
NCBI GI	g3202025
BLAST score	184
E value	8.0e-99
Match length	428
% identity	86
NCBI Description	Mesembryanthemum crystallinum stromal L-ascorbate peroxidase precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	190443
Contig ID	319_1.R1039
5'-most EST	g5048116
Method	BLASTX
NCBI GI	g2828280
BLAST score	1041
E value	1.0e-113
Match length	207
% identity	93
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|emb|CAA16762| (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No.	190444
Contig ID	319_2.R1039
5'-most EST	g5046076
Method	BLASTX
NCBI GI	g2828280
BLAST score	687
E value	2.0e-76
Match length	162
% identity	84
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|emb|CAA16762| (AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	190445
Contig ID	319_3.R1039
5'-most EST	LIB3048-003-Q1-L1-C9
Method	BLASTN
NCBI GI	g2828278
BLAST score	35
E value	5.0e-10
Match length	87
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	190446
Contig ID	320_1.R1039
5'-most EST	LIB3048-003-Q1-L1-D1
Method	BLASTX
NCBI GI	g1076685
BLAST score	481
E value	3.0e-48
Match length	190
% identity	37
NCBI Description	SPF1 protein - sweet potato >gi|484261|dbj|BAA06278| (D30038) SPF1 protein [Ipomoea batatas]

Seq. No.	190447
Contig ID	323_1.R1039
5'-most EST	LIB3048-003-Q1-L1-D12
Method	BLASTX
NCBI GI	g4432860
BLAST score	932
E value	1.0e-100
Match length	316
% identity	18
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	190448
Contig ID	324_1.R1039
5'-most EST	LIB3048-039-Q1-L1-B2

Seq. No.	190449
Contig ID	325_1.R1039

5'-most EST	LIB3197-012-P1-M1-C11
Method	BLASTX
NCBI GI	g139780
BLAST score	329
E value	3.0e-30
Match length	112
% identity	59
NCBI Description	WOUND-INDUCED PROTEIN 1 >gi|82293|pir||JQ0398 wun1 protein - potato

Seq. No.	190450
Contig ID	325_2.R1039
5'-most EST	LIB3166-011-P1-K1-B1
Method	BLASTX
NCBI GI	g4185146
BLAST score	603
E value	2.0e-87
Match length	205
% identity	73
NCBI Description	(AC005724) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	190451
Contig ID	325_3.R1039
5'-most EST	LIB3048-010-Q1-L1-H1

Seq. No.	190452
Contig ID	326_1.R1039
5'-most EST	LIB3048-003-Q1-L1-D6
Method	BLASTX
NCBI GI	g3132696
BLAST score	1356
E value	1.0e-150
Match length	305
% identity	88
NCBI Description	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No.	190453
Contig ID	327_1.R1039
5'-most EST	LIB3048-047-Q1-L1-C1
Method	BLASTX
NCBI GI	g4337025
BLAST score	1144
E value	1.0e-125
Match length	328
% identity	67
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	190454
Contig ID	329_1.R1039
5'-most EST	LIB3272-036-P1-K1-H12

Seq. No.	190455
Contig ID	330_1.R1039
5'-most EST	LIB3048-003-Q1-L1-E1

Seq. No.	190456

Contig ID	331_1.R1039
5'-most EST	uC-gsflmaxxa061d11b1
Method	BLASTX
NCBI GI	g899608
BLAST score	1474
E value	1.0e-164
Match length	296
% identity	36
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	190457
Contig ID	331_2.R1039
5'-most EST	LIB3189-043-P1-K1-D9
Method	BLASTX
NCBI GI	g70644
BLAST score	1779
E value	0.0e+00
Match length	380
% identity	51
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	190458
Contig ID	331_3.R1039
5'-most EST	g5044987
Method	BLASTX
NCBI GI	g322750
BLAST score	658
E value	7.0e-69
Match length	128
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi|170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	190459
Contig ID	331_4.R1039
5'-most EST	g3326258
Method	BLASTX
NCBI GI	g421929
BLAST score	498
E value	4.0e-50
Match length	211
% identity	8
NCBI Description	ubiquitin - tomato >gi|312160|emb|CAA51679| (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	190460
Contig ID	331_5.R1039
5'-most EST	LIB3272-018-P1-K1-C6
Method	BLASTX
NCBI GI	g100934
BLAST score	1088
E value	1.0e-119
Match length	229
% identity	19
NCBI Description	ubiquitin precursor Ubi-1 - maize >gi|422037|pir||S20926 ubiquitin precursor Ubi-2 - maize >gi|248337|bbs|94465

	(S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays] >gi|248339|bbs|94467 (S94466) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays]
Seq. No.	190461
Contig ID	331_6.R1039
5'-most EST	g5047243
Method	BLASTX
NCBI GI	g3126967
BLAST score	1025
E value	1.0e-112
Match length	237
% identity	23
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.	190462
Contig ID	331_7.R1039
5'-most EST	LIB3166-011-P1-K1-C11
Method	BLASTX
NCBI GI	g322750
BLAST score	658
E value	5.0e-69
Match length	128
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi|170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]
Seq. No.	190463
Contig ID	331_8.R1039
5'-most EST	uC-gsronu33B141e03b1
Method	BLASTX
NCBI GI	g1332579
BLAST score	503
E value	2.0e-69
Match length	142
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]
Seq. No.	190464
Contig ID	331_9.R1039
5'-most EST	uC-gsflnu33B115d04b1
Method	BLASTX
NCBI GI	g322750
BLAST score	639
E value	1.0e-66
Match length	128
% identity	97
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi|170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]
Seq. No.	190465
Contig ID	331_12.R1039
5'-most EST	LIB3189-002-P1-K1-E9
Method	BLASTX

NCBI GI	g2144734
BLAST score	848
E value	3.0e-91
Match length	205
% identity	33
NCBI Description	polyubiquitin / ribosomal protein CEP52 - Trypanosoma cruzi >gi|162337 (J03945) ubiquitin precursor [Trypanosoma cruzi]

Seq. No.	190466
Contig ID	331_13.R1039
5'-most EST	uC-gsflnu33B145g08b1
Method	BLASTX
NCBI GI	g322750
BLAST score	641
E value	4.0e-67
Match length	128
% identity	97
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi|170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	190467
Contig ID	331_14.R1039
5'-most EST	LIB3272-031-P1-K1-G1
Method	BLASTX
NCBI GI	g3695408
BLAST score	295
E value	2.0e-26
Match length	86
% identity	72
NCBI Description	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No.	190468
Contig ID	331_15.R1039
5'-most EST	LIB3197-040-Q1-M1-H1
Method	BLASTN
NCBI GI	g347063
BLAST score	156
E value	4.0e-82
Match length	391
% identity	85
NCBI Description	Brassica rapa ubiquitin/ribosomal protein mRNA, complete cds

Seq. No.	190469
Contig ID	331_19.R1039
5'-most EST	LIB3148-024-Q1-K1-D3
Method	BLASTX
NCBI GI	g322750
BLAST score	502
E value	2.0e-62
Match length	128
% identity	89
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco

>gi|170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No.	190470
Contig ID	334_1.R1039
5'-most EST	LIB3048-011-Q1-L1-G2
Method	BLASTX
NCBI GI	g3249105
BLAST score	473
E value	1.0e-47
Match length	137
% identity	64
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb|X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	190471
Contig ID	335_1.R1039
5'-most EST	LIB3048-003-Q1-L1-E3
Method	BLASTX
NCBI GI	g3334659
BLAST score	507
E value	3.0e-51
Match length	222
% identity	45
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	190472
Contig ID	336_1.R1039
5'-most EST	LIB3048-003-Q1-L1-G8

Seq. No.	190473
Contig ID	337_1.R1039
5'-most EST	uC-gsronu33B127d05b1
Method	BLASTX
NCBI GI	g2462836
BLAST score	407
E value	3.0e-81
Match length	337
% identity	55
NCBI Description	(AF000657) beta-glucanase [Arabidopsis thaliana]

Seq. No.	190474
Contig ID	337_2.R1039
5'-most EST	LIB3048-042-Q1-L1-G7

Seq. No.	190475
Contig ID	338_1.R1039
5'-most EST	LIB3048-022-Q1-L1-C5
Method	BLASTX
NCBI GI	g3461815
BLAST score	182
E value	3.0e-25
Match length	80
% identity	76
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 190476

Contig ID	339_1.R1039
5'-most EST	LIB3148-043-Q1-K1-G6
Method	BLASTX
NCBI GI	g1352664
BLAST score	1298
E value	1.0e-143
Match length	310
% identity	85
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi|2117984|pir||S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi|473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi|4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	190477
Contig ID	339_3.R1039
5'-most EST	LIB3146-051-Q1-K1-B4
Method	BLASTX
NCBI GI	g3297819
BLAST score	654
E value	8.0e-69
Match length	130
% identity	94
NCBI Description	(AL031032) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	190478
Contig ID	339_5.R1039
5'-most EST	LIB3146-049-Q1-K1-D5
Method	BLASTX
NCBI GI	g3776005
BLAST score	463
E value	4.0e-46
Match length	93
% identity	96
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	190479
Contig ID	339_7.R1039
5'-most EST	LIB3147-055-Q1-K1-B8

Seq. No.	190480
Contig ID	339_14.R1039
5'-most EST	uC-gsronu33B158h04b2

Seq. No.	190481
Contig ID	339_16.R1039
5'-most EST	LIB3148-050-Q1-K1-D7
Method	BLASTX
NCBI GI	g1352664
BLAST score	193
E value	7.0e-15
Match length	55
% identity	85
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC

SUBUNIT >gi|2117984|pir||S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi|473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi|4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	190482
Contig ID	339_20.R1039
5'-most EST	LIB3146-047-Q1-K1-B4
Method	BLASTX
NCBI GI	g2262118
BLAST score	173
E value	3.0e-12
Match length	40
% identity	85
NCBI Description	(AC002343) cell division protein isolog [Arabidopsis thaliana]

Seq. No.	190483
Contig ID	340_1.R1039
5'-most EST	LIB3048-015-Q1-L1-A1

Seq. No.	190484
Contig ID	341_1.R1039
5'-most EST	g5048533
Method	BLASTX
NCBI GI	g2243118
BLAST score	412
E value	2.0e-55
Match length	140
% identity	74
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]

Seq. No.	190485
Contig ID	342_1.R1039
5'-most EST	LIB3048-012-Q1-L1-D1

Seq. No.	190486
Contig ID	344_1.R1039
5'-most EST	g5050502
Method	BLASTX
NCBI GI	g1617270
BLAST score	1238
E value	1.0e-136
Match length	266
% identity	85
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	190487
Contig ID	344_2.R1039
5'-most EST	g5045783
Method	BLASTX
NCBI GI	g2706450
BLAST score	941
E value	1.0e-102
Match length	216

% identity	84
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	190488
Contig ID	344_3.R1039
5'-most EST	LIB3048-010-Q1-L1-A5
Method	BLASTX
NCBI GI	g1694621
BLAST score	1297
E value	1.0e-143
Match length	300
% identity	83
NCBI Description	(D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No.	190489
Contig ID	344_4.R1039
5'-most EST	LIB3197-003-P1-M1-F1
Method	BLASTX
NCBI GI	g393707
BLAST score	810
E value	1.0e-86
Match length	217
% identity	73
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	190490
Contig ID	344_6.R1039
5'-most EST	g5049143
Method	BLASTX
NCBI GI	g2500047
BLAST score	879
E value	7.0e-95
Match length	195
% identity	84
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi|534916|emb|CAA85362| (Z36894) soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	190491
Contig ID	344_7.R1039
5'-most EST	LIB3148-028-Q1-K1-C9
Method	BLASTX
NCBI GI	g2706450
BLAST score	371
E value	2.0e-35
Match length	82
% identity	84
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	190492
Contig ID	344_11.R1039
5'-most EST	LIB3197-040-Q1-M1-C9
Method	BLASTX
NCBI GI	g2706450

BLAST score	232
E value	1.0e-24
Match length	84
% identity	77
NCBI Description	(AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	190493
Contig ID	344_13.R1039
5'-most EST	LIB3146-060-Q1-K1-C3
Method	BLASTX
NCBI GI	g2500047
BLAST score	498
E value	2.0e-50
Match length	110
% identity	82
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi|534916|emb|CAA85362| (Z36894) soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No.	190494
Contig ID	345_1.R1039
5'-most EST	LIB3048-003-Q1-L1-F3
Method	BLASTX
NCBI GI	g1483218
BLAST score	463
E value	2.0e-46
Match length	138
% identity	59
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	190495
Contig ID	355_1.R1039
5'-most EST	g5045903
Method	BLASTN
NCBI GI	g3868723
BLAST score	36
E value	2.0e-10
Match length	156
% identity	81
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	190496
Contig ID	358_1.R1039
5'-most EST	LIB3083-048-Q1-G1-F2
Method	BLASTX
NCBI GI	g2920706
BLAST score	462
E value	2.0e-54
Match length	464
% identity	33
NCBI Description	(Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 190497

Contig ID	358_3.R1039
5'-most EST	LIB3048-031-Q1-L1-D1
Method	BLASTX
NCBI GI	g2181180
BLAST score	243
E value	1.0e-20
Match length	133
% identity	37
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	190498
Contig ID	359_1.R1039
5'-most EST	LIB3083-109-Q1-L1-A1
Method	BLASTN
NCBI GI	g1009231
BLAST score	51
E value	1.0e-19
Match length	91
% identity	89
NCBI Description	Nicotiana tabacum EF-1-alpha-related GTP-binding protein (SUP1) mRNA, complete cds

Seq. No.	190499
Contig ID	362_1.R1039
5'-most EST	LIB3048-010-Q1-L1-F2
Method	BLASTX
NCBI GI	g2230757
BLAST score	329
E value	2.0e-30
Match length	150
% identity	49
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	190500
Contig ID	363_1.R1039
5'-most EST	g5048150
Method	BLASTX
NCBI GI	g1708236
BLAST score	799
E value	1.0e-112
Match length	289
% identity	72
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi|2129617|pir||JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi|1143390|emb|CAA58763| (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi|1586548|prf||2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	190501
Contig ID	363_2.R1039
5'-most EST	uC-gsflnu33B093d12b1
Method	BLASTX
NCBI GI	g4098521
BLAST score	990

E value	1.0e-107
Match length	208
% identity	89
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi|4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana]

Seq. No.	190502
Contig ID	363_3.R1039
5'-most EST	g5045078
Method	BLASTX
NCBI GI	g4098521
BLAST score	730
E value	3.0e-77
Match length	152
% identity	88
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi|4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana]

Seq. No.	190503
Contig ID	363_4.R1039
5'-most EST	LIB3145-035-Q1-K1-E2
Method	BLASTX
NCBI GI	g1708236
BLAST score	899
E value	3.0e-97
Match length	197
% identity	83
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi|2129617|pir||JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi|1143390|emb|CAA58763| (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi|1586548|prf||2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	190504
Contig ID	364_1.R1039
5'-most EST	LIB3083-099-Q1-L1-G6
Method	BLASTX
NCBI GI	g1169534
BLAST score	2108
E value	0.0e+00
Match length	445
% identity	92
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi|542019|pir||S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean >gi|433609|emb|CAA82232| (Z28386) enolase [Ricinus communis]

Seq. No.	190505
Contig ID	364_2.R1039
5'-most EST	LIB3147-050-Q1-K1-F1
Method	BLASTX

09396450 - 110000

NCBI GI	g119354
BLAST score	489
E value	2.0e-49
Match length	101
% identity	94
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi|82082|pir||JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi|19281|emb|CAA41115| (X58108) enolase [Lycopersicon esculentum]

Seq. No.	190506
Contig ID	364_3.R1039
5'-most EST	LIB3048-037-Q1-L1-G11
Method	BLASTX
NCBI GI	g82083
BLAST score	688
E value	2.0e-72
Match length	167
% identity	83
NCBI Description	phosphopyruvate hydratase (EC 4.2.1.11) - tomato (fragment) >gi|1161573|emb|CAA41116| (X58109) enolase [Lycopersicon esculentum]

Seq. No.	190507
Contig ID	364_4.R1039
5'-most EST	LIB3272-017-P1-K1-D9
Method	BLASTX
NCBI GI	g119350
BLAST score	560
E value	1.0e-57
Match length	121
% identity	90
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi|81608|pir||JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi|16271|emb|CAA41114| (X58107) enolase [Arabidopsis thaliana]

Seq. No.	190508
Contig ID	366_1.R1039
5'-most EST	LIB3048-037-Q1-L1-B1
Method	BLASTX
NCBI GI	g1399275
BLAST score	1172
E value	1.0e-129
Match length	237
% identity	92
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi|2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	190509
Contig ID	368_1.R1039
5'-most EST	LIB3048-003-Q1-L1-H5
Method	BLASTX

NCBI GI	g2465925
BLAST score	294
E value	3.0e-26
Match length	127
% identity	50
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	190510
Contig ID	369_1.R1039
5'-most EST	LIB3147-045-Q1-K1-A5
Method	BLASTX
NCBI GI	g2738949
BLAST score	1044
E value	1.0e-114
Match length	250
% identity	78
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	190511
Contig ID	369_2.R1039
5'-most EST	g5045164
Method	BLASTX
NCBI GI	g2738949
BLAST score	1025
E value	1.0e-111
Match length	244
% identity	79
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	190512
Contig ID	369_3.R1039
5'-most EST	uC-gsronu33B158d04b2
Method	BLASTX
NCBI GI	g2738949
BLAST score	708
E value	6.0e-75
Match length	145
% identity	90
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No.	190513
Contig ID	369_5.R1039
5'-most EST	g3325592
Method	BLASTX
NCBI GI	g2738949
BLAST score	572
E value	6.0e-59
Match length	121
% identity	87
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 190514

Contig ID	369_10.R1039
5'-most EST	uC-gsflnu33B143b07b1
Method	BLASTX
NCBI GI	g804973
BLAST score	396
E value	3.0e-38
Match length	117
% identity	68
NCBI Description	(X81376) L-ascorbate peroxidase [Capsicum annuum]

Seq. No.	190515
Contig ID	370_1.R1039
5'-most EST	LIB3048-022-Q1-L1-E8

Seq. No.	190516
Contig ID	371_1.R1039
5'-most EST	LIB3048-026-Q1-L1-A6

Seq. No.	190517
Contig ID	372_1.R1039
5'-most EST	uC-gsronu33B164f03b2
Method	BLASTX
NCBI GI	g3158376
BLAST score	366
E value	5.0e-35
Match length	128
% identity	59
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	190518
Contig ID	373_1.R1039
5'-most EST	LIB3272-019-P1-K1-H4
Method	BLASTX
NCBI GI	g1657374
BLAST score	471
E value	2.0e-47
Match length	102
% identity	85
NCBI Description	(X96853) endo-beta-1,4-glucanase [Prunus persica] >gi|1657380|emb|CAA65600| (X96856) endo-beta-1,4-glucanase [Prunus persica]

Seq. No.	190519
Contig ID	375_1.R1039
5'-most EST	LIB3135-051-Q1-K1-C1
Method	BLASTX
NCBI GI	g81790
BLAST score	164
E value	8.0e-11
Match length	191
% identity	13
NCBI Description	hypothetical protein - soybean

Seq. No.	190520
Contig ID	375_2.R1039
5'-most EST	LIB3166-055-P1-K1-C12
Method	BLASTX

NCBI GI	g81790
BLAST score	166
E value	4.0e-11
Match length	151
% identity	9
NCBI Description	hypothetical protein - soybean

Seq. No.	190521
Contig ID	375_3.R1039
5'-most EST	LIB3135-008-Q1-K1-F4
Method	BLASTX
NCBI GI	g81790
BLAST score	190
E value	8.0e-14
Match length	206
% identity	15
NCBI Description	hypothetical protein - soybean

Seq. No.	190522
Contig ID	375_4.R1039
5'-most EST	LIB3135-060-Q1-K1-B9
Method	BLASTN
NCBI GI	g2829205
BLAST score	78
E value	1.0e-35
Match length	426
% identity	20
NCBI Description	Gossypium hirsutum cultivar Siokra 1-2 proline-rich protein precursor (PRP) mRNA, complete cds

Seq. No.	190523
Contig ID	376_1.R1039
5'-most EST	LIB3120-002-Q1-K1-A12
Method	BLASTX
NCBI GI	g3924597
BLAST score	557
E value	7.0e-57
Match length	287
% identity	41
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	190524
Contig ID	376_2.R1039
5'-most EST	LIB3048-011-Q1-L1-C5
Method	BLASTX
NCBI GI	g3924598
BLAST score	160
E value	2.0e-10
Match length	149
% identity	36
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	190525
Contig ID	376_3.R1039
5'-most EST	g3326710

Seq. No.	190526

Contig ID	376_4.R1039
5'-most EST	g3326326
Method	BLASTX
NCBI GI	g3924597
BLAST score	219
E value	2.0e-17
Match length	137
% identity	32
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	190527
Contig ID	376_5.R1039
5'-most EST	uC-gsronu33B144h07b1
Method	BLASTX
NCBI GI	g3924597
BLAST score	318
E value	6.0e-29
Match length	198
% identity	38
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	190528
Contig ID	376_6.R1039
5'-most EST	LIB3135-052-Q1-K1-G9

Seq. No.	190529
Contig ID	376_8.R1039
5'-most EST	uC-gsronu33B031e01b1

Seq. No.	190530
Contig ID	376_9.R1039
5'-most EST	uC-gsronu33B139h06b1

Seq. No.	190531
Contig ID	377_1.R1039
5'-most EST	LIB3048-019-Q1-L1-F12
Method	BLASTX
NCBI GI	g4335752
BLAST score	255
E value	5.0e-22
Match length	127
% identity	43
NCBI Description	(AC006284) putative myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	190532
Contig ID	379_1.R1039
5'-most EST	LIB3048-024-Q1-L1-A6
Method	BLASTX
NCBI GI	g1170660
BLAST score	192
E value	1.0e-14
Match length	55
% identity	73
NCBI Description	MEVALONATE KINASE (MK) >gi|541880|pir||S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi|456614|emb|CAA54820| (X77793) mevalonate kinase

[Arabidopsis thaliana]

Seq. No.	190533
Contig ID	380_1.R1039
5'-most EST	LIB3048-004-Q1-L1-B9
Method	BLASTX
NCBI GI	g2895866
BLAST score	253
E value	1.0e-21
Match length	89
% identity	60
NCBI Description	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]

Seq. No.	190534
Contig ID	381_1.R1039
5'-most EST	uC-gsflmaxxa042d12b1
Method	BLASTX
NCBI GI	g2454182
BLAST score	1684
E value	0.0e+00
Match length	430
% identity	77
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	190535
Contig ID	381_2.R1039
5'-most EST	LIB3048-051-Q1-L1-B7

Seq. No.	190536
Contig ID	382_1.R1039
5'-most EST	LIB3272-043-P1-K1-D9
Method	BLASTX
NCBI GI	g2979555
BLAST score	459
E value	1.0e-45
Match length	196
% identity	51
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	190537
Contig ID	383_1.R1039
5'-most EST	g5049876
Method	BLASTX
NCBI GI	g3892712
BLAST score	653
E value	3.0e-68
Match length	151
% identity	83
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein [Arabidopsis thaliana]

Seq. No.	190538
Contig ID	384_1.R1039
5'-most EST	LIB3272-020-P1-K1-A9

Seq. No.	190539
Contig ID	385_1.R1039
5'-most EST	LIB3197-050-Q1-M1-C9
Method	BLASTX
NCBI GI	g548770
BLAST score	1797
E value	0.0e+00
Match length	389
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi|481228|pir||S38359 ribosomal protein L3 - rice >gi|303853|dbj|BAA02155| (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	190540
Contig ID	385_2.R1039
5'-most EST	LIB3147-019-Q1-K1-B6
Method	BLASTX
NCBI GI	g132939
BLAST score	665
E value	8.0e-70
Match length	170
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi|81657|pir||JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi|166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	190541
Contig ID	385_3.R1039
5'-most EST	LIB3083-113-Q1-L1-H9

Seq. No.	190542
Contig ID	386_1.R1039
5'-most EST	g5050435
Method	BLASTX
NCBI GI	g3329294
BLAST score	255
E value	9.0e-22
Match length	188
% identity	31
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	190543
Contig ID	387_1.R1039
5'-most EST	LIB3048-039-Q1-L1-B1
Method	BLASTX
NCBI GI	g3738295
BLAST score	773
E value	2.0e-82
Match length	236
% identity	67
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	190544
Contig ID	388_1.R1039
5'-most EST	g5044674
Method	BLASTN

NCBI GI g556421
BLAST score 47
E value 4.0e-17
Match length 55
% identity 96
NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No. 190545
Contig ID 390_1.R1039
5'-most EST LIB3048-027-Q1-L1-B6

Seq. No. 190546
Contig ID 391_1.R1039
5'-most EST uC-gsflmaxxa074h08b1
Method BLASTX
NCBI GI g2462746
BLAST score 1852
E value 0.0e+00
Match length 408
% identity 84
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No. 190547
Contig ID 391_2.R1039
5'-most EST LIB3189-030-P1-K1-E4
Method BLASTX
NCBI GI g2462746
BLAST score 592
E value 2.0e-61
Match length 136
% identity 79
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No. 190548
Contig ID 392_1.R1039
5'-most EST LIB3165-058-P1-K1-G2

Seq. No. 190549
Contig ID 392_2.R1039
5'-most EST LIB3165-013-P1-K1-F9

Seq. No. 190550
Contig ID 396_1.R1039
5'-most EST LIB3149-049-Q1-K1-H1

Seq. No. 190551
Contig ID 399_1.R1039
5'-most EST g3326082

Seq. No. 190552
Contig ID 400_1.R1039
5'-most EST LIB3048-013-Q1-L1-D2

Seq. No. 190553

Contig ID	402_1.R1039
5'-most EST	uC-gsronu33B116h12b1
Method	BLASTX
NCBI GI	g629602
BLAST score	1272
E value	0.0e+00
Match length	553
% identity	77
NCBI Description	probable imbibition protein - wild cabbage >gi|488787|emb|CAA55893| (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	190554
Contig ID	404_1.R1039
5'-most EST	LIB3048-052-Q1-L1-G11
Method	BLASTX
NCBI GI	g3047114
BLAST score	438
E value	2.0e-43
Match length	113
% identity	73
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	190555
Contig ID	405_1.R1039
5'-most EST	LIB3048-005-Q1-L1-A11

Seq. No.	190556
Contig ID	406_1.R1039
5'-most EST	LIB3048-024-Q1-L1-B3
Method	BLASTX
NCBI GI	g2507422
BLAST score	318
E value	2.0e-29
Match length	112
% identity	84
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi|3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	190557
Contig ID	409_1.R1039
5'-most EST	LIB3048-008-Q1-L1-C10
Method	BLASTN
NCBI GI	g310566
BLAST score	152
E value	2.0e-79
Match length	995
% identity	82
NCBI Description	Soybean glutamate 1-semialdehyde aminotransferase mRNA, complete cds

Seq. No.	190558
Contig ID	413_1.R1039
5'-most EST	LIB3048-036-Q1-L1-C5

Seq. No.	190559
Contig ID	414_1.R1039
5'-most EST	LIB3196-059-P1-M1-E2
Method	BLASTX
NCBI GI	g4426565
BLAST score	225
E value	4.0e-18
Match length	184
% identity	33
NCBI Description	(AF031483) unknown [Rattus norvegicus]

Seq. No.	190560
Contig ID	414_2.R1039
5'-most EST	LIB3120-054-P1-K1-A6
Method	BLASTX
NCBI GI	g4426565
BLAST score	342
E value	4.0e-33
Match length	281
% identity	32
NCBI Description	(AF031483) unknown [Rattus norvegicus]

Seq. No.	190561
Contig ID	418_1.R1039
5'-most EST	LIB3048-041-Q1-L1-A1
Method	BLASTX
NCBI GI	g529353
BLAST score	331
E value	1.0e-30
Match length	153
% identity	47
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	190562
Contig ID	420_1.R1039
5'-most EST	LIB3048-012-Q1-L1-E3

Seq. No.	190563
Contig ID	421_1.R1039
5'-most EST	LIB3048-005-Q1-L1-B6
Method	BLASTX
NCBI GI	g4204295
BLAST score	119
E value	3.0e-10
Match length	129
% identity	37
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	190564
Contig ID	422_1.R1039
5'-most EST	uC-gsronu33B080e05b1
Method	BLASTX
NCBI GI	g3834314
BLAST score	746
E value	2.0e-79
Match length	159

% identity	88
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi|2257490 from S. pombe clone 1750 gb|AB004534. ESTs gb|T46079 and gb|AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	190565
Contig ID	424_1.R1039
5'-most EST	LIB3149-026-Q1-K1-H4
Method	BLASTX
NCBI GI	g1370589
BLAST score	215
E value	6.0e-17
Match length	96
% identity	53
NCBI Description	(X98304) protein induced upon tuberization [Solanum demissum]

Seq. No.	190566
Contig ID	424_2.R1039
5'-most EST	g3325865
Method	BLASTX
NCBI GI	g1370589
BLAST score	223
E value	8.0e-18
Match length	98
% identity	53
NCBI Description	(X98304) protein induced upon tuberization [Solanum demissum]

Seq. No.	190567
Contig ID	424_3.R1039
5'-most EST	LIB3166-038-P1-K1-A9

Seq. No.	190568
Contig ID	428_1.R1039
5'-most EST	LIB3048-022-Q1-L1-F4

Seq. No.	190569
Contig ID	429_1.R1039
5'-most EST	uC-gsflmaxxa089b06b1
Method	BLASTX
NCBI GI	g542058
BLAST score	540
E value	3.0e-55
Match length	144
% identity	67
NCBI Description	HSR203J protein - common tobacco >gi|444002|emb|CAA54393| (X77136) HSR203J [Nicotiana tabacum]

Seq. No.	190570
Contig ID	430_1.R1039
5'-most EST	LIB3048-054-Q1-L1-H8

Seq. No.	190571
Contig ID	431_1.R1039
5'-most EST	g3326238

Method	BLASTX
NCBI GI	g2760837
BLAST score	246
E value	1.0e-20
Match length	129
% identity	36
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	190572
Contig ID	432_1.R1039
5'-most EST	LIB3048-005-Q1-L1-C8
Method	BLASTX
NCBI GI	g2911052
BLAST score	553
E value	6.0e-57
Match length	132
% identity	80
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	190573
Contig ID	434_1.R1039
5'-most EST	LIB3048-005-Q1-L1-D10

Seq. No.	190574
Contig ID	435_1.R1039
5'-most EST	LIB3048-019-Q1-L1-B7
Method	BLASTX
NCBI GI	g4510406
BLAST score	371
E value	2.0e-35
Match length	114
% identity	64
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	190575
Contig ID	436_1.R1039
5'-most EST	uC-gsflmaxxa089d04b1
Method	BLASTX
NCBI GI	g1076668
BLAST score	2243
E value	0.0e+00
Match length	471
% identity	88
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi|639834|emb|CAA58823| (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	190576
Contig ID	438_1.R1039
5'-most EST	LIB3272-028-P1-K1-B8
Method	BLASTX
NCBI GI	g120667
BLAST score	1431
E value	1.0e-159
Match length	320
% identity	86
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi|81622|pir||JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi|166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi|166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	190577
Contig ID	438_2.R1039
5'-most EST	LIB3149-061-Q1-K1-A3
Method	BLASTX
NCBI GI	g120669
BLAST score	817
E value	2.0e-87
Match length	191
% identity	83
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|66014|pir||DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi|19566|emb|CAA42905| (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	190578
Contig ID	438_3.R1039
5'-most EST	g5045482
Method	BLASTX
NCBI GI	g462141
BLAST score	1016
E value	1.0e-111
Match length	231
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH) >gi|1085816|pir||S38570 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Atriplex nummularia >gi|409575 (U02886) glyceraldehyde-3-phosphate dehydrogenase [Atriplex nummularia] >gi|414607|emb|CAA53269| (X75597) glyceraldehyde-3-phosphate dehydrogenase [Atriplex nummularia]

Seq. No.	190579
Contig ID	438_4.R1039
5'-most EST	LIB3147-022-Q1-K1-B9
Method	BLASTX
NCBI GI	g3023816
BLAST score	299
E value	7.0e-27
Match length	59
% identity	95
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	190580
Contig ID	438_5.R1039
5'-most EST	uC-gsflmaxxa041g09b1
Method	BLASTX

NCBI GI g585241
BLAST score 165
E value 7.0e-11
Match length 64
% identity 56
NCBI Description HISTONE H1 >gi|629668|pir||S45662 histone H1 - tomato >gi|424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No. 190581
Contig ID 438_6.R1039
5'-most EST uC-gsflmaxxa042e12b1
Method BLASTX
NCBI GI g120672
BLAST score 815
E value 3.0e-87
Match length 180
% identity 88
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|66016|pir||DEPZG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - parsley >gi|20549|emb|CAA42902| (X60344) glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]

Seq. No. 190582
Contig ID 438_7.R1039
5'-most EST uC-gsflmaxxa048d08b1
Method BLASTX
NCBI GI g120669
BLAST score 656
E value 7.0e-69
Match length 152
% identity 83
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|66014|pir||DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi|19566|emb|CAA42905| (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 190583
Contig ID 442_1.R1039
5'-most EST g3326368

Seq. No. 190584
Contig ID 443_1.R1039
5'-most EST g5046184
Method BLASTX
NCBI GI g1361983
BLAST score 695
E value 2.0e-73
Match length 209
% identity 67
NCBI Description ARP protein - Arabidopsis thaliana >gi|886434|emb|CAA89858| (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 190585
Contig ID 444_1.R1039
5'-most EST LIB3048-005-Q1-L1-D9

Seq. No.	190586
Contig ID	447_1.R1039
5'-most EST	LIB3120-039-P1-K1-A7
Method	BLASTX
NCBI GI	g1345979
BLAST score	325
E value	4.0e-30
Match length	128
% identity	53
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi|459962 (L29215) plastid omega-6 desaturase [Glycine max]

Seq. No.	190587
Contig ID	448_1.R1039
5'-most EST	LIB3048-005-Q1-L1-E2
Method	BLASTX
NCBI GI	g3915037
BLAST score	1273
E value	1.0e-141
Match length	275
% identity	89
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi|2570067|emb|CAA04512| (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No.	190588
Contig ID	450_1.R1039
5'-most EST	LIB3048-019-Q1-L1-D9
Method	BLASTX
NCBI GI	g4544409
BLAST score	464
E value	2.0e-46
Match length	145
% identity	64
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No.	190589
Contig ID	453_1.R1039
5'-most EST	uC-gsronu33B076e05b1
Method	BLASTX
NCBI GI	g4138647
BLAST score	935
E value	1.0e-101
Match length	225
% identity	77
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	190590
Contig ID	453_2.R1039
5'-most EST	LIB3135-049-Q1-K1-C10
Method	BLASTX
NCBI GI	g4138647
BLAST score	472
E value	2.0e-47

Match length	117
% identity	74
NCBI Description	(AJ011939) peroxidase [Trifolium repens]

Seq. No.	190591
Contig ID	453_3.R1039
5'-most EST	LIB3166-005-P1-K1-F11
Method	BLASTX
NCBI GI	g4468978
BLAST score	468
E value	1.0e-46
Match length	171
% identity	57
NCBI Description	(AL035605) peroxidase-like protein [Arabidopsis thaliana]

Seq. No.	190592
Contig ID	454_1.R1039
5'-most EST	LIB3048-005-Q1-L1-E8
Method	BLASTX
NCBI GI	g4406818
BLAST score	434
E value	5.0e-43
Match length	101
% identity	74
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	190593
Contig ID	456_1.R1039
5'-most EST	LIB3048-020-Q1-L1-F8

Seq. No.	190594
Contig ID	457_1.R1039
5'-most EST	LIB3048-035-Q1-L1-B12
Method	BLASTX
NCBI GI	g872116
BLAST score	1163
E value	1.0e-128
Match length	266
% identity	58
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	190595
Contig ID	459_1.R1039
5'-most EST	LIB3048-005-Q1-L1-F12

Seq. No.	190596
Contig ID	463_1.R1039
5'-most EST	LIB3048-033-Q1-L1-H10

Seq. No.	190597
Contig ID	467_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A3
Method	BLASTX
NCBI GI	g3608155
BLAST score	336
E value	2.0e-31

Match length	146
% identity	48
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	190598
Contig ID	468_1.R1039
5'-most EST	LIB3145-007-Q1-K1-E7
Method	BLASTX
NCBI GI	g3935168
BLAST score	377
E value	3.0e-36
Match length	164
% identity	52
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	190599
Contig ID	470_1.R1039
5'-most EST	LIB3048-008-Q1-L1-A1
Method	BLASTX
NCBI GI	g2146797
BLAST score	1082
E value	1.0e-159
Match length	367
% identity	64
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi|1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi|1587210|prf||2206331A protein disulfide isomerase [Ricinus communis]

Seq. No.	190600
Contig ID	470_2.R1039
5'-most EST	LIB3148-039-Q1-K1-H7

Seq. No.	190601
Contig ID	473_1.R1039
5'-most EST	LIB3048-012-Q1-L1-D7
Method	BLASTX
NCBI GI	g3548802
BLAST score	372
E value	1.0e-35
Match length	142
% identity	50
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi|4335769|gb|AAD17446| (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	190602
Contig ID	475_1.R1039
5'-most EST	LIB3048-054-Q1-L1-B11

Seq. No.	190603
Contig ID	476_1.R1039
5'-most EST	LIB3083-020-Q1-L1-D3
Method	BLASTX
NCBI GI	g3882211
BLAST score	434
E value	2.0e-48

Match length 228
% identity 48
NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]

Seq. No. 190604
Contig ID 477_1.R1039
5'-most EST LIB3048-031-Q1-L1-H2

Seq. No. 190605
Contig ID 479_1.R1039
5'-most EST uC-gsf1nu33B015h11b1
Method BLASTX
NCBI GI g4432859
BLAST score 479
E value 8.0e-48
Match length 235
% identity 48
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 190606
Contig ID 479_2.R1039
5'-most EST g5047833
Method BLASTX
NCBI GI g4432859
BLAST score 485
E value 1.0e-48
Match length 201
% identity 56
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 190607
Contig ID 479_3.R1039
5'-most EST LIB3166-002-Q1-K1-D2
Method BLASTX
NCBI GI g4432859
BLAST score 439
E value 5.0e-43
Match length 201
% identity 51
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 190608
Contig ID 479_4.R1039
5'-most EST LIB3083-056-Q1-L1-F2
Method BLASTX
NCBI GI g4432859
BLAST score 233
E value 5.0e-19
Match length 180
% identity 44
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 190609
Contig ID 480_1.R1039
5'-most EST LIB3048-005-Q1-L1-H11
Method BLASTX
NCBI GI g2317729

BLAST score 480
E value 4.0e-48
Match length 114
% identity 82
NCBI Description (AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No. 190610
Contig ID 481_1.R1039
5'-most EST LIB3197-012-P1-M1-G9

Seq. No. 190611
Contig ID 482_1.R1039
5'-most EST LIB3048-012-Q1-L1-B11
Method BLASTX
NCBI GI g1245182
BLAST score 587
E value 1.0e-103
Match length 199
% identity 83
NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 190612
Contig ID 484_1.R1039
5'-most EST uC-gsflmaxxa028e04b1

Seq. No. 190613
Contig ID 485_1.R1039
5'-most EST LIB3048-046-Q1-L1-D7
Method BLASTX
NCBI GI g2760347
BLAST score 1901
E value 0.0e+00
Match length 387
% identity 50
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]

Seq. No. 190614
Contig ID 485_2.R1039
5'-most EST LIB3189-028-P1-K1-H4
Method BLASTX
NCBI GI g902584
BLAST score 879
E value 7.0e-95
Match length 177
% identity 17
NCBI Description (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea mays]

Seq. No. 190615
Contig ID 485_3.R1039
5'-most EST LIB3048-025-Q1-L1-C2
Method BLASTX
NCBI GI g3335355
BLAST score 332
E value 7.0e-44
Match length 149

% identity	18
NCBI Description	(AC004512) Match to polyubiquitin DNA gb|L05401 from A. thaliana. Contains insertion of mitochondrial NADH dehydrogenase gb|X82618 and gb|X98301. May be a pseudogene with an expressed insert. EST gb|AA586248 comes from this region. [Arabi

Seq. No.	190616
Contig ID	485_5.R1039
5'-most EST	LIB3166-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g1362008
BLAST score	480
E value	2.0e-60
Match length	158
% identity	17
NCBI Description	ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No.	190617
Contig ID	485_6.R1039
5'-most EST	LIB3148-058-Q1-K1-D12
Method	BLASTX
NCBI GI	g170352
BLAST score	370
E value	9.0e-66
Match length	150
% identity	15
NCBI Description	(M74101) hexameric polyubiquitin [Nicotiana sylvestris] >gi|870792 (L05361) polyubiquitin [Arabidopsis thaliana] >gi|4115333 (L81139) ubiquitin [Pisum sativum] >gi|4115335 (L81140) ubiquitin [Pisum sativum]

Seq. No.	190618
Contig ID	485_7.R1039
5'-most EST	LIB3272-015-P1-K1-H12
Method	BLASTX
NCBI GI	g4115337
BLAST score	845
E value	1.0e-90
Match length	237
% identity	17
NCBI Description	(L81141) ubiquitin [Pisum sativum]

Seq. No.	190619
Contig ID	485_9.R1039
5'-most EST	LIB3196-012-P1-M1-A9
Method	BLASTX
NCBI GI	g1684855
BLAST score	338
E value	8.0e-32
Match length	106
% identity	16
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	190620
Contig ID	485_13.R1039
5'-most EST	LIB3048-019-Q1-L1-D12

Method	BLASTX
NCBI GI	g100934
BLAST score	618
E value	2.0e-64
Match length	184
% identity	10
NCBI Description	ubiquitin precursor Ubi-1 - maize >gi|422037|pir||S20926 ubiquitin precursor Ubi-2 - maize >gi|248337|bbs|94465 (S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays] >gi|248339|bbs|94467 (S94466) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays]

Seq. No.	190621
Contig ID	486_1.R1039
5'-most EST	LIB3048-030-Q1-L1-C5
Method	BLASTX
NCBI GI	g3044212
BLAST score	1039
E value	1.0e-133
Match length	271
% identity	86
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	190622
Contig ID	487_1.R1039
5'-most EST	LIB3272-009-P1-K1-C7
Method	BLASTX
NCBI GI	g113742
BLAST score	494
E value	6.0e-63
Match length	403
% identity	38
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi|147142 (M15273) peptidase N [Escherichia coli] >gi|147144 (M15676) aminopeptidase N [Escherichia coli] >gi|1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi|4062498|dbj|BAA35684| (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	190623
Contig ID	487_2.R1039
5'-most EST	LIB3135-022-Q1-K1-E3
Method	BLASTX
NCBI GI	g113742
BLAST score	420
E value	4.0e-41
Match length	188
% identity	46
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi|147142 (M15273) peptidase N [Escherichia coli] >gi|147144 (M15676) aminopeptidase N [Escherichia coli] >gi|1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi|4062498|dbj|BAA35684| (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No. 190624
Contig ID 488_1.R1039
5'-most EST LIB3048-005-Q1-L1-H9

Seq. No. 190625
Contig ID 489_1.R1039
5'-most EST LIB3048-020-Q1-L1-G9
Method BLASTX
NCBI GI g2980770
BLAST score 515
E value 2.0e-52
Match length 116
% identity 83
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 190626
Contig ID 490_1.R1039
5'-most EST LIB3048-027-Q1-L1-D9
Method BLASTX
NCBI GI g2244759
BLAST score 481
E value 1.0e-48
Match length 117
% identity 71
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 190627
Contig ID 492_1.R1039
5'-most EST LIB3048-037-Q1-L1-B7
Method BLASTX
NCBI GI g1346387
BLAST score 670
E value 1.0e-70
Match length 143
% identity 90
NCBI Description KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi|1045042|emb|CAA63130| (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi|4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]

Seq. No. 190628
Contig ID 494_1.R1039
5'-most EST LIB3146-030-Q1-K1-B2

Seq. No. 190629
Contig ID 495_1.R1039
5'-most EST LIB3048-013-Q1-L1-F2
Method BLASTX
NCBI GI g1076511
BLAST score 580
E value 4.0e-60
Match length 141
% identity 82
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi|758250|emb|CAA59799| (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

09604.0050

Seq. No.	190630
Contig ID	497_1.R1039
5'-most EST	uC-gsflmaxxa027h02b1
Method	BLASTX
NCBI GI	g4204313
BLAST score	559
E value	2.0e-57
Match length	125
% identity	85
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	190631
Contig ID	498_1.R1039
5'-most EST	LIB3048-006-Q1-L1-A9
Method	BLASTX
NCBI GI	g4099482
BLAST score	356
E value	2.0e-33
Match length	242
% identity	33
NCBI Description	(U87791) eRFS [Homo sapiens]

Seq. No.	190632
Contig ID	499_1.R1039
5'-most EST	uC-gsflmaxxa096h07b1

Seq. No.	190633
Contig ID	499_2.R1039
5'-most EST	uC-gsronu33B036e11b1
Method	BLASTX
NCBI GI	g3334320
BLAST score	1148
E value	1.0e-126
Match length	307
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi|2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	190634
Contig ID	499_3.R1039
5'-most EST	LIB3147-036-Q1-K1-E8
Method	BLASTX
NCBI GI	g3334320
BLAST score	671
E value	1.0e-70
Match length	142
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi|2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	190635
Contig ID	500_1.R1039
5'-most EST	LIB3146-017-Q1-K1-D7

Seq. No.	190636

Contig ID	504_1.R1039
5'-most EST	LIB3048-011-Q1-L1-H6
Method	BLASTX
NCBI GI	g2102691
BLAST score	302
E value	2.0e-27
Match length	107
% identity	59
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	190637
Contig ID	505_1.R1039
5'-most EST	g5050451
Method	BLASTX
NCBI GI	g2129826
BLAST score	836
E value	1.0e-150
Match length	315
% identity	85
NCBI Description	dynamin-like protein phragmoplastin 5 - soybean >gi|1218004 (U36430) SDL5A [Glycine max]

Seq. No.	190638
Contig ID	505_3.R1039
5'-most EST	LIB3048-036-Q1-L1-A6
Method	BLASTX
NCBI GI	g2129825
BLAST score	479
E value	3.0e-48
Match length	108
% identity	84
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi|1217994 (U25547) SDL [Glycine max]

Seq. No.	190639
Contig ID	505_5.R1039
5'-most EST	LIB3083-112-Q1-L1-B7
Method	BLASTX
NCBI GI	g2129826
BLAST score	602
E value	1.0e-62
Match length	132
% identity	89
NCBI Description	dynamin-like protein phragmoplastin 5 - soybean >gi|1218004 (U36430) SDL5A [Glycine max]

Seq. No.	190640
Contig ID	507_1.R1039
5'-most EST	LIB3048-033-Q1-L1-B5
Method	BLASTX
NCBI GI	g3142303
BLAST score	336
E value	3.0e-31
Match length	153
% identity	47
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb|U92650 from A. thaliana and canalicular multi-drug

resistance protein gb|L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	190641
Contig ID	507_2.R1039
5'-most EST	uC-gsronu33B148d12b1
Method	BLASTX
NCBI GI	g2980641
BLAST score	283
E value	9.0e-42
Match length	195
% identity	46
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	190642
Contig ID	510_1.R1039
5'-most EST	LIB3048-026-Q1-L1-C5

Seq. No.	190643
Contig ID	512_1.R1039
5'-most EST	LIB3135-053-Q1-K1-A1
Method	BLASTX
NCBI GI	g3269288
BLAST score	802
E value	1.0e-85
Match length	204
% identity	77
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	190644
Contig ID	512_2.R1039
5'-most EST	LIB3272-015-P1-K1-E8

Seq. No.	190645
Contig ID	515_1.R1039
5'-most EST	LIB3197-005-P1-M1-A4
Method	BLASTX
NCBI GI	g1346180
BLAST score	382
E value	1.0e-36
Match length	85
% identity	85
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi|496233 (L31374) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	190646
Contig ID	516_1.R1039
5'-most EST	LIB3048-029-Q1-L1-B7
Method	BLASTX
NCBI GI	g1155261
BLAST score	614
E value	6.0e-64
Match length	148
% identity	81
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	190647
Contig ID	518_1.R1039
5'-most EST	LIB3083-116-Q1-L1-H2
Method	BLASTX
NCBI GI	g2262173
BLAST score	397
E value	2.0e-38
Match length	146
% identity	56
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	190648
Contig ID	523_1.R1039
5'-most EST	LIB3048-052-Q1-L1-E9

Seq. No.	190649
Contig ID	524_1.R1039
5'-most EST	g5045299
Method	BLASTX
NCBI GI	g4335751
BLAST score	621
E value	1.0e-100
Match length	247
% identity	68
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	190650
Contig ID	531_1.R1039
5'-most EST	LIB3048-006-Q1-L1-E10

Seq. No.	190651
Contig ID	532_1.R1039
5'-most EST	uC-gsronu33B099b04b1
Method	BLASTX
NCBI GI	g2088647
BLAST score	809
E value	9.0e-87
Match length	188
% identity	83
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi|3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	190652
Contig ID	534_1.R1039
5'-most EST	LIB3165-034-P1-K3-F1
Method	BLASTX
NCBI GI	g4455225
BLAST score	844
E value	1.0e-90
Match length	195
% identity	73
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	190653
Contig ID	537_1.R1039
5'-most EST	LIB3048-042-Q1-L1-A3
Method	BLASTX
NCBI GI	g4490732
BLAST score	688
E value	3.0e-72
Match length	221
% identity	67
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	190654
Contig ID	537_2.R1039
5'-most EST	LIB3166-018-P1-K1-F1
Method	BLASTX
NCBI GI	g4490732
BLAST score	1834
E value	0.0e+00
Match length	374
% identity	90
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	190655
Contig ID	538_1.R1039
5'-most EST	LIB3048-012-Q1-L1-G4
Method	BLASTX
NCBI GI	g1407705
BLAST score	1054
E value	1.0e-115
Match length	236
% identity	79
NCBI Description	(U60202) lipoxygenase [Solanum tuberosum]

Seq. No.	190656
Contig ID	539_1.R1039
5'-most EST	LIB3197-011-P1-M1-D3
Method	BLASTX
NCBI GI	g3367591
BLAST score	345
E value	3.0e-32
Match length	166
% identity	39
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	190657
Contig ID	540_1.R1039
5'-most EST	g5049712
Method	BLASTX
NCBI GI	g3785978
BLAST score	456
E value	4.0e-45
Match length	193
% identity	61
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	190658
Contig ID	542_1.R1039
5'-most EST	LIB3048-021-Q1-L1-F3

Seq. No.	190659
Contig ID	543_1.R1039
5'-most EST	uC-gsflnu33B146c05b1

Seq. No.	190660
Contig ID	544_1.R1039
5'-most EST	LIB3048-006-Q1-L1-F12
Method	BLASTN
NCBI GI	g304040
BLAST score	226
E value	1.0e-124
Match length	313
% identity	94
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	190661
Contig ID	546_1.R1039
5'-most EST	LIB3048-019-Q1-L1-B3

Seq. No.	190662
Contig ID	555_1.R1039
5'-most EST	LIB3147-052-Q1-K1-D9
Method	BLASTX
NCBI GI	g112863
BLAST score	686
E value	2.0e-72
Match length	139
% identity	86
NCBI Description	STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR >gi|100227|pir||S12209 hypothetical protein - tomato >gi|19162|emb|CAA38979| (X55193) 9612 [Lycopersicon esculentum]

Seq. No.	190663
Contig ID	555_2.R1039
5'-most EST	LIB3048-006-Q1-L1-G12
Method	BLASTX
NCBI GI	g2463509
BLAST score	500
E value	1.0e-50
Match length	132
% identity	73
NCBI Description	(Y09541) pectate lyase [Zinnia elegans]

Seq. No.	190664
Contig ID	556_1.R1039
5'-most EST	LIB3165-006-P1-K3-C11
Method	BLASTX
NCBI GI	g2369714
BLAST score	2140
E value	0.0e+00
Match length	473
% identity	88

NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	190665
Contig ID	556_2.R1039
5'-most EST	uC-gsflmaxxa040h03b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	1343
E value	1.0e-149
Match length	270
% identity	94
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	190666
Contig ID	556_3.R1039
5'-most EST	LIB3146-056-Q1-K1-D12
Method	BLASTX
NCBI GI	g2369714
BLAST score	267
E value	1.0e-31
Match length	115
% identity	76
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	190667
Contig ID	556_4.R1039
5'-most EST	LIB3149-055-Q1-K1-F5
Method	BLASTX
NCBI GI	g2369714
BLAST score	305
E value	8.0e-28
Match length	72
% identity	82
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	190668
Contig ID	557_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C4

Seq. No.	190669
Contig ID	557_2.R1039
5'-most EST	g5046752
Method	BLASTX
NCBI GI	g728882
BLAST score	772
E value	2.0e-82
Match length	159
% identity	92
NCBI Description	ADP-RIBOSYLATION FACTOR 3 >gi|541846|pir||S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana >gi|453191|emb|CAA54564| (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

Seq. No.	190670
Contig ID	557_3.R1039
5'-most EST	LIB3146-046-Q1-K1-B2
Method	BLASTX

NCBI GI	g2665890
BLAST score	378
E value	2.0e-36
Match length	90
% identity	79
NCBI Description	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No.	190671
Contig ID	557_4.R1039
5'-most EST	g3325664
Method	BLASTX
NCBI GI	g2665890
BLAST score	879
E value	9.0e-95
Match length	212
% identity	79
NCBI Description	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No.	190672
Contig ID	559_1.R1039
5'-most EST	LIB3272-009-P1-K1-D6
Method	BLASTX
NCBI GI	g3184082
BLAST score	377
E value	5.0e-36
Match length	201
% identity	40
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	190673
Contig ID	560_1.R1039
5'-most EST	LIB3145-041-Q1-K1-G6
Method	BLASTX
NCBI GI	g728744
BLAST score	445
E value	4.0e-44
Match length	131
% identity	67
NCBI Description	AUXIN-INDUCED PROTEIN PCNT115 >gi|100305|pir||S16390 auxin-induced protein - common tobacco >gi|19799|emb|CAA39708| (X56267) auxin-induced protein [Nicotiana tabacum]

Seq. No.	190674
Contig ID	562_1.R1039
5'-most EST	LIB3048-006-Q1-L1-G9
Method	BLASTX
NCBI GI	g4204265
BLAST score	315
E value	3.0e-67
Match length	236
% identity	61
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	190675
Contig ID	566_1.R1039
5'-most EST	LIB3048-040-Q1-L1-A2
Method	BLASTX
NCBI GI	g1352088
BLAST score	1419
E value	1.0e-174
Match length	399
% identity	78
NCBI Description	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi|624676 (U19481) citrate synthase precursor [Citrus maxima]

Seq. No.	190676
Contig ID	567_1.R1039
5'-most EST	LIB3048-008-Q1-L1-C9
Method	BLASTX
NCBI GI	g1363325
BLAST score	321
E value	3.0e-29
Match length	179
% identity	60
NCBI Description	RNA helicase HEL117 - rat >gi|897915 (U25746) RNA helicase [Rattus norvegicus]

Seq. No.	190677
Contig ID	568_1.R1039
5'-most EST	LIB3189-007-P1-K1-F3
Method	BLASTX
NCBI GI	g464980
BLAST score	805
E value	6.0e-86
Match length	152
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi|166422 (L06967) ubiquitin carrier protein [Medicago sativa]

Seq. No.	190678
Contig ID	569_1.R1039
5'-most EST	LIB3048-006-Q1-L1-H6

Seq. No.	190679
Contig ID	573_1.R1039
5'-most EST	LIB3048-033-Q1-L1-A6
Method	BLASTX
NCBI GI	g282881
BLAST score	199
E value	2.0e-15
Match length	122
% identity	39
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi|166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	190680
Contig ID	574_1.R1039
5'-most EST	LIB3048-052-Q1-L1-H9

09655-0050

Method	BLASTX
NCBI GI	g730241
BLAST score	316
E value	4.0e-29
Match length	123
% identity	50
NCBI Description	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi|473947|dbj|BAA06126| (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo sapiens]

Seq. No.	190681
Contig ID	575_1.R1039
5'-most EST	LIB3048-033-Q1-L1-H1

Seq. No.	190682
Contig ID	576_1.R1039
5'-most EST	LIB3048-007-Q1-L1-A2
Method	BLASTX
NCBI GI	g2909781
BLAST score	469
E value	3.0e-47
Match length	118
% identity	79
NCBI Description	(AF020288) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	190683
Contig ID	578_1.R1039
5'-most EST	LIB3048-013-Q1-L1-E1

Seq. No.	190684
Contig ID	579_1.R1039
5'-most EST	LIB3272-052-P1-K1-G8
Method	BLASTX
NCBI GI	g2497538
BLAST score	243
E value	1.0e-20
Match length	94
% identity	56
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	190685
Contig ID	580_1.R1039
5'-most EST	LIB3048-020-Q1-L1-E10
Method	BLASTX
NCBI GI	g1778370
BLAST score	600
E value	2.0e-62
Match length	142
% identity	79
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	190686

Contig ID	581_1.R1039
5'-most EST	LIB3048-029-Q1-L1-H7
Method	BLASTX
NCBI GI	g1703200
BLAST score	625
E value	2.0e-65
Match length	128
% identity	92
NCBI Description	PROTEIN KINASE AFC2 >gi|601789 (U16177) protein kinase [Arabidopsis thaliana] >gi|642130|dbj|BAA08214| (D45353) protein kinase [Arabidopsis thaliana] >gi|4220516|emb|CAA22989| (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	190687
Contig ID	584_1.R1039
5'-most EST	LIB3048-007-Q1-L1-B1
Method	BLASTX
NCBI GI	g1169782
BLAST score	746
E value	2.0e-79
Match length	189
% identity	76
NCBI Description	FUSCA PROTEIN FUS6 >gi|432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	190688
Contig ID	594_1.R1039
5'-most EST	LIB3048-007-Q1-L1-B8

Seq. No.	190689
Contig ID	596_1.R1039
5'-most EST	LIB3048-013-Q1-L1-E5
Method	BLASTX
NCBI GI	g2739381
BLAST score	557
E value	4.0e-57
Match length	175
% identity	61
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	190690
Contig ID	596_2.R1039
5'-most EST	LIB3048-038-Q1-L1-C1
Method	BLASTX
NCBI GI	g2739381
BLAST score	563
E value	5.0e-70
Match length	204
% identity	66
NCBI Description	(AC002505) putative patatin [Arabidopsis thaliana]

Seq. No.	190691
Contig ID	597_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C10
Method	BLASTX
NCBI GI	g4468046

BLAST score	477
E value	1.0e-72
Match length	279
% identity	53
NCBI Description	(X69192) catechol methyltransferase [Vanilla planifolia]

Seq. No.	190692
Contig ID	599_1.R1039
5'-most EST	LIB3083-015-Q1-L2-B1
Method	BLASTX
NCBI GI	g2833388
BLAST score	2156
E value	0.0e+00
Match length	519
% identity	78
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi|629660|pir||S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi|437042|emb|CAA52273| (X74160) starch (bacterial glycogen) synthase [Manihot esculenta]

Seq. No.	190693
Contig ID	599_2.R1039
5'-most EST	uC-gsflmaxxa042f12b1
Method	BLASTX
NCBI GI	g3688123
BLAST score	412
E value	1.0e-40
Match length	143
% identity	65
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	190694
Contig ID	599_3.R1039
5'-most EST	uC-gsflmaxxa048f10b1
Method	BLASTN
NCBI GI	g437041
BLAST score	57
E value	3.0e-23
Match length	125
% identity	86
NCBI Description	M.esculenta mRNA for granule-bound starch synthase

Seq. No.	190695
Contig ID	601_1.R1039
5'-most EST	LIB3145-030-Q1-K1-G3
Method	BLASTX
NCBI GI	g4544454
BLAST score	504
E value	2.0e-84
Match length	181
% identity	86
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	190696
Contig ID	602_1.R1039

5'-most EST	LIB3048-007-Q1-L1-C4
Method	BLASTX
NCBI GI	g3096935
BLAST score	526
E value	2.0e-53
Match length	237
% identity	47
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	190697
Contig ID	604_1.R1039
5'-most EST	LIB3048-020-Q1-L1-G6
Method	BLASTN
NCBI GI	g1465367
BLAST score	37
E value	3.0e-11
Match length	57
% identity	91
NCBI Description	A.thaliana mRNA for RAP-1 protein

Seq. No.	190698
Contig ID	609_1.R1039
5'-most EST	LIB3048-033-Q1-L1-H11

Seq. No.	190699
Contig ID	610_1.R1039
5'-most EST	LIB3166-010-P1-K1-C11
Method	BLASTX
NCBI GI	g4558547
BLAST score	293
E value	2.0e-26
Match length	146
% identity	45
NCBI Description	(AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190700
Contig ID	612_1.R1039
5'-most EST	LIB3048-032-Q1-L1-G11

Seq. No.	190701
Contig ID	613_1.R1039
5'-most EST	LIB3048-007-Q1-L1-D4

Seq. No.	190702
Contig ID	614_1.R1039
5'-most EST	LIB3048-034-Q1-L1-B11
Method	BLASTX
NCBI GI	g3434971
BLAST score	206
E value	4.0e-16
Match length	95
% identity	54
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	190703
Contig ID	615_1.R1039

5'-most EST LIB3048-033-Q1-L1-E2

Seq. No. 190704
Contig ID 619_1.R1039
5'-most EST LIB3048-049-Q1-L1-C12

Seq. No. 190705
Contig ID 625_1.R1039
5'-most EST g5046153
Method BLASTX
NCBI GI g1749596
BLAST score 717
E value 1.0e-75
Match length 222
% identity 60
NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No. 190706
Contig ID 625_2.R1039
5'-most EST LIB3083-006-Q1-L1-F1
Method BLASTX
NCBI GI g113116
BLAST score 1302
E value 1.0e-144
Match length 491
% identity 51
NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi|111396|pir||A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi|203490 (J05210) ATP citrate-lyase [Rattus norvegicus]

Seq. No. 190707
Contig ID 625_3.R1039
5'-most EST g3326424
Method BLASTX
NCBI GI g4107343
BLAST score 272
E value 1.0e-23
Match length 139
% identity 40
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq. No. 190708
Contig ID 626_1.R1039
5'-most EST LIB3272-048-P1-K1-E7

Seq. No. 190709
Contig ID 627_1.R1039
5'-most EST LIB3048-029-Q1-L1-E8

Seq. No. 190710
Contig ID 628_1.R1039
5'-most EST LIB3166-033-P1-K1-B6
Method BLASTX
NCBI GI g477819
BLAST score 1220

E value	1.0e-134
Match length	313
% identity	76
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi|410634|bbs|136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	190711
Contig ID	629_1.R1039
5'-most EST	uC-gsflmaxxa098f11b1
Method	BLASTX
NCBI GI	g4262250
BLAST score	577
E value	2.0e-59
Match length	159
% identity	75
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	190712
Contig ID	629_2.R1039
5'-most EST	LIB3145-001-P1-K1-F3
Method	BLASTN
NCBI GI	g4262221
BLAST score	61
E value	2.0e-25
Match length	383
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	190713
Contig ID	632_1.R1039
5'-most EST	LIB3120-053-P1-K1-C7
Method	BLASTX
NCBI GI	g3421134
BLAST score	737
E value	1.0e-100
Match length	289
% identity	70
NCBI Description	(AF045666) arginine decarboxylase [Theobroma cacao]

Seq. No.	190714
Contig ID	632_2.R1039
5'-most EST	uC-gsronu33B160e09b1
Method	BLASTX
NCBI GI	g2347054
BLAST score	749
E value	1.0e-79
Match length	198
% identity	73
NCBI Description	(X96791) arginine decarboxylase [Vitis vinifera]

Seq. No.	190715
Contig ID	632_3.R1039
5'-most EST	uC-gsronu33B108e08b1

Method	BLASTX
NCBI GI	g2347054
BLAST score	632
E value	8.0e-66
Match length	183
% identity	67
NCBI Description	(X96791) arginine decarboxylase [Vitis vinifera]

Seq. No.	190716
Contig ID	634_1.R1039
5'-most EST	uC-gsronu33B138e11b1
Method	BLASTX
NCBI GI	g2739279
BLAST score	735
E value	1.0e-77
Match length	273
% identity	53
NCBI Description	(AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi|2791348|emb|CAA11154| (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No.	190717
Contig ID	637_1.R1039
5'-most EST	g5045364
Method	BLASTX
NCBI GI	g1171978
BLAST score	624
E value	6.0e-65
Match length	229
% identity	26
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi|304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi|2911051|emb|CAA17561| (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	190718
Contig ID	637_2.R1039
5'-most EST	LIB3147-023-Q1-K1-D7
Method	BLASTX
NCBI GI	g1171978
BLAST score	227
E value	2.0e-18
Match length	89
% identity	48
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi|304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi|2911051|emb|CAA17561| (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	190719
Contig ID	638_1.R1039
5'-most EST	LIB3048-019-Q1-L1-E2
Method	BLASTX
NCBI GI	g4530126
BLAST score	429
E value	2.0e-42
Match length	116

% identity	72
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	190720
Contig ID	640_1.R1039
5'-most EST	uC-gsflnu33B093b01b1
Method	BLASTX
NCBI GI	g2129955
BLAST score	382
E value	6.0e-38
Match length	128
% identity	59
NCBI Description	photoassimilate-responsive protein PAR-1b precursor - common tobacco >gi|871487|emb|CAA58731| (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No.	190721
Contig ID	640_2.R1039
5'-most EST	LIB3048-007-Q1-L1-G1
Method	BLASTX
NCBI GI	g2129956
BLAST score	304
E value	7.0e-38
Match length	147
% identity	52
NCBI Description	photoassimilate-responsive protein PAR-1c precursor - common tobacco >gi|871489|emb|CAA58732| (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]

Seq. No.	190722
Contig ID	641_2.R1039
5'-most EST	LIB3048-041-Q1-L1-F2
Method	BLASTX
NCBI GI	g3831455
BLAST score	175
E value	1.0e-12
Match length	69
% identity	77
NCBI Description	(AC005700) putative ubiquitin activating enzyme [Arabidopsis thaliana]

Seq. No.	190723
Contig ID	642_1.R1039
5'-most EST	g3326391
Method	BLASTX
NCBI GI	g4455365
BLAST score	153
E value	8.0e-10
Match length	31
% identity	87
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	190724
Contig ID	642_2.R1039

5'-most EST	LIB3048-038-Q1-L1-D10
Method	BLASTX
NCBI GI	g4455365
BLAST score	272
E value	8.0e-24
Match length	57
% identity	81
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	190725
Contig ID	642_3.R1039
5'-most EST	LIB3048-038-Q1-L1-G8
Method	BLASTX
NCBI GI	g166949
BLAST score	305
E value	1.0e-47
Match length	289
% identity	42
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No.	190726
Contig ID	649_1.R1039
5'-most EST	LIB3048-025-Q1-L1-A6

Seq. No.	190727
Contig ID	652_1.R1039
5'-most EST	LIB3165-038-Q1-K1-A4
Method	BLASTX
NCBI GI	g2827551
BLAST score	159
E value	3.0e-10
Match length	112
% identity	46
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	190728
Contig ID	652_2.R1039
5'-most EST	g5050719
Method	BLASTX
NCBI GI	g2827551
BLAST score	411
E value	1.0e-39
Match length	216
% identity	49
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	190729
Contig ID	653_1.R1039
5'-most EST	LIB3166-009-P1-K1-H3
Method	BLASTX
NCBI GI	g3599974
BLAST score	347
E value	2.0e-32
Match length	169
% identity	43
NCBI Description	(AF038651) GTP pyrophosphokinase [Corynebacterium

glutamicum]

Seq. No.	190730
Contig ID	657_1.R1039
5'-most EST	LIB3189-022-P1-K1-D2
Method	BLASTX
NCBI GI	g3377797
BLAST score	767
E value	2.0e-81
Match length	181
% identity	84
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	190731
Contig ID	657_2.R1039
5'-most EST	LIB3083-051-Q1-L1-F8
Method	BLASTX
NCBI GI	g3377797
BLAST score	781
E value	3.0e-83
Match length	183
% identity	84
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	190732
Contig ID	657_3.R1039
5'-most EST	LIB3083-101-Q1-L1-A12
Method	BLASTX
NCBI GI	g3377797
BLAST score	445
E value	3.0e-44
Match length	117
% identity	75
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	190733
Contig ID	657_4.R1039
5'-most EST	uC-gsronu33B018a08b1
Method	BLASTX
NCBI GI	g3377797
BLAST score	247
E value	5.0e-21
Match length	53
% identity	94
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	190734
Contig ID	662_1.R1039
5'-most EST	LIB3048-008-Q1-L1-A10
Method	BLASTN
NCBI GI	g3449322
BLAST score	76
E value	3.0e-34
Match length	256
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	190735
Contig ID	664_1.R1039
5'-most EST	uC-gsflnu33B109c08b1
Method	BLASTX
NCBI GI	g2569938
BLAST score	240
E value	7.0e-20
Match length	153
% identity	38
NCBI Description	(Y15193) GAI [Arabidopsis thaliana]

Seq. No.	190736
Contig ID	665_1.R1039
5'-most EST	uC-gsflmaxxa098c03b1
Method	BLASTX
NCBI GI	g3549670
BLAST score	651
E value	4.0e-68
Match length	154
% identity	81
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	190737
Contig ID	666_1.R1039
5'-most EST	uC-gsflnu33B114b05b1
Method	BLASTX
NCBI GI	g4101626
BLAST score	545
E value	1.0e-55
Match length	152
% identity	67
NCBI Description	(AF005096) desaturase/cytochrome b5 protein [Ricinus communis]

Seq. No.	190738
Contig ID	668_1.R1039
5'-most EST	LIB3048-008-Q1-L1-D4
Method	BLASTX
NCBI GI	g3641836
BLAST score	742

E value 1.0e-78
Match length 252
% identity 73
NCBI Description (AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 190739
Contig ID 670_1.R1039
5'-most EST g3326493
Method BLASTX
NCBI GI g2642450
BLAST score 1302
E value 1.0e-144
Match length 326
% identity 76
NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi|3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 190740
Contig ID 673_1.R1039
5'-most EST LIB3048-053-Q1-L1-B11

Seq. No. 190741
Contig ID 676_1.R1039
5'-most EST uC-gsronu33B098d10b1
Method BLASTX
NCBI GI g4138265
BLAST score 720
E value 1.0e-108
Match length 245
% identity 74
NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No. 190742
Contig ID 676_2.R1039
5'-most EST LIB3048-051-Q1-L1-F9
Method BLASTX
NCBI GI g2388580
BLAST score 275
E value 2.0e-24
Match length 67
% identity 69
NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002 (gb|1253956). [Arabidopsis thaliana]

Seq. No. 190743
Contig ID 677_1.R1039
5'-most EST uC-gsronu33B109d07b1
Method BLASTX
NCBI GI g4210330
BLAST score 2262
E value 0.0e+00
Match length 490
% identity 85
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit

[Arabidopsis thaliana]

Seq. No.	190744
Contig ID	677_2.R1039
5'-most EST	uC-gsronu33B109d01b1
Method	BLASTX
NCBI GI	g2827711
BLAST score	593
E value	2.0e-61
Match length	182
% identity	60
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	190745
Contig ID	678_1.R1039
5'-most EST	g5044895
Method	BLASTX
NCBI GI	g2995953
BLAST score	379
E value	4.0e-36
Match length	104
% identity	70
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No.	190746
Contig ID	681_1.R1039
5'-most EST	LIB3166-040-P1-K1-D7
Method	BLASTX
NCBI GI	g2465923
BLAST score	213
E value	5.0e-17
Match length	123
% identity	22
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	190747
Contig ID	682_1.R1039
5'-most EST	LIB3048-008-Q1-L1-B9
Method	BLASTX
NCBI GI	g4314376
BLAST score	270
E value	2.0e-23
Match length	199
% identity	38
NCBI Description	(AC006232) similar to PIG-L [Arabidopsis thaliana]

Seq. No.	190748
Contig ID	683_1.R1039
5'-most EST	LIB3048-008-Q1-L1-C1
Method	BLASTX
NCBI GI	g2245064
BLAST score	168
E value	7.0e-12
Match length	71
% identity	52

09604-1000

NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	190749
Contig ID	685_1.R1039
5'-most EST	LIB3048-008-Q1-L1-C11
Method	BLASTX
NCBI GI	g3065814
BLAST score	332
E value	8.0e-31
Match length	190
% identity	44
NCBI Description	(AF058714) sodium-dicarboxylate cotransporter SDCT1 [Rattus norvegicus] >gi|3168585|dbj|BAA28609| (AB001321) sodium-dependent dicarboxylate transporter [Rattus norvegicus]
Seq. No.	190750
Contig ID	687_1.R1039
5'-most EST	g3326059
Method	BLASTX
NCBI GI	g3450842
BLAST score	381
E value	2.0e-36
Match length	113
% identity	65
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
Seq. No.	190751
Contig ID	687_2.R1039
5'-most EST	LIB3048-053-Q1-L1-A7
Method	BLASTX
NCBI GI	g3450842
BLAST score	283
E value	6.0e-25
Match length	157
% identity	48
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
Seq. No.	190752
Contig ID	688_1.R1039
5'-most EST	LIB3048-024-Q1-L1-F1
Seq. No.	190753
Contig ID	689_1.R1039
5'-most EST	LIB3048-031-Q1-L1-F6
Method	BLASTX
NCBI GI	g2827561
BLAST score	224
E value	2.0e-18
Match length	117
% identity	41
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi|3292809|emb|CAA19799| (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	190754
Contig ID	692_1.R1039
5'-most EST	LIB3048-008-Q1-L1-C8

Seq. No.	190755
Contig ID	695_1.R1039
5'-most EST	LIB3083-050-Q1-L1-F6
Method	BLASTN
NCBI GI	g1495250
BLAST score	33
E value	9.0e-09
Match length	171
% identity	87
NCBI Description	A.thaliana mRNA for heat-shock protein

Seq. No.	190756
Contig ID	697_1.R1039
5'-most EST	g5050148
Method	BLASTX
NCBI GI	g1176081
BLAST score	340
E value	2.0e-31
Match length	156
% identity	46
NCBI Description	HYPOTHETICAL PROTEIN HI0671 >gi|1074478|pir||F64156 hypothetical protein HI0671 - Haemophilus influenzae (strain Rd KW20) >gi|1573672 (U32750) conserved hypothetical protein [Haemophilus influenzae Rd]

Seq. No.	190757
Contig ID	698_1.R1039
5'-most EST	LIB3048-008-Q1-L1-H10
Method	BLASTX
NCBI GI	g3287683
BLAST score	382
E value	6.0e-37
Match length	135
% identity	16
NCBI Description	(AC003979) Similar to apoptosis protein MA-3 gb|D50465 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	190758
Contig ID	699_1.R1039
5'-most EST	LIB3197-054-Q1-M1-E1
Method	BLASTX
NCBI GI	g136739
BLAST score	1975
E value	0.0e+00
Match length	464
% identity	82
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi|67061|pir||XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi|218001|dbj|BAA00570| (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	190759

Contig ID 701_1.R1039
5'-most EST LIB3197-059-Q1-M1-B7
Method BLASTX
NCBI GI g3319355
BLAST score 1961
E value 0.0e+00
Match length 426
% identity 91
NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No. 190760
Contig ID 702_1.R1039
5'-most EST LIB3048-015-Q1-L1-H10
Method BLASTX
NCBI GI g4105798
BLAST score 858
E value 1.0e-114
Match length 271
% identity 62
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 190761
Contig ID 704_1.R1039
5'-most EST LIB3048-025-Q1-L1-E8
Method BLASTX
NCBI GI g4204265
BLAST score 572
E value 8.0e-59
Match length 233
% identity 54
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 190762
Contig ID 707_1.R1039
5'-most EST LIB3048-008-Q1-L1-E11

Seq. No. 190763
Contig ID 711_1.R1039
5'-most EST LIB3048-027-Q1-L1-A1

Seq. No. 190764
Contig ID 713_1.R1039
5'-most EST LIB3272-019-P1-K1-A11
Method BLASTX
NCBI GI g231675
BLAST score 696
E value 1.0e-113
Match length 331
% identity 67
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi|282955|pir||S23525 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common tobacco >gi|19839|emb|CAA44216| (X62343) cinnamyl-alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 190765
Contig ID 713_2.R1039

5'-most EST	LIB3272-018-P1-K1-G7
Method	BLASTX
NCBI GI	g3913185
BLAST score	429
E value	2.0e-42
Match length	133
% identity	59
NCBI Description	CINNAMYL ALCOHOL DEHYDROGENASE (CAD) >gi|2984653 (AF038561) cinnamyl alcohol dehydrogenase; CAD [Eucalyptus globulus]

Seq. No.	190766
Contig ID	714_1.R1039
5'-most EST	LIB3048-023-Q1-L1-F6
Method	BLASTX
NCBI GI	g2911059
BLAST score	631
E value	5.0e-66
Match length	146
% identity	87
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	190767
Contig ID	715_1.R1039
5'-most EST	LIB3048-008-Q1-L1-E9
Method	BLASTX
NCBI GI	g2244987
BLAST score	229
E value	5.0e-19
Match length	98
% identity	48
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No.	190768
Contig ID	716_1.R1039
5'-most EST	LIB3272-058-P1-K1-H7
Method	BLASTX
NCBI GI	g3602981
BLAST score	195
E value	8.0e-15
Match length	87
% identity	51
NCBI Description	(AF041468) acetohydroxyacid synthetase small subunit [Guillardia theta]

Seq. No.	190769
Contig ID	717_1.R1039
5'-most EST	LIB3145-057-Q1-K1-E9
Method	BLASTN
NCBI GI	g166411
BLAST score	251
E value	1.0e-138
Match length	1146
% identity	81
NCBI Description	Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 190770

Contig ID	717_2.R1039
5'-most EST	uC-gsronu33B125e07b1
Method	BLASTX
NCBI GI	g417073
BLAST score	1773
E value	0.0e+00
Match length	415
% identity	81
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi|484529|pir||JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi|166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	190771
Contig ID	718_1.R1039
5'-most EST	uC-gsronu33B021c06b1
Method	BLASTX
NCBI GI	g4262174
BLAST score	797
E value	2.0e-85
Match length	194
% identity	71
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	190772
Contig ID	723_1.R1039
5'-most EST	LIB3149-004-P1-K1-B10
Method	BLASTX
NCBI GI	g1706323
BLAST score	487
E value	5.0e-49
Match length	164
% identity	57
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi|2118242|pir||S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi|871008|emb|CAA61121| (X87847) ornithine decarboxylase [Datura stramonium]

Seq. No.	190773
Contig ID	725_1.R1039
5'-most EST	LIB3083-023-Q1-L1-G5

Seq. No.	190774
Contig ID	727_1.R1039
5'-most EST	LIB3135-050-Q1-K1-H10
Method	BLASTX
NCBI GI	g3176708
BLAST score	269
E value	1.0e-23
Match length	104
% identity	53
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	190775
Contig ID	734_1.R1039
5'-most EST	LIB3189-014-P1-K1-E8

Method	BLASTX
NCBI GI	g2935298
BLAST score	2485
E value	0.0e+00
Match length	578
% identity	85
NCBI Description	(AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No.	190776
Contig ID	736_1.R1039
5'-most EST	LIB3189-032-P1-K1-H2
Method	BLASTX
NCBI GI	g2244971
BLAST score	1113
E value	1.0e-122
Match length	281
% identity	74
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190777
Contig ID	737_1.R1039
5'-most EST	LIB3048-025-Q1-L1-F8
Method	BLASTX
NCBI GI	g2498706
BLAST score	150
E value	4.0e-13
Match length	63
% identity	60
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi|1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi|3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	190778
Contig ID	742_2.R1039
5'-most EST	LIB3272-023-P1-K1-C8
Method	BLASTX
NCBI GI	g1619300
BLAST score	934
E value	1.0e-101
Match length	207
% identity	86
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	190779
Contig ID	742_3.R1039
5'-most EST	LIB3048-008-Q1-L1-H3
Method	BLASTX
NCBI GI	g1619300
BLAST score	314
E value	8.0e-29
Match length	74
% identity	78
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	190780

Contig ID	742_4.R1039
5'-most EST	uC-gsronu33B082a07b1
Method	BLASTX
NCBI GI	g1619300
BLAST score	318
E value	2.0e-29
Match length	65
% identity	91
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	190781
Contig ID	744_1.R1039
5'-most EST	LIB3196-056-P1-M1-A3
Method	BLASTX
NCBI GI	g119791
BLAST score	659
E value	5.0e-69
Match length	236
% identity	62
NCBI Description	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) >gi|1084385|pir||S22450 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor - Cuphea lanceolata >gi|18046|emb|CAA45866| (X64566) 3-oxoacyl-[acyl-carrier protein] reductase [Cuphea lanceolata] >gi|228929|prf||1814446A beta ketoacyl-ACP reductase [Cuphea lanceolata]

Seq. No.	190782
Contig ID	745_1.R1039
5'-most EST	LIB3197-057-Q1-M1-E10
Method	BLASTX
NCBI GI	g1644427
BLAST score	543
E value	2.0e-55
Match length	122
% identity	84
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	190783
Contig ID	745_2.R1039
5'-most EST	g3326297
Method	BLASTX
NCBI GI	g1644427
BLAST score	451
E value	1.0e-44
Match length	118
% identity	75
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	190784
Contig ID	745_4.R1039
5'-most EST	g5044418
Method	BLASTX
NCBI GI	g1644427
BLAST score	886
E value	1.0e-95

Match length 200
% identity 81
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No. 190785
Contig ID 749_1.R1039
5'-most EST LIB3048-009-Q1-L1-A10

Seq. No. 190786
Contig ID 750_1.R1039
5'-most EST LIB3048-020-Q1-L1-H7

Seq. No. 190787
Contig ID 751_1.R1039
5'-most EST LIB3048-031-Q1-L1-E3
Method BLASTX
NCBI GI g4558664
BLAST score 310
E value 2.0e-28
Match length 145
% identity 10
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 190788
Contig ID 756_1.R1039
5'-most EST LIB3048-042-Q1-L1-C1
Method BLASTX
NCBI GI g2459440
BLAST score 455
E value 4.0e-45
Match length 251
% identity 35
NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 190789
Contig ID 757_1.R1039
5'-most EST LIB3048-050-Q1-L1-D11
Method BLASTX
NCBI GI g1729760
BLAST score 1076
E value 1.0e-118
Match length 191
% identity 99
NCBI Description (Z68152) chitinase [Gossypium hirsutum]

Seq. No. 190790
Contig ID 761_1.R1039
5'-most EST LIB3135-049-Q1-K1-F9

Seq. No. 190791
Contig ID 764_1.R1039
5'-most EST LIB3048-009-Q1-L1-C11

Seq. No. 190792
Contig ID 765_1.R1039
5'-most EST LIB3048-027-Q1-L1-A5
Method BLASTX

NCBI GI	g3643607
BLAST score	1014
E value	1.0e-110
Match length	268
% identity	71
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	190793
Contig ID	767_1.R1039
5'-most EST	LIB3048-009-Q1-L1-C4
Method	BLASTX
NCBI GI	g3874447
BLAST score	251
E value	5.0e-35
Match length	266
% identity	35
NCBI Description	(Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com

Seq. No.	190794
Contig ID	771_1.R1039
5'-most EST	LIB3048-036-Q1-L1-A4
Method	BLASTX
NCBI GI	g3075394
BLAST score	510
E value	6.0e-52
Match length	130
% identity	78
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi|3559809|emb|CAA09311| (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	190795
Contig ID	772_1.R1039
5'-most EST	LIB3048-034-Q1-L1-B6

Seq. No.	190796
Contig ID	772_2.R1039
5'-most EST	LIB3165-020-P1-K1-H6
Method	BLASTX
NCBI GI	g1078406
BLAST score	293
E value	4.0e-26
Match length	204
% identity	36
NCBI Description	SWH1 protein (version 2) - yeast (Saccharomyces cerevisiae) >gi|402658|emb|CAA52646| (X74552) SWH1 [Saccharomyces cerevisiae] >gi|1090523|prf||2019253A oxysterol-binding protein-like protein [Saccharomyces cerevisiae]

Seq. No.	190797
Contig ID	774_1.R1039
5'-most EST	LIB3048-009-Q1-L1-D2
Method	BLASTX
NCBI GI	g4377331

BLAST score 381
E value 2.0e-36
Match length 168
% identity 48
NCBI Description (AE001681) cytosine deaminase [Chlamydia pneumoniae]

Seq. No. 190798
Contig ID 778_1.R1039
5'-most EST LIB3166-036-P1-K1-A8
Method BLASTX
NCBI GI g2760345
BLAST score 544
E value 2.0e-74
Match length 151
% identity 26
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]

Seq. No. 190799
Contig ID 782_1.R1039
5'-most EST LIB3083-112-Q1-L1-H7

Seq. No. 190800
Contig ID 783_1.R1039
5'-most EST LIB3048-020-Q1-L1-C7
Method BLASTX
NCBI GI g4539383
BLAST score 677
E value 3.0e-71
Match length 185
% identity 67
NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 190801
Contig ID 788_1.R1039
5'-most EST LIB3048-022-Q1-L1-D1
Method BLASTX
NCBI GI g2443329
BLAST score 709
E value 3.0e-95
Match length 249
% identity 73
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 190802
Contig ID 789_3.R1039
5'-most EST LIB3048-020-Q1-L1-H6

Seq. No. 190803
Contig ID 791_1.R1039
5'-most EST LIB3048-035-Q1-L1-H9
Method BLASTX
NCBI GI g3212865
BLAST score 524
E value 1.0e-53
Match length 130
% identity 79

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 190804
Contig ID 797_1.R1039
5'-most EST g3325569
Method BLASTX
NCBI GI g1531758
BLAST score 766
E value 1.0e-81
Match length 197
% identity 76
NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi|3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 190805
Contig ID 799_1.R1039
5'-most EST LIB3048-017-Q1-L1-D11
Method BLASTX
NCBI GI g2832642
BLAST score 310
E value 3.0e-30
Match length 124
% identity 25
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 190806
Contig ID 801_1.R1039
5'-most EST LIB3272-039-P1-K1-D4
Method BLASTX
NCBI GI g2911059
BLAST score 503
E value 6.0e-51
Match length 116
% identity 83
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 190807
Contig ID 803_1.R1039
5'-most EST LIB3048-009-Q1-L1-G5

Seq. No. 190808
Contig ID 806_1.R1039
5'-most EST LIB3048-019-Q1-L1-H7
Method BLASTX
NCBI GI g3420906
BLAST score 237
E value 4.0e-22
Match length 72
% identity 59
NCBI Description (AF080595) zinc finger protein; WRKY1 [Pimpinella brachycarpa]

Seq. No. 190809
Contig ID 809_1.R1039
5'-most EST LIB3048-050-Q1-L1-D5
Method BLASTX
NCBI GI g3461814

BLAST score 784
E value 9.0e-84
Match length 208
% identity 72
NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 190810
Contig ID 810_1.R1039
5'-most EST uC-gsflnu33B115e10b1
Method BLASTX
NCBI GI g1777386
BLAST score 475
E value 1.0e-47
Match length 177
% identity 48
NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]

Seq. No. 190811
Contig ID 812_1.R1039
5'-most EST LIB3048-009-Q1-L1-H4
Method BLASTX
NCBI GI g2632105
BLAST score 291
E value 3.0e-26
Match length 84
% identity 69
NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi|4539426|emb|CAB38959.1| (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 190812
Contig ID 815_1.R1039
5'-most EST LIB3048-010-Q1-L1-A12
Method BLASTX
NCBI GI g2827546
BLAST score 351
E value 3.0e-33
Match length 147
% identity 47
NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No. 190813
Contig ID 816_1.R1039
5'-most EST LIB3048-047-Q1-L1-D10

Seq. No. 190814
Contig ID 818_1.R1039
5'-most EST g3325965
Method BLASTX
NCBI GI g548488
BLAST score 648
E value 1.0e-67
Match length 197
% identity 63
NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi|166325 (L12019) polygalacturonase [Actinidia deliciosa]

Seq. No.	190815
Contig ID	821_1.R1039
5'-most EST	LIB3146-052-Q1-K1-F4
Method	BLASTX
NCBI GI	g1272410
BLAST score	536
E value	7.0e-55
Match length	110
% identity	91
NCBI Description	(U52045) immunophilin precursor [Vicia faba]

Seq. No.	190816
Contig ID	822_1.R1039
5'-most EST	LIB3048-010-Q1-L1-A8
Method	BLASTX
NCBI GI	g4432844
BLAST score	194
E value	8.0e-15
Match length	84
% identity	51
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	190817
Contig ID	823_1.R1039
5'-most EST	LIB3048-025-Q1-L1-E2
Method	BLASTX
NCBI GI	g3687223
BLAST score	393
E value	5.0e-49
Match length	211
% identity	59
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190818
Contig ID	823_2.R1039
5'-most EST	LIB3083-114-Q1-L1-C10
Method	BLASTX
NCBI GI	g3687223
BLAST score	159
E value	1.0e-10
Match length	117
% identity	32
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190819
Contig ID	824_1.R1039
5'-most EST	LIB3048-029-Q1-L1-C1
Method	BLASTX
NCBI GI	g116923
BLAST score	932
E value	1.0e-101
Match length	338
% identity	58
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi|111414|pir||S13520 beta-COP protein - rat >gi|55819|emb|CAA40505| (X57228) beta COP [Rattus

norvegicus]

Seq. No.	190820
Contig ID	824_2.R1039
5'-most EST	LIB3135-046-Q1-K1-D9
Method	BLASTX
NCBI GI	g116923
BLAST score	150
E value	4.0e-11
Match length	64
% identity	64
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi|111414|pir||S13520 beta-COP protein - rat >gi|55819|emb|CAA40505| (X57228) beta COP [Rattus norvegicus]

Seq. No.	190821
Contig ID	827_1.R1039
5'-most EST	LIB3083-015-Q1-L2-B2
Method	BLASTN
NCBI GI	g4165340
BLAST score	38
E value	1.0e-11
Match length	191
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	190822
Contig ID	829_1.R1039
5'-most EST	g5050704
Method	BLASTX
NCBI GI	g3080401
BLAST score	871
E value	7.0e-94
Match length	206
% identity	79
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi|4455265|emb|CAB36801.1| (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	190823
Contig ID	830_1.R1039
5'-most EST	LIB3048-031-Q1-L1-C2
Method	BLASTX
NCBI GI	g3033397
BLAST score	1027
E value	1.0e-143
Match length	333
% identity	75
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	190824
Contig ID	834_1.R1039
5'-most EST	LIB3048-010-Q1-L1-C1
Method	BLASTX
NCBI GI	g3287693

BLAST score	1425
E value	1.0e-158
Match length	301
% identity	87
NCBI Description	(AC003979) Similar to LIM17 gene product gb|1653769 from the genome of Synechocystis sp. gb|D90916. [Arabidopsis thaliana]

Seq. No.	190825
Contig ID	835_1.R1039
5'-most EST	LIB3048-010-Q1-L1-C10
Method	BLASTX
NCBI GI	g4105798
BLAST score	463
E value	2.0e-46
Match length	101
% identity	71
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	190826
Contig ID	839_1.R1039
5'-most EST	uC-gsflnu33B070h07b1
Method	BLASTX
NCBI GI	g2440035
BLAST score	762
E value	3.0e-81
Match length	187
% identity	79
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	190827
Contig ID	841_2.R1039
5'-most EST	LIB3048-027-Q1-L1-D2

Seq. No.	190828
Contig ID	845_1.R1039
5'-most EST	LIB3048-019-Q1-L1-D8

Seq. No.	190829
Contig ID	847_1.R1039
5'-most EST	LIB3048-010-Q1-L1-D10
Method	BLASTX
NCBI GI	g4539423
BLAST score	370
E value	2.0e-35
Match length	97
% identity	73
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	190830
Contig ID	848_1.R1039
5'-most EST	LIB3048-053-Q1-L1-D10
Method	BLASTX
NCBI GI	g4580523
BLAST score	268
E value	4.0e-23

Match length	219
% identity	34
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	190831
Contig ID	849_1.R1039
5'-most EST	LIB3048-010-Q1-L1-D12
Method	BLASTX
NCBI GI	g542200
BLAST score	333
E value	3.0e-31
Match length	123
% identity	49
NCBI Description	hypothetical protein - garden asparagus >gi|452714|emb|CAA54526| (X77320) unknown [Asparagus officinalis]

Seq. No.	190832
Contig ID	853_2.R1039
5'-most EST	LIB3149-014-Q1-K1-H11
Method	BLASTX
NCBI GI	g134025
BLAST score	475
E value	2.0e-47
Match length	107
% identity	86
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi|70913|pir||R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi|11863|emb|CAA77378| (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi|225232|prf||1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	190833
Contig ID	854_1.R1039
5'-most EST	LIB3048-042-Q1-L1-D2
Method	BLASTX
NCBI GI	g4539423
BLAST score	846
E value	5.0e-91
Match length	182
% identity	88
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	190834
Contig ID	856_1.R1039
5'-most EST	LIB3048-010-Q1-L1-D8

Seq. No.	190835
Contig ID	857_1.R1039
5'-most EST	LIB3048-034-Q1-L1-B1
Method	BLASTX
NCBI GI	g3336903
BLAST score	476
E value	7.0e-48
Match length	127
% identity	72

NCBI Description	(Y10809) bZIP DNA-binding protein [Petroselinum crispum]
Seq. No.	190836
Contig ID	859_1.R1039
5'-most EST	LIB3048-010-Q1-L1-E11
Method	BLASTX
NCBI GI	g1488647
BLAST score	1180
E value	1.0e-130
Match length	298
% identity	79
NCBI Description	(X99937) RNA helicase [Spinacia oleracea]
Seq. No.	190837
Contig ID	860_1.R1039
5'-most EST	LIB3048-010-Q1-L1-E12
Method	BLASTX
NCBI GI	g2088651
BLAST score	364
E value	1.0e-34
Match length	132
% identity	52
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	190838
Contig ID	862_1.R1039
5'-most EST	g3326203
Method	BLASTX
NCBI GI	g2231034
BLAST score	692
E value	2.0e-75
Match length	175
% identity	83
NCBI Description	(Y12785) MAP kinase I [Petroselinum crispum]
Seq. No.	190839
Contig ID	862_2.R1039
5'-most EST	LIB3048-026-Q1-L1-A2
Method	BLASTX
NCBI GI	g2499607
BLAST score	1507
E value	1.0e-168
Match length	322
% identity	87
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi|629544|pir||S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi|457398|dbj|BAA04866| (D21839) MAP kinase [Arabidopsis thaliana]
Seq. No.	190840
Contig ID	864_1.R1039
5'-most EST	g5047184
Method	BLASTX
NCBI GI	g2529703
BLAST score	891

E value	4.0e-96
Match length	228
% identity	76
NCBI Description	(AF000142) class II knotted-like homeodomain protein [Lycopersicon esculentum]

Seq. No.	190841
Contig ID	870_1.R1039
5'-most EST	LIB3048-010-Q1-L1-G5
Method	BLASTX
NCBI GI	g3169028
BLAST score	397
E value	2.0e-38
Match length	227
% identity	42
NCBI Description	(AL023702) putative cationic amino acid transporter [Streptomyces coelicolor]

Seq. No.	190842
Contig ID	874_1.R1039
5'-most EST	LIB3048-036-Q1-L1-C4
Method	BLASTX
NCBI GI	g4406819
BLAST score	610
E value	5.0e-66
Match length	178
% identity	76
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	190843
Contig ID	875_1.R1039
5'-most EST	LIB3196-008-P1-M1-F10

Seq. No.	190844
Contig ID	876_1.R1039
5'-most EST	LIB3048-035-Q1-L1-A10
Method	BLASTX
NCBI GI	g3582328
BLAST score	319
E value	2.0e-29
Match length	125
% identity	50
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190845
Contig ID	878_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C8
Method	BLASTX
NCBI GI	g267146
BLAST score	554
E value	5.0e-57
Match length	151
% identity	66
NCBI Description	DNA TOPOISOMERASE I >gi|99762|pir||S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi|16558|emb|CAA40763| (X57544) topoisomerase I [Arabidopsis thaliana] >gi|445137|prf||1908437A

topoisomerase I [Arabidopsis thaliana]

Seq. No.	190846
Contig ID	879_1.R1039
5'-most EST	g5045747
Method	BLASTX
NCBI GI	g543867
BLAST score	1298
E value	1.0e-143
Match length	325
% identity	82
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi|1076684|pir||A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi|303626|dbj|BAA03526| (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	190847
Contig ID	879_2.R1039
5'-most EST	LIB3197-010-P1-M1-H7
Method	BLASTX
NCBI GI	g2702263
BLAST score	352
E value	4.0e-33
Match length	115
% identity	70
NCBI Description	(AC003033) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	190848
Contig ID	879_3.R1039
5'-most EST	g5049318
Method	BLASTX
NCBI GI	g543867
BLAST score	407
E value	2.0e-39
Match length	156
% identity	64
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi|1076684|pir||A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi|303626|dbj|BAA03526| (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	190849
Contig ID	881_1.R1039
5'-most EST	LIB3048-040-Q1-L1-D6
Method	BLASTX
NCBI GI	g1176658
BLAST score	172
E value	3.0e-12
Match length	65
% identity	52
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi|726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	190850
Contig ID	882_1.R1039
5'-most EST	LIB3048-022-Q1-L1-A7
Method	BLASTX
NCBI GI	g2623299
BLAST score	284
E value	2.0e-25
Match length	105
% identity	51
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190851
Contig ID	883_1.R1039
5'-most EST	LIB3197-049-Q1-M1-D8
Method	BLASTX
NCBI GI	g4337001
BLAST score	493
E value	2.0e-49
Match length	153
% identity	64
NCBI Description	(AF118129) Tsi1-interacting protein TSIP1 [Nicotiana tabacum]

Seq. No.	190852
Contig ID	888_1.R1039
5'-most EST	LIB3166-008-P1-K1-C10
Method	BLASTX
NCBI GI	g2149640
BLAST score	426
E value	2.0e-63
Match length	170
% identity	75
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	190853
Contig ID	889_1.R1039
5'-most EST	LIB3048-010-Q1-L1-G8
Method	BLASTX
NCBI GI	g465012
BLAST score	686
E value	3.0e-93
Match length	247
% identity	72
NCBI Description	URICASE II CLONE PCCLNUO-02 (URATE OXIDASE) >gi|1086285|pir||S38910 uricase - Canavalia lineata >gi|432631|emb|CAA53905| (X76287) uricase [Canavalia lineata]

Seq. No.	190854
Contig ID	893_1.R1039
5'-most EST	LIB3147-003-Q1-K1-D1
Method	BLASTX
NCBI GI	g4204297
BLAST score	1677
E value	0.0e+00
Match length	485
% identity	74

NCBI Description	(AC003027) ADK1 [Arabidopsis thaliana]
Seq. No.	190855
Contig ID	894_1.R1039
5'-most EST	LIB3048-022-Q1-L1-D3
Seq. No.	190856
Contig ID	895_1.R1039
5'-most EST	LIB3166-008-P1-K1-B11
Seq. No.	190857
Contig ID	895_2.R1039
5'-most EST	g3326562
Seq. No.	190858
Contig ID	895_3.R1039
5'-most EST	LIB3272-009-P1-K1-A4
Seq. No.	190859
Contig ID	896_1.R1039
5'-most EST	LIB3189-043-P1-K1-E8
Method	BLASTX
NCBI GI	g1170507
BLAST score	1822
E value	0.0e+00
Match length	390
% identity	90
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi|100276|pir||S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi|19699|emb|CAA43514| (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
Seq. No.	190860
Contig ID	896_2.R1039
5'-most EST	LIB3165-040-Q1-K1-B9
Method	BLASTX
NCBI GI	g1170507
BLAST score	172
E value	4.0e-12
Match length	45
% identity	80
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi|100276|pir||S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi|19699|emb|CAA43514| (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
Seq. No.	190861
Contig ID	899_1.R1039
5'-most EST	LIB3048-034-Q1-L1-A2
Method	BLASTX
NCBI GI	g4262142
BLAST score	332
E value	5.0e-31
Match length	105
% identity	58

NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	190862
Contig ID	906_1.R1039
5'-most EST	LIB3048-031-Q1-L1-F7
Method	BLASTX
NCBI GI	g4455340
BLAST score	442
E value	7.0e-44
Match length	116
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	190863
Contig ID	907_1.R1039
5'-most EST	LIB3048-031-Q1-L1-G8
Method	BLASTX
NCBI GI	g4539400
BLAST score	589
E value	4.0e-61
Match length	138
% identity	80
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	190864
Contig ID	912_1.R1039
5'-most EST	uC-gsflnu33B138b01b1
Method	BLASTX
NCBI GI	g4455364
BLAST score	778
E value	1.0e-82
Match length	309
% identity	52
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	190865
Contig ID	912_2.R1039
5'-most EST	LIB3146-027-Q1-K1-A5
Method	BLASTX
NCBI GI	g2662415
BLAST score	173
E value	4.0e-12
Match length	56
% identity	54
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No.	190866
Contig ID	912_3.R1039
5'-most EST	uC-gsflnu33B085f05b1
Method	BLASTN
NCBI GI	g169712
BLAST score	50
E value	6.0e-19
Match length	136
% identity	90

NCBI Description	Ricinus communis metallothionein (RCMIT) mRNA, complete cds
Seq. No.	190867
Contig ID	912_5.R1039
5'-most EST	LIB3197-002-P1-M1-C2
Method	BLASTX
NCBI GI	g3318611
BLAST score	1430
E value	1.0e-159
Match length	357
% identity	79
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]
Seq. No.	190868
Contig ID	912_10.R1039
5'-most EST	LIB3149-040-Q1-K1-G5
Method	BLASTX
NCBI GI	g3318611
BLAST score	261
E value	5.0e-23
Match length	57
% identity	97
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]
Seq. No.	190869
Contig ID	915_1.R1039
5'-most EST	uC-gsflmaxxa042d05b1
Method	BLASTX
NCBI GI	g3334138
BLAST score	452
E value	8.0e-45
Match length	111
% identity	74
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]
Seq. No.	190870
Contig ID	915_2.R1039
5'-most EST	uC-gsflmaxxa039b01b1
Method	BLASTX
NCBI GI	g3334138
BLAST score	688
E value	1.0e-72
Match length	143
% identity	86
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]
Seq. No.	190871
Contig ID	916_1.R1039
5'-most EST	LIB3272-031-P1-K1-B12
Method	BLASTX
NCBI GI	g542200
BLAST score	678
E value	3.0e-71

Match length	211
% identity	64
NCBI Description	hypothetical protein - garden asparagus >gi|452714|emb|CAA54526| (X77320) unknown [Asparagus officinalis]

Seq. No.	190872
Contig ID	916_3.R1039
5'-most EST	LIB3083-006-Q1-L1-C1
Method	BLASTX
NCBI GI	g2642215
BLAST score	317
E value	6.0e-29
Match length	75
% identity	80
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	190873
Contig ID	916_6.R1039
5'-most EST	LIB3272-022-P1-K1-C5
Method	BLASTX
NCBI GI	g643469
BLAST score	426
E value	9.0e-42
Match length	118
% identity	69
NCBI Description	(U19886) unknown [Lycopersicon esculentum]

Seq. No.	190874
Contig ID	920_1.R1039
5'-most EST	g5044756
Method	BLASTX
NCBI GI	g3204134
BLAST score	1489
E value	0.0e+00
Match length	546
% identity	76
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	190875
Contig ID	920_2.R1039
5'-most EST	g3326380
Method	BLASTX
NCBI GI	g3204134
BLAST score	238
E value	9.0e-20
Match length	51
% identity	82
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	190876
Contig ID	920_3.R1039
5'-most EST	uC-gsflnu33B059d09b1

Seq. No.	190877
Contig ID	927_1.R1039
5'-most EST	LIB3048-036-Q1-L1-G7

Method	BLASTX
NCBI GI	g2290683
BLAST score	510
E value	7.0e-52
Match length	111
% identity	83
NCBI Description	(AF000136) basic cellulase [Citrus sinensis]

Seq. No.	190878
Contig ID	929_1.R1039
5'-most EST	LIB3048-012-Q1-L1-E5
Method	BLASTX
NCBI GI	g4185136
BLAST score	493
E value	7.0e-50
Match length	131
% identity	67
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	190879
Contig ID	930_1.R1039
5'-most EST	uC-gsflnu33B061h04b1
Method	BLASTX
NCBI GI	g2956783
BLAST score	350
E value	7.0e-33
Match length	151
% identity	48
NCBI Description	(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]

Seq. No.	190880
Contig ID	932_1.R1039
5'-most EST	LIB3048-034-Q1-L1-H1
Method	BLASTX
NCBI GI	g1841464
BLAST score	881
E value	6.0e-95
Match length	189
% identity	84
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	190881
Contig ID	932_2.R1039
5'-most EST	LIB3145-048-Q1-K1-F9
Method	BLASTX
NCBI GI	g1841464
BLAST score	303
E value	2.0e-27
Match length	105
% identity	35
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	190882
Contig ID	934_1.R1039
5'-most EST	LIB3189-043-P1-K1-B8

Method	BLASTX
NCBI GI	g1709007
BLAST score	187
E value	8.0e-14
Match length	107
% identity	40
NCBI Description	O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE) >gi|607830 (U10904) O-succinylhomoserine sulfhydrylase [Pseudomonas aeruginosa]

Seq. No.	190883
Contig ID	937_1.R1039
5'-most EST	LIB3189-011-P1-K1-C4
Method	BLASTX
NCBI GI	g2827715
BLAST score	506
E value	3.0e-51
Match length	185
% identity	10
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	190884
Contig ID	941_1.R1039
5'-most EST	g5050323
Method	BLASTX
NCBI GI	g3393062
BLAST score	623
E value	9.0e-65
Match length	233
% identity	51
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	190885
Contig ID	941_3.R1039
5'-most EST	LIB3272-005-P1-K1-B8
Method	BLASTX
NCBI GI	g3393062
BLAST score	442
E value	6.0e-44
Match length	116
% identity	67
NCBI Description	(Y17386) putative In2.1 protein [Triticum aestivum]

Seq. No.	190886
Contig ID	948_1.R1039
5'-most EST	LIB3083-066-Q1-L1-E8
Method	BLASTX
NCBI GI	g1174621
BLAST score	956
E value	1.0e-103
Match length	392
% identity	47
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi|1083259|pir||JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi|695625|emb|CAA85521| (Z37164) CCTtheta, theta subunit

of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	190887
Contig ID	960_1.R1039
5'-most EST	LIB3166-028-P1-K1-B10
Method	BLASTX
NCBI GI	g2129921
BLAST score	194
E value	2.0e-14
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi|758694 (U12573) putative [Catharanthus roseus]

Seq. No.	190888
Contig ID	960_2.R1039
5'-most EST	g5047423
Method	BLASTX
NCBI GI	g2687584
BLAST score	723
E value	1.0e-129
Match length	348
% identity	68
NCBI Description	(AF033100) S-adenosylmethionine decarboxylase [Nicotiana tabacum]

Seq. No.	190889
Contig ID	960_4.R1039
5'-most EST	uC-gsflmaxxa070f10b1
Method	BLASTX
NCBI GI	g2129921
BLAST score	195
E value	8.0e-15
Match length	51
% identity	75
NCBI Description	hypothetical protein 1 - Madagascar periwinkle >gi|758694 (U12573) putative [Catharanthus roseus]

Seq. No.	190890
Contig ID	961_1.R1039
5'-most EST	uC-gsflnu33B111c10b1
Method	BLASTX
NCBI GI	g2398521
BLAST score	306
E value	1.0e-27
Match length	183
% identity	45
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	190891
Contig ID	961_2.R1039
5'-most EST	LIB3048-031-Q1-L1-C6
Method	BLASTX
NCBI GI	g2398521
BLAST score	344
E value	2.0e-32
Match length	134

% identity	55
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	190892
Contig ID	962_1.R1039
5'-most EST	LIB3048-019-Q1-L1-G3

Seq. No.	190893
Contig ID	965_1.R1039
5'-most EST	LIB3048-035-Q1-L1-C10

Seq. No.	190894
Contig ID	967_1.R1039
5'-most EST	LIB3048-031-Q1-L1-G5

Seq. No.	190895
Contig ID	968_1.R1039
5'-most EST	LIB3165-057-P1-K1-G7
Method	BLASTX
NCBI GI	g1001309
BLAST score	386
E value	7.0e-37
Match length	234
% identity	35
NCBI Description	(D64006) aspartate aminotransferase [Synechocystis sp.]

Seq. No.	190896
Contig ID	970_1.R1039
5'-most EST	LIB3272-015-P1-K1-B11
Method	BLASTX
NCBI GI	g1706918
BLAST score	492
E value	3.0e-49
Match length	199
% identity	48
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi|498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	190897
Contig ID	970_3.R1039
5'-most EST	uC-gsflnu33B078b07b1
Method	BLASTX
NCBI GI	g1706918
BLAST score	285
E value	3.0e-25
Match length	115
% identity	46
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi|498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	190898
Contig ID	972_1.R1039
5'-most EST	LIB3135-018-Q1-K1-E9
Method	BLASTX
NCBI GI	g3947733
BLAST score	431
E value	1.0e-42

Match length	147
% identity	59
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	190899
Contig ID	976_1.R1039
5'-most EST	uC-gsronu33B157b08b1
Method	BLASTX
NCBI GI	g2506139
BLAST score	777
E value	8.0e-83
Match length	184
% identity	83
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi|1314049|emb|CAA91901| (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	190900
Contig ID	976_2.R1039
5'-most EST	LIB3048-024-Q1-L1-H5
Method	BLASTX
NCBI GI	g2506139
BLAST score	321
E value	1.0e-29
Match length	82
% identity	78
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi|1314049|emb|CAA91901| (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	190901
Contig ID	978_1.R1039
5'-most EST	LIB3083-105-Q1-L1-H7
Method	BLASTX
NCBI GI	g1076627
BLAST score	1040
E value	1.0e-113
Match length	236
% identity	87
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi|790479|emb|CAA58701| (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	190902
Contig ID	978_2.R1039
5'-most EST	LIB3166-056-P1-K1-A11
Method	BLASTX
NCBI GI	g3608171
BLAST score	428
E value	3.0e-42
Match length	113
% identity	75
NCBI Description	(D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No.	190903
Contig ID	981_1.R1039

5'-most EST	g5045589
Method	BLASTX
NCBI GI	g3183247
BLAST score	770
E value	7.0e-82
Match length	289
% identity	53
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi|3880615|emb|CAB07131| (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB

Seq. No.	190904
Contig ID	981_2.R1039
5'-most EST	LIB3048-011-Q1-L1-H7
Method	BLASTX
NCBI GI	g3183247
BLAST score	207
E value	5.0e-16
Match length	61
% identity	61
NCBI Description	PUTATIVE GTP-BINDING PROTEIN W08E3.3 >gi|3880615|emb|CAB07131| (Z92773) predicted using Genefinder; Similarity to Yeast hypothetical 44.2 KD protein, putative GTP-binding protein (SW:P38219); cDNA EST EMBL:D64516 comes from this gene; cDNA EST EMBL:D65777 comes from this gene; cDNA EST EMB

Seq. No.	190905
Contig ID	984_1.R1039
5'-most EST	g3325558
Method	BLASTX
NCBI GI	g82131
BLAST score	402
E value	6.0e-39
Match length	129
% identity	67
NCBI Description	beta-glucanase (EC 3.2.1.-) precursor - curled-leaved tobacco (fragment) >gi|829281|emb|CAA30261| (X07280) beta-glucanase [Nicotiana plumbaginifolia]

Seq. No.	190906
Contig ID	984_2.R1039
5'-most EST	LIB3135-029-Q1-K1-C5
Method	BLASTX
NCBI GI	g1706547
BLAST score	693
E value	1.0e-108
Match length	326
% identity	66
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi|2129912|pir||S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi|1184668 (U22147)

beta-1,3-glucanase [Hevea brasiliensis]

Seq. No.	190907
Contig ID	986_1.R1039
5'-most EST	g5048347
Method	BLASTX
NCBI GI	g2244841
BLAST score	233
E value	4.0e-19
Match length	70
% identity	57
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190908
Contig ID	986_2.R1039
5'-most EST	g5050337
Method	BLASTX
NCBI GI	g2244841
BLAST score	159
E value	2.0e-10
Match length	60
% identity	45
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190909
Contig ID	987_1.R1039
5'-most EST	g5044903
Method	BLASTX
NCBI GI	g3928758
BLAST score	311
E value	3.0e-28
Match length	96
% identity	57
NCBI Description	(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi|4454462|gb|AAD20909| (AC006234) putative lipoic acid synthase [Arabidopsis thaliana]

Seq. No.	190910
Contig ID	994_1.R1039
5'-most EST	LIB3196-016-P1-M1-C8
Method	BLASTX
NCBI GI	g3738257
BLAST score	904
E value	1.0e-97
Match length	191
% identity	92
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	190911
Contig ID	994_2.R1039
5'-most EST	LIB3048-012-Q1-L1-B10
Method	BLASTX
NCBI GI	g3738257
BLAST score	1262
E value	1.0e-139
Match length	317

% identity	80
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	190912
Contig ID	994_3.R1039
5'-most EST	uC-gsronu33B171c10b1
Method	BLASTX
NCBI GI	g3738257
BLAST score	429
E value	3.0e-42
Match length	90
% identity	94
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	190913
Contig ID	994_7.R1039
5'-most EST	LIB3166-045-P1-K1-D2
Method	BLASTX
NCBI GI	g3759177
BLAST score	320
E value	2.0e-29
Match length	91
% identity	73
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi|3759179|dbj|BAA33807| (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	190914
Contig ID	1001_1.R1039
5'-most EST	LIB3197-001-P1-M1-E1
Method	BLASTX
NCBI GI	g2570164
BLAST score	475
E value	1.0e-47
Match length	137
% identity	62
NCBI Description	(D45183) chitinase [Chenopodium amaranticolor]

Seq. No.	190915
Contig ID	1004_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C3
Method	BLASTX
NCBI GI	g3328231
BLAST score	264
E value	8.0e-23
Match length	201
% identity	31
NCBI Description	(AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus laevis]

Seq. No.	190916
Contig ID	1005_1.R1039
5'-most EST	LIB3048-012-Q1-L1-C1

Seq. No. 190917

Contig ID	1012_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C6
Method	BLASTX
NCBI GI	g3420050
BLAST score	379
E value	4.0e-36
Match length	229
% identity	38
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190918
Contig ID	1013_1.R1039
5'-most EST	uC-gsflnu33B036h10b1
Method	BLASTX
NCBI GI	g2970051
BLAST score	1010
E value	1.0e-110
Match length	228
% identity	84
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	190919
Contig ID	1013_2.R1039
5'-most EST	LIB3048-025-Q1-L1-A4
Method	BLASTX
NCBI GI	g3123745
BLAST score	249
E value	3.0e-21
Match length	68
% identity	71
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	190920
Contig ID	1013_4.R1039
5'-most EST	LIB3083-102-Q1-L1-G2
Method	BLASTN
NCBI GI	g2970050
BLAST score	45
E value	4.0e-16
Match length	109
% identity	85
NCBI Description	Vigna radiata mRNA for ARG10, complete cds

Seq. No.	190921
Contig ID	1013_5.R1039
5'-most EST	LIB3148-034-Q1-K1-H11
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	5.0e-11
Match length	48
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	190922
Contig ID	1013_6.R1039
5'-most EST	LIB3146-018-Q1-K1-G1

Method	BLASTX
NCBI GI	g2970051
BLAST score	397
E value	3.0e-38
Match length	108
% identity	72
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	190923
Contig ID	1014_1.R1039
5'-most EST	LIB3048-012-Q1-L1-C8

Seq. No.	190924
Contig ID	1015_1.R1039
5'-most EST	LIB3189-046-P1-K1-B2
Method	BLASTX
NCBI GI	g3941289
BLAST score	609
E value	3.0e-63
Match length	198
% identity	57
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	190925
Contig ID	1017_1.R1039
5'-most EST	LIB3272-002-P1-K1-H10
Method	BLASTX
NCBI GI	g3668089
BLAST score	188
E value	4.0e-14
Match length	91
% identity	42
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	190926
Contig ID	1018_1.R1039
5'-most EST	LIB3166-022-P1-K1-E6
Method	BLASTX
NCBI GI	g3608412
BLAST score	775
E value	1.0e-82
Match length	251
% identity	59
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	190927
Contig ID	1019_1.R1039
5'-most EST	LIB3135-050-Q1-K1-B7
Method	BLASTX
NCBI GI	g1076501
BLAST score	315
E value	1.0e-28
Match length	88
% identity	67
NCBI Description	cell wall protein - alfalfa >gi|3818416 (AF028841) proline-rich cell wall protein [Medicago sativa]

Seq. No.	190928
Contig ID	1021_1.R1039
5'-most EST	LIB3189-031-P1-K1-D7
Method	BLASTX
NCBI GI	g3790102
BLAST score	485
E value	7.0e-49
Match length	102
% identity	85
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	190929
Contig ID	1022_1.R1039
5'-most EST	uC-gsflnu33B070d01b1
Method	BLASTX
NCBI GI	g2500378
BLAST score	369
E value	4.0e-35
Match length	82
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	190930
Contig ID	1022_2.R1039
5'-most EST	LIB3048-012-Q1-L1-D5
Method	BLASTX
NCBI GI	g2500378
BLAST score	437
E value	3.0e-43
Match length	94
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	190931
Contig ID	1022_3.R1039
5'-most EST	LIB3146-023-Q1-K1-G12
Method	BLASTX
NCBI GI	g2500378
BLAST score	338
E value	2.0e-31
Match length	91
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	190932
Contig ID	1023_1.R1039
5'-most EST	LIB3048-019-Q1-L1-E6
Method	BLASTX
NCBI GI	g3894159
BLAST score	172
E value	3.0e-12
Match length	80
% identity	41
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190933
Contig ID	1025_1.R1039
5'-most EST	LIB3189-023-P1-K1-C1
Method	BLASTX
NCBI GI	g4455288
BLAST score	350
E value	4.0e-33
Match length	86
% identity	78
NCBI Description	(AL035527) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	190934
Contig ID	1027_1.R1039
5'-most EST	LIB3048-054-Q1-L1-C10
Method	BLASTX
NCBI GI	g464365
BLAST score	195
E value	3.0e-30
Match length	105
% identity	69
NCBI Description	PEROXIDASE P7 >gi|66306|pir||OPNB7 peroxidase (EC 1.11.1.7) - turnip

Seq. No.	190935
Contig ID	1027_2.R1039
5'-most EST	g3326040
Method	BLASTN
NCBI GI	g1781331
BLAST score	36
E value	1.0e-10
Match length	63
% identity	97
NCBI Description	S.oleracea mRNA for peroxidase, clone PC23

Seq. No.	190936
Contig ID	1029_1.R1039
5'-most EST	LIB3048-018-Q1-L1-C10

Seq. No.	190937
Contig ID	1029_2.R1039
5'-most EST	LIB3146-022-Q1-K1-C3
Method	BLASTX
NCBI GI	g4508073
BLAST score	1097
E value	1.0e-120
Match length	322
% identity	64
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	190938
Contig ID	1032_1.R1039
5'-most EST	LIB3048-012-Q1-L1-E4

Seq. No.	190939
Contig ID	1035_1.R1039
5'-most EST	LIB3048-012-Q1-L1-E7

Method	BLASTN
NCBI GI	g2281081
BLAST score	144
E value	7.0e-75
Match length	683
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	190940
Contig ID	1038_1.R1039
5'-most EST	LIB3048-012-Q1-L1-F1
Method	BLASTX
NCBI GI	g3540180
BLAST score	352
E value	2.0e-33
Match length	143
% identity	57
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	190941
Contig ID	1039_1.R1039
5'-most EST	LIB3048-019-Q1-L1-H4

Seq. No.	190942
Contig ID	1043_1.R1039
5'-most EST	LIB3272-002-P1-K1-E11
Method	BLASTN
NCBI GI	g3241927
BLAST score	44
E value	3.0e-15
Match length	251
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	190943
Contig ID	1045_1.R1039
5'-most EST	LIB3189-003-P1-K1-F5
Method	BLASTX
NCBI GI	g1346422
BLAST score	238
E value	3.0e-22
Match length	145
% identity	41
NCBI Description	SERINE PALMITOYLTRANSFERASE 2 (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2) >gi|2130481|pir||JC5183 serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) >gi|1001947 (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] >gi|2414613|emb|CAB16362| (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No.	190944
Contig ID	1046_1.R1039
5'-most EST	g3326497
Method	BLASTX

NCBI GI	g3914940
BLAST score	808
E value	2.0e-86
Match length	213
% identity	75
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi|2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	190945
Contig ID	1050_1.R1039
5'-most EST	LIB3048-012-Q1-L1-G10
Method	BLASTX
NCBI GI	g4580531
BLAST score	248
E value	3.0e-21
Match length	125
% identity	47
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	190946
Contig ID	1053_1.R1039
5'-most EST	LIB3272-009-P1-K1-E5
Method	BLASTX
NCBI GI	g1657621
BLAST score	1460
E value	1.0e-162
Match length	362
% identity	78
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi|3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	190947
Contig ID	1053_2.R1039
5'-most EST	LIB3083-080-Q1-L1-C2
Method	BLASTX
NCBI GI	g1657621
BLAST score	538
E value	4.0e-55
Match length	127
% identity	79
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi|3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	190948
Contig ID	1056_1.R1039
5'-most EST	uC-gsflnu33B083a03b1
Method	BLASTX
NCBI GI	g3608485
BLAST score	1085
E value	1.0e-119
Match length	223
% identity	92
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No.	190949

Contig ID	1057_1.R1039
5'-most EST	LIB3166-001-Q1-K1-H12
Method	BLASTX
NCBI GI	g2088648
BLAST score	165
E value	3.0e-11
Match length	110
% identity	40
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190950
Contig ID	1059_1.R1039
5'-most EST	LIB3048-012-Q1-L1-G8
Method	BLASTX
NCBI GI	g4115371
BLAST score	356
E value	6.0e-34
Match length	110
% identity	65
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	190951
Contig ID	1060_1.R1039
5'-most EST	LIB3189-008-P1-K1-D1
Method	BLASTX
NCBI GI	g2911044
BLAST score	508
E value	2.0e-51
Match length	132
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	190952
Contig ID	1066_1.R1039
5'-most EST	LIB3048-012-Q1-L1-H4
Method	BLASTX
NCBI GI	g3450842
BLAST score	494
E value	6.0e-50
Match length	131
% identity	72
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	190953
Contig ID	1068_1.R1039
5'-most EST	LIB3272-034-P1-K1-C1
Method	BLASTX
NCBI GI	g3242723
BLAST score	447
E value	4.0e-44
Match length	211
% identity	44
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	190954

Contig ID	1070_1.R1039
5'-most EST	LIB3048-022-Q1-L1-H11
Method	BLASTX
NCBI GI	g3461820
BLAST score	214
E value	4.0e-17
Match length	52
% identity	69
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	190955
Contig ID	1072_1.R1039
5'-most EST	LIB3048-012-Q1-L1-H9

Seq. No.	190956
Contig ID	1073_1.R1039
5'-most EST	LIB3135-002-Q1-K1-B4
Method	BLASTX
NCBI GI	g1617272
BLAST score	624
E value	1.0e-105
Match length	276
% identity	68
NCBI Description	(Z72151) AMP-binding protein [Brassica napus]

Seq. No.	190957
Contig ID	1075_1.R1039
5'-most EST	LIB3048-039-Q1-L1-B8
Method	BLASTX
NCBI GI	g1084349
BLAST score	481
E value	2.0e-48
Match length	129
% identity	77
NCBI Description	aldehyde dehydrogenase homolog btg-26 - rape >gi|913941|bbs|164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494 aa] [Brassica napus]

Seq. No.	190958
Contig ID	1077_1.R1039
5'-most EST	LIB3048-026-Q1-L1-D7

Seq. No.	190959
Contig ID	1078_1.R1039
5'-most EST	uC-gsflnu33B050b11b1
Method	BLASTX
NCBI GI	g1616614
BLAST score	871
E value	7.0e-94
Match length	183
% identity	92
NCBI Description	(Y08425) small GTP-binding protein [Nicotiana plumbaginifolia]

Seq. No.	190960
Contig ID	1081_1.R1039

5'-most EST	LIB3048-030-Q1-L1-H4
Seq. No.	190961
Contig ID	1082_1.R1039
5'-most EST	LIB3048-013-Q1-L1-A7
Method	BLASTX
NCBI GI	g3176687
BLAST score	469
E value	8.0e-47
Match length	129
% identity	67
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb|Z97344. ESTs gb|H37594, gb|R65023, gb|H37578 and gb|R64855 come from this gene. [Arabidopsis thaliana]
Seq. No.	190962
Contig ID	1082_2.R1039
5'-most EST	LIB3146-059-Q1-K1-A9
Method	BLASTX
NCBI GI	g2245136
BLAST score	727
E value	6.0e-77
Match length	190
% identity	71
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
Seq. No.	190963
Contig ID	1085_1.R1039
5'-most EST	LIB3189-044-P1-K1-C7
Method	BLASTX
NCBI GI	g4580460
BLAST score	668
E value	3.0e-77
Match length	202
% identity	75
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]
Seq. No.	190964
Contig ID	1085_2.R1039
5'-most EST	LIB3166-024-P1-K1-G11
Method	BLASTX
NCBI GI	g4580460
BLAST score	471
E value	3.0e-47
Match length	101
% identity	92
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]
Seq. No.	190965
Contig ID	1088_1.R1039
5'-most EST	LIB3165-025-P1-K1-A9
Method	BLASTX
NCBI GI	g3063392

BLAST score	481
E value	2.0e-48
Match length	127
% identity	76
NCBI Description	(AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No.	190966
Contig ID	1090_1.R1039
5'-most EST	LIB3048-013-Q1-L1-B3

Seq. No.	190967
Contig ID	1091_1.R1039
5'-most EST	LIB3147-006-Q1-K1-B6

Seq. No.	190968
Contig ID	1092_1.R1039
5'-most EST	LIB3048-037-Q1-L1-C8
Method	BLASTX
NCBI GI	g4239845
BLAST score	488
E value	6.0e-49
Match length	147
% identity	67
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	190969
Contig ID	1092_2.R1039
5'-most EST	LIB3145-031-Q1-K1-B8
Method	BLASTX
NCBI GI	g2224933
BLAST score	300
E value	6.0e-27
Match length	99
% identity	64
NCBI Description	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] >gi|2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]

Seq. No.	190970
Contig ID	1098_1.R1039
5'-most EST	LIB3048-029-Q1-L1-G6
Method	BLASTX
NCBI GI	g2739376
BLAST score	341
E value	7.0e-35
Match length	100
% identity	78
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	190971
Contig ID	1099_1.R1039
5'-most EST	g3325601

Seq. No.	190972
Contig ID	1101_1.R1039
5'-most EST	LIB3048-029-Q1-L1-A10
Method	BLASTX

NCBI GI	g2129550
BLAST score	570
E value	5.0e-59
Match length	126
% identity	85
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi|2129554|pir||S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi|836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi|836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi|4454034|emb|CAA23031.1| (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	190973
Contig ID	1104_1.R1039
5'-most EST	uC-gsflmaxxa026b03b1
Method	BLASTX
NCBI GI	g4262226
BLAST score	225
E value	8.0e-18
Match length	111
% identity	49
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	190974
Contig ID	1104_2.R1039
5'-most EST	uC-gsronu33B108e02b1
Method	BLASTX
NCBI GI	g1172995
BLAST score	245
E value	1.0e-20
Match length	95
% identity	56
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi|1083790|pir||S52084 ribosomal protein L22 - rat >gi|710295|emb|CAA55204| (X78444) ribosomal protein L22 [Rattus norvegicus] >gi|1093952|prf||2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	190975
Contig ID	1104_3.R1039
5'-most EST	LIB3149-042-Q1-K1-C4
Method	BLASTX
NCBI GI	g1172995
BLAST score	252
E value	2.0e-21
Match length	98
% identity	55
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi|1083790|pir||S52084 ribosomal protein L22 - rat >gi|710295|emb|CAA55204| (X78444) ribosomal protein L22 [Rattus norvegicus] >gi|1093952|prf||2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	190976
Contig ID	1104_4.R1039

5'-most EST	LIB3148-054-Q1-K1-E7
Method	BLASTX
NCBI GI	g1172995
BLAST score	268
E value	3.0e-23
Match length	107
% identity	52
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi|1083790|pir||S52084 ribosomal protein L22 - rat >gi|710295|emb|CAA55204| (X78444) ribosomal protein L22 [Rattus norvegicus] >gi|1093952|prf||2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	190977
Contig ID	1104_5.R1039
5'-most EST	LIB3166-036-P1-K1-B12

Seq. No.	190978
Contig ID	1107_1.R1039
5'-most EST	LIB3048-020-Q1-L1-B11

Seq. No.	190979
Contig ID	1108_1.R1039
5'-most EST	LIB3196-049-P1-M1-F5
Method	BLASTX
NCBI GI	g3212859
BLAST score	671
E value	2.0e-70
Match length	202
% identity	43
NCBI Description	(AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No.	190980
Contig ID	1111_1.R1039
5'-most EST	LIB3048-022-Q1-L1-B2

Seq. No.	190981
Contig ID	1112_1.R1039
5'-most EST	LIB3048-013-Q1-L1-D12
Method	BLASTX
NCBI GI	g3688181
BLAST score	172
E value	6.0e-12
Match length	69
% identity	57
NCBI Description	(AL031804) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	190982
Contig ID	1123_1.R1039
5'-most EST	LIB3048-013-Q1-L1-E12
Method	BLASTX
NCBI GI	g2281115
BLAST score	575
E value	2.0e-59
Match length	135
% identity	83

NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	190983
Contig ID	1124_1.R1039
5'-most EST	LIB3048-052-Q1-L1-F9
Method	BLASTX
NCBI GI	g3510603
BLAST score	182
E value	2.0e-13
Match length	87
% identity	40
NCBI Description	(AF044209) nuclear receptor co-repressor N-CoR [Homo sapiens]

Seq. No.	190984
Contig ID	1129_1.R1039
5'-most EST	LIB3135-022-Q1-K1-D2
Method	BLASTX
NCBI GI	g479386
BLAST score	1365
E value	1.0e-151
Match length	285
% identity	91
NCBI Description	isocitrate dehydrogenase - soybean

Seq. No.	190985
Contig ID	1129_2.R1039
5'-most EST	LIB3146-014-Q1-K1-G4
Method	BLASTX
NCBI GI	g169989
BLAST score	854
E value	6.0e-92
Match length	175
% identity	92
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine max]

Seq. No.	190986
Contig ID	1130_1.R1039
5'-most EST	g3325946
Method	BLASTX
NCBI GI	g1808656
BLAST score	2092
E value	0.0e+00
Match length	463
% identity	83
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	190987
Contig ID	1134_2.R1039
5'-most EST	LIB3148-034-Q1-K1-B11
Method	BLASTX
NCBI GI	g217909
BLAST score	411
E value	3.0e-40
Match length	89

% identity	91
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]

Seq. No.	190988
Contig ID	1137_1.R1039
5'-most EST	LIB3048-023-Q1-L1-F8

Seq. No.	190989
Contig ID	1139_1.R1039
5'-most EST	LIB3048-047-Q1-L1-B11
Method	BLASTX
NCBI GI	g2435395
BLAST score	882
E value	1.0e-180
Match length	394
% identity	80
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	190990
Contig ID	1139_2.R1039
5'-most EST	LIB3048-038-Q1-L1-D1
Method	BLASTX
NCBI GI	g2435395
BLAST score	656
E value	1.0e-83
Match length	187
% identity	83
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	190991
Contig ID	1140_1.R1039
5'-most EST	LIB3272-051-P1-K1-G10
Method	BLASTX
NCBI GI	g2499945
BLAST score	709
E value	1.0e-74
Match length	237
% identity	60
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi|1076363|pir||S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi|443818|emb|CAA50686| (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No.	190992
Contig ID	1140_2.R1039
5'-most EST	LIB3272-014-P1-K1-D8
Method	BLASTX
NCBI GI	g2499946
BLAST score	1238
E value	1.0e-136
Match length	327
% identity	74
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi|747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No.	190993
Contig ID	1142_1.R1039
5'-most EST	uC-gsronu33B055g01b1
Method	BLASTX
NCBI GI	g121953
BLAST score	167
E value	5.0e-11
Match length	38
% identity	87
NCBI Description	HISTONE H1 >gi|81905|pir||S00033 histone H1.b - garden pea >gi|20762|emb|CAA29123| (X05636) H1 histone (AA 1-263) [Pisum sativum]

Seq. No.	190994
Contig ID	1143_1.R1039
5'-most EST	LIB3048-013-Q1-L1-G1

Seq. No.	190995
Contig ID	1148_1.R1039
5'-most EST	LIB3048-013-Q1-L1-G3
Method	BLASTX
NCBI GI	g4539399
BLAST score	362
E value	2.0e-34
Match length	75
% identity	95
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	190996
Contig ID	1151_1.R1039
5'-most EST	LIB3165-001-Q1-K1-C3
Method	BLASTX
NCBI GI	g4027897
BLAST score	716
E value	7.0e-76
Match length	153
% identity	84
NCBI Description	(AF049353) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	190997
Contig ID	1152_1.R1039
5'-most EST	LIB3165-036-P1-K1-D9
Method	BLASTX
NCBI GI	g4455180
BLAST score	278
E value	9.0e-25
Match length	106
% identity	57
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	190998
Contig ID	1153_1.R1039
5'-most EST	LIB3048-013-Q1-L1-G8

Seq. No.	190999
Contig ID	1161_1.R1039
5'-most EST	LIB3083-050-Q1-L1-D1
Method	BLASTX
NCBI GI	g2827555
BLAST score	528
E value	7.0e-54
Match length	174
% identity	64
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	191000
Contig ID	1163_1.R1039
5'-most EST	LIB3048-013-Q1-L1-H7
Method	BLASTN
NCBI GI	g3785968
BLAST score	34
E value	1.0e-09
Match length	82
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191001
Contig ID	1164_1.R1039
5'-most EST	LIB3048-013-Q1-L1-H8
Method	BLASTX
NCBI GI	g4455155
BLAST score	341
E value	4.0e-32
Match length	69
% identity	90
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	191002
Contig ID	1169_1.R1039
5'-most EST	g3325686

Seq. No.	191003
Contig ID	1170_1.R1039
5'-most EST	g5048129
Method	BLASTX
NCBI GI	g2708750
BLAST score	1084
E value	1.0e-118
Match length	420
% identity	53
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	191004
Contig ID	1173_1.R1039
5'-most EST	uC-gsflnu33B132a03b1
Method	BLASTX

NCBI GI	g2660664
BLAST score	830
E value	5.0e-89
Match length	229
% identity	72
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	191005
Contig ID	1174_1.R1039
5'-most EST	LIB3048-048-Q1-L1-A4
Method	BLASTX
NCBI GI	g3287834
BLAST score	305
E value	4.0e-28
Match length	77
% identity	78
NCBI Description	(+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE SYNTHASE) >gi|2147016|pir||S68366 (+)-delta-cadinene synthase isozyme XC14 - Gossypium arboreum >gi|1045314 (U23205) (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]

Seq. No.	191006
Contig ID	1178_1.R1039
5'-most EST	LIB3048-027-Q1-L1-G1
Method	BLASTX
NCBI GI	g3492803
BLAST score	332
E value	5.0e-31
Match length	139
% identity	51
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	191007
Contig ID	1179_2.R1039
5'-most EST	LIB3048-025-Q1-L1-G11
Method	BLASTX
NCBI GI	g2245060
BLAST score	486
E value	6.0e-54
Match length	191
% identity	59
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	191008
Contig ID	1187_1.R1039
5'-most EST	LIB3120-019-Q1-K1-E1
Method	BLASTX
NCBI GI	g3080400
BLAST score	751
E value	8.0e-80
Match length	175
% identity	82
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi|4455264|emb|CAB36800.1| (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	191009
Contig ID	1192_1.R1039
5'-most EST	LIB3048-014-Q1-L1-D2

Seq. No.	191010
Contig ID	1194_1.R1039
5'-most EST	LIB3048-021-Q1-L1-D11

Seq. No.	191011
Contig ID	1197_1.R1039
5'-most EST	LIB3189-016-P1-K1-D4
Method	BLASTX
NCBI GI	g133409
BLAST score	733
E value	7.0e-78
Match length	161
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN >gi|66962|pir||RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast >gi|11860|emb|CAA77376| (Z00044) RNA polymerase alpha subunit [Nicotiana tabacum] >gi|225228|prf||1211235BK RNA polymerase alpha [Nicotiana tabacum]

Seq. No.	191012
Contig ID	1198_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A6

Seq. No.	191013
Contig ID	1203_1.R1039
5'-most EST	LIB3048-031-Q1-L1-A8
Method	BLASTX
NCBI GI	g2832675
BLAST score	259
E value	5.0e-22
Match length	111
% identity	49
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191014
Contig ID	1205_1.R1039
5'-most EST	LIB3048-047-Q1-L1-B4
Method	BLASTX
NCBI GI	g3080435
BLAST score	181
E value	2.0e-16
Match length	62
% identity	68
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	191015
Contig ID	1206_1.R1039
5'-most EST	LIB3048-040-Q1-L1-B5

Seq. No.	191016
Contig ID	1212_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A5

Seq. No.	191017
Contig ID	1215_1.R1039
5'-most EST	LIB3166-043-P1-K1-G6
Method	BLASTX
NCBI GI	g1220196
BLAST score	1608
E value	1.0e-180
Match length	382
% identity	79
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.	191018
Contig ID	1215_3.R1039
5'-most EST	LIB3145-030-Q1-K1-H9
Method	BLASTX
NCBI GI	g1840425
BLAST score	166
E value	3.0e-11
Match length	44
% identity	68
NCBI Description	(U36586) alcohol dehydrogenase [Vitis vinifera]

Seq. No.	191019
Contig ID	1215_6.R1039
5'-most EST	LIB3166-009-P1-K1-D6
Method	BLASTX
NCBI GI	g1944216
BLAST score	296
E value	3.0e-27
Match length	97
% identity	70
NCBI Description	(D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	191020
Contig ID	1217_1.R1039
5'-most EST	LIB3048-018-Q1-L1-H2

Seq. No.	191021
Contig ID	1219_1.R1039
5'-most EST	LIB3083-095-Q1-L1-D8

Seq. No.	191022
Contig ID	1220_1.R1039
5'-most EST	LIB3148-016-Q1-K1-H12
Method	BLASTN
NCBI GI	g2924768
BLAST score	37
E value	2.0e-11
Match length	69
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191023
Contig ID	1226_1.R1039
5'-most EST	LIB3048-046-Q1-L1-D9

Method	BLASTX
NCBI GI	g1256509
BLAST score	388
E value	1.0e-37
Match length	86
% identity	79
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	191024
Contig ID	1230_1.R1039
5'-most EST	LIB3048-019-Q1-L1-G7
Method	BLASTX
NCBI GI	g2342724
BLAST score	334
E value	3.0e-31
Match length	146
% identity	60
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	191025
Contig ID	1231_1.R1039
5'-most EST	uC-gsflnu33B003g09b1
Method	BLASTX
NCBI GI	g3925703
BLAST score	1146
E value	1.0e-126
Match length	253
% identity	89
NCBI Description	(X95905) 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	191026
Contig ID	1235_1.R1039
5'-most EST	LIB3048-033-Q1-L1-A12

Seq. No.	191027
Contig ID	1237_1.R1039
5'-most EST	g5048146
Method	BLASTX
NCBI GI	g2959324
BLAST score	1057
E value	1.0e-115
Match length	236
% identity	36
NCBI Description	(Y15224) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	191028
Contig ID	1242_1.R1039
5'-most EST	LIB3166-036-P1-K1-D9
Method	BLASTX
NCBI GI	g4336426
BLAST score	431
E value	2.0e-42
Match length	124
% identity	66
NCBI Description	(AF090835) Ca2+-dependent protein kinase [Mesembryanthemum crystallinum]

Seq. No.	191029
Contig ID	1245_1.R1039
5'-most EST	LIB3272-002-P1-K1-C12
Method	BLASTX
NCBI GI	g2351380
BLAST score	593
E value	4.0e-61
Match length	317
% identity	40
NCBI Description	(U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi|4503515|ref|NP_003747.1|pEIF3S3| UNKNOWN

Seq. No.	191030
Contig ID	1247_1.R1039
5'-most EST	LIB3197-049-Q1-M1-H4
Method	BLASTX
NCBI GI	g2130051
BLAST score	853
E value	8.0e-92
Match length	203
% identity	75
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi|1296807|emb|CAA64544| (X95256) xylose isomerase [Hordeum vulgare] >gi|1588664|prf||2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	191031
Contig ID	1250_1.R1039
5'-most EST	LIB3048-051-Q1-L1-C12
Method	BLASTX
NCBI GI	g1652467
BLAST score	217
E value	3.0e-17
Match length	65
% identity	63
NCBI Description	(D90905) hypothetical protein [Synechocystis sp.]

Seq. No.	191032
Contig ID	1252_1.R1039
5'-most EST	LIB3048-022-Q1-L1-G8

Seq. No.	191033
Contig ID	1254_1.R1039
5'-most EST	LIB3048-020-Q1-L1-D11
Method	BLASTX
NCBI GI	g119640
BLAST score	353
E value	2.0e-33
Match length	125
% identity	54
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN E8) >gi|82109|pir||S01642 ripening protein E8 - tomato >gi|19199|emb|CAA31789| (X13437) E8 protein [Lycopersicon esculentum]

Seq. No.	191034
Contig ID	1256_1.R1039

5'-most EST	LIB3048-015-Q1-L1-C2
Method	BLASTX
NCBI GI	g3077640
BLAST score	352
E value	2.0e-33
Match length	131
% identity	53
NCBI Description	(AJ223151) O-methyltransferase [Prunus dulcis]

Seq. No.	191035
Contig ID	1259_1.R1039
5'-most EST	LIB3048-015-Q1-L1-C5

Seq. No.	191036
Contig ID	1263_1.R1039
5'-most EST	LIB3048-026-Q1-L1-E7

Seq. No.	191037
Contig ID	1265_1.R1039
5'-most EST	LIB3166-016-P1-K1-F3

Seq. No.	191038
Contig ID	1268_1.R1039
5'-most EST	uC-gsronu33B147c01b1
Method	BLASTX
NCBI GI	g3075392
BLAST score	809
E value	1.0e-86
Match length	202
% identity	73
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	191039
Contig ID	1271_1.R1039
5'-most EST	LIB3048-035-Q1-L1-D9
Method	BLASTX
NCBI GI	g2275204
BLAST score	329
E value	1.0e-30
Match length	82
% identity	73
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	191040
Contig ID	1276_1.R1039
5'-most EST	LIB3166-039-P1-K1-D9
Method	BLASTX
NCBI GI	g2983447
BLAST score	351
E value	5.0e-33
Match length	198
% identity	40
NCBI Description	(AE000714) large subunit of isopropylmalate isomerase [Aquifex aeolicus]

Seq. No.	191041
Contig ID	1277_1.R1039
5'-most EST	LIB3166-009-P1-K1-D2
Method	BLASTX
NCBI GI	g2632254
BLAST score	455
E value	4.0e-45
Match length	121
% identity	72
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	191042
Contig ID	1278_1.R1039
5'-most EST	LIB3166-040-P1-K1-H6
Method	BLASTX
NCBI GI	g1200205
BLAST score	730
E value	3.0e-77
Match length	148
% identity	90
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	191043
Contig ID	1278_2.R1039
5'-most EST	uC-gsronu33B036f10b1
Method	BLASTX
NCBI GI	g1200205
BLAST score	221
E value	5.0e-18
Match length	67
% identity	67
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	191044
Contig ID	1282_1.R1039
5'-most EST	LIB3048-015-Q1-L1-G8

Seq. No.	191045
Contig ID	1283_1.R1039
5'-most EST	LIB3048-015-Q1-L1-E5

Seq. No.	191046
Contig ID	1284_1.R1039
5'-most EST	LIB3048-015-Q1-L1-E6
Method	BLASTX
NCBI GI	g2829918
BLAST score	701
E value	4.0e-74
Match length	180
% identity	77
NCBI Description	(AC002291) similar to "tub" protein gp|U82468|2072162 [Arabidopsis thaliana]

Seq. No.	191047
Contig ID	1285_1.R1039
5'-most EST	LIB3196-020-P1-M1-E12

Seq. No.	191048
Contig ID	1287_1.R1039
5'-most EST	LIB3166-034-P1-K1-B4
Method	BLASTX
NCBI GI	g1076515
BLAST score	464
E value	2.0e-46
Match length	175
% identity	56
NCBI Description	pectinesterase precursor - kidney bean >gi|732913|emb|CAA59482| (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No.	191049
Contig ID	1289_1.R1039
5'-most EST	uC-gsronu33B011h04b1
Method	BLASTX
NCBI GI	g4539296
BLAST score	581
E value	1.0e-59
Match length	164
% identity	61
NCBI Description	(AL049480) putative pathogenesis-related protein [Arabidopsis thaliana]

Seq. No.	191050
Contig ID	1291_1.R1039
5'-most EST	LIB3135-046-Q1-K1-F4
Method	BLASTX
NCBI GI	g1871182
BLAST score	202
E value	7.0e-33
Match length	121
% identity	64
NCBI Description	(U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No.	191051
Contig ID	1297_1.R1039
5'-most EST	uC-gsronu33B090g05b1
Method	BLASTX
NCBI GI	g3559805
BLAST score	870
E value	1.0e-93
Match length	206
% identity	75
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	191052
Contig ID	1297_2.R1039
5'-most EST	uC-gsronu33B109a06b1
Method	BLASTX
NCBI GI	g3559805
BLAST score	718
E value	4.0e-76
Match length	169
% identity	76

NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	191053
Contig ID	1299_1.R1039
5'-most EST	g3326024

Seq. No.	191054
Contig ID	1301_1.R1039
5'-most EST	LIB3048-015-Q1-L1-G10

Seq. No.	191055
Contig ID	1303_1.R1039
5'-most EST	LIB3083-108-Q1-L1-D5
Method	BLASTX
NCBI GI	g4406759
BLAST score	176
E value	2.0e-12
Match length	137
% identity	44
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191056
Contig ID	1303_2.R1039
5'-most EST	LIB3165-055-P1-K1-C1
Method	BLASTX
NCBI GI	g4406759
BLAST score	257
E value	5.0e-22
Match length	117
% identity	44
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191057
Contig ID	1308_1.R1039
5'-most EST	LIB3148-011-Q1-K1-F3
Method	BLASTX
NCBI GI	g169211
BLAST score	375
E value	5.0e-36
Match length	86
% identity	88
NCBI Description	(M90294) ethylene-forming enzyme [Petunia hybrida] >gi|445591|prf||1909343A ethylene-forming enzyme [Petunia x hybrida]

Seq. No.	191058
Contig ID	1315_1.R1039
5'-most EST	LIB3048-015-Q1-L1-H3
Method	BLASTX
NCBI GI	g4220528
BLAST score	687
E value	1.0e-112
Match length	232
% identity	82
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	191059
Contig ID	1317_1.R1039
5'-most EST	LIB3048-015-Q1-L1-H5
Method	BLASTX
NCBI GI	g4558659
BLAST score	207
E value	7.0e-18
Match length	102
% identity	49
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	191060
Contig ID	1319_1.R1039
5'-most EST	LIB3145-023-Q1-K1-G11
Method	BLASTX
NCBI GI	g1169200
BLAST score	218
E value	1.0e-17
Match length	119
% identity	42
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR >gi|421829|pir||S33706 DNA-damage resistance protein - Arabidopsis thaliana >gi|166694 (M98455) [Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	191061
Contig ID	1324_1.R1039
5'-most EST	uC-gsflmaxxa002f04b1

Seq. No.	191062
Contig ID	1324_2.R1039
5'-most EST	LIB3048-053-Q1-L1-A8

Seq. No.	191063
Contig ID	1326_1.R1039
5'-most EST	LIB3048-016-Q1-L1-A5
Method	BLASTX
NCBI GI	g1150932
BLAST score	561
E value	8.0e-58
Match length	146
% identity	73
NCBI Description	(X88864) cyclin [Medicago sativa]

Seq. No.	191064
Contig ID	1326_2.R1039
5'-most EST	LIB3166-011-P1-K1-A9

Seq. No.	191065
Contig ID	1328_1.R1039
5'-most EST	uC-gsflnu33B079h02b1
Method	BLASTX
NCBI GI	g1350720
BLAST score	419

E value 5.0e-41
Match length 88
% identity 88
NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 191066
Contig ID 1328_2.R1039
5'-most EST LIB3166-013-P1-K1-E1
Method BLASTN
NCBI GI g1777727
BLAST score 138
E value 2.0e-71
Match length 190
% identity 93
NCBI Description Gossypium hirsutum 18S ribosomal RNA gene, partial sequence

Seq. No. 191067
Contig ID 1330_1.R1039
5'-most EST LIB3048-016-Q1-L1-A9

Seq. No. 191068
Contig ID 1331_1.R1039
5'-most EST LIB3166-013-P1-K1-B2
Method BLASTN
NCBI GI g3451055
BLAST score 43
E value 1.0e-14
Match length 165
% identity 87
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No. 191069
Contig ID 1333_1.R1039
5'-most EST LIB3166-013-P1-K1-G11

Seq. No. 191070
Contig ID 1335_1.R1039
5'-most EST LIB3048-051-Q1-L1-C7
Method BLASTX
NCBI GI g2244792
BLAST score 665
E value 1.0e-69
Match length 140
% identity 83
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 191071
Contig ID 1337_1.R1039
5'-most EST LIB3048-033-Q1-L1-D7

Seq. No. 191072
Contig ID 1343_1.R1039
5'-most EST LIB3048-016-Q1-L1-C11
Method BLASTX
NCBI GI g4220445
BLAST score 147

E value	8.0e-09
Match length	178
% identity	17
NCBI Description	(AC006216) Similar to gi|3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb|AC003673. [Arabidopsis thaliana]

Seq. No.	191073
Contig ID	1344_1.R1039
5'-most EST	LIB3048-042-Q1-L1-B11
Method	BLASTX
NCBI GI	g1518540
BLAST score	554
E value	4.0e-57
Match length	123
% identity	85
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	191074
Contig ID	1346_1.R1039
5'-most EST	LIB3048-016-Q1-L1-C3

Seq. No.	191075
Contig ID	1349_1.R1039
5'-most EST	LIB3048-054-Q1-L1-D4
Method	BLASTX
NCBI GI	g119748
BLAST score	422
E value	1.0e-41
Match length	94
% identity	89
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi|67241|pir||PASPY fructose-bisphosphatase (EC 3.1.3.11), cytosolic - spinach >gi|21245|emb|CAA43860| (X61690) fructose-bisphosphatase [Spinacia oleracea]

Seq. No.	191076
Contig ID	1350_1.R1039
5'-most EST	g3325609
Method	BLASTX
NCBI GI	g3435196
BLAST score	559
E value	2.0e-57
Match length	187
% identity	60
NCBI Description	(AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	191077
Contig ID	1358_1.R1039
5'-most EST	uC-gsronu33B046g02b1
Method	BLASTX
NCBI GI	g2827548
BLAST score	152
E value	6.0e-10
Match length	90
% identity	41

NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	191078
Contig ID	1365_1.R1039
5'-most EST	LIB3048-052-Q1-L1-D3
Method	BLASTX
NCBI GI	g2244898
BLAST score	738
E value	3.0e-79
Match length	207
% identity	71
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	191079
Contig ID	1373_1.R1039
5'-most EST	LIB3083-088-Q1-L1-E6
Method	BLASTX
NCBI GI	g4263695
BLAST score	472
E value	5.0e-47
Match length	276
% identity	10
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	191080
Contig ID	1382_1.R1039
5'-most EST	LIB3048-026-Q1-L1-G1
Method	BLASTX
NCBI GI	g1723239
BLAST score	573
E value	6.0e-59
Match length	201
% identity	55
NCBI Description	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I >gi|1177358|emb|CAA93234| (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]

Seq. No.	191081
Contig ID	1383_1.R1039
5'-most EST	LIB3196-024-P1-M1-H9
Method	BLASTX
NCBI GI	g4128133
BLAST score	787
E value	8.0e-84
Match length	331
% identity	47
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	191082
Contig ID	1385_1.R1039
5'-most EST	LIB3048-016-Q1-L1-G2

Seq. No.	191083
Contig ID	1386_1.R1039

5'-most EST	LIB3272-046-P1-K1-E11
Method	BLASTX
NCBI GI	g285741
BLAST score	1365
E value	1.0e-151
Match length	425
% identity	64
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	191084
Contig ID	1387_1.R1039
5'-most EST	g5050748
Method	BLASTX
NCBI GI	g3892055
BLAST score	889
E value	4.0e-96
Match length	212
% identity	76
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	191085
Contig ID	1388_1.R1039
5'-most EST	LIB3166-053-P1-K1-C7
Method	BLASTX
NCBI GI	g3288883
BLAST score	470
E value	4.0e-47
Match length	137
% identity	69
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	191086
Contig ID	1390_1.R1039
5'-most EST	LIB3048-033-Q1-L1-C12
Method	BLASTX
NCBI GI	g2369766
BLAST score	832
E value	1.0e-137
Match length	283
% identity	84
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	191087
Contig ID	1390_2.R1039
5'-most EST	LIB3135-018-Q1-K1-A5
Method	BLASTX
NCBI GI	g2369766
BLAST score	237
E value	1.0e-19
Match length	45
% identity	98
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	191088
Contig ID	1390_4.R1039
5'-most EST	uC-gsronu33B178b06b1

Method	BLASTX
NCBI GI	g2369766
BLAST score	402
E value	2.0e-61
Match length	195
% identity	64
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	191089
Contig ID	1396_1.R1039
5'-most EST	LIB3048-036-Q1-L1-F5

Seq. No.	191090
Contig ID	1397_1.R1039
5'-most EST	LIB3048-023-Q1-L1-G4
Method	BLASTX
NCBI GI	g3096919
BLAST score	333
E value	7.0e-46
Match length	110
% identity	85
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	191091
Contig ID	1398_1.R1039
5'-most EST	LIB3272-005-P1-K1-A12
Method	BLASTX
NCBI GI	g70645
BLAST score	1901
E value	0.0e+00
Match length	381
% identity	100
NCBI Description	ubiquitin precursor - garden pea >gi|20589|emb|CAA34886| (X17020) polyubiquitin (AA 1-381) [Pisum sativum] >gi|4115339 (L81142) ubiquitin [Pisum sativum] >gi|226707|prf||1603402A poly-ubiquitin [Pisum sativum]

Seq. No.	191092
Contig ID	1400_1.R1039
5'-most EST	LIB3166-001-Q1-K1-C11
Method	BLASTX
NCBI GI	g1495804
BLAST score	713
E value	1.0e-75
Match length	158
% identity	85
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	191093
Contig ID	1402_1.R1039
5'-most EST	LIB3048-033-Q1-L1-F8

Seq. No.	191094
Contig ID	1403_1.R1039
5'-most EST	LIB3165-028-P1-K1-F2
Method	BLASTX

NCBI GI g2244905
BLAST score 656
E value 1.0e-68
Match length 203
% identity 61
NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 191095
Contig ID 1404_1.R1039
5'-most EST LIB3048-019-Q1-L1-G6
Method BLASTX
NCBI GI g3746059
BLAST score 805
E value 3.0e-86
Match length 204
% identity 69
NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi|4432812|gb|AAD20662| (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 191096
Contig ID 1409_1.R1039
5'-most EST LIB3272-021-P1-K1-C11
Method BLASTX
NCBI GI g4455210
BLAST score 570
E value 2.0e-58
Match length 229
% identity 54
NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No. 191097
Contig ID 1417_1.R1039
5'-most EST LIB3048-034-Q1-L1-E7

Seq. No. 191098
Contig ID 1418_1.R1039
5'-most EST g5047458
Method BLASTX
NCBI GI g2507426
BLAST score 1276
E value 1.0e-141
Match length 393
% identity 64
NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (ALANINE--TRNA LIGASE) (ALARS) >gi|1673365|emb|CAA80380| (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No. 191099
Contig ID 1429_1.R1039
5'-most EST LIB3272-045-P1-K1-B1
Method BLASTX
NCBI GI g1769887
BLAST score 454

E value	3.0e-45
Match length	106
% identity	78
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	191100
Contig ID	1431_1.R1039
5'-most EST	LIB3048-029-Q1-L1-D1

Seq. No.	191101
Contig ID	1432_1.R1039
5'-most EST	LIB3135-028-Q1-K1-H1
Method	BLASTX
NCBI GI	g1076746
BLAST score	1400
E value	1.0e-155
Match length	312
% identity	88
NCBI Description	heat shock protein 70 - rice (fragment) >gi|763160|emb|CAA47948| (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	191102
Contig ID	1432_2.R1039
5'-most EST	g3326230
Method	BLASTX
NCBI GI	g116343
BLAST score	400
E value	1.0e-38
Match length	213
% identity	40
NCBI Description	BASIC ENDOCHITINASE PRECURSOR

Seq. No.	191103
Contig ID	1432_3.R1039
5'-most EST	uC-gsflnu33B100a04b1
Method	BLASTX
NCBI GI	g584928
BLAST score	317
E value	3.0e-41
Match length	242
% identity	40
NCBI Description	ENDOCHITINASE CH25 PRECURSOR >gi|2118034|pir||S59953 chitinase (EC 3.2.1.14) class I precursor - rape >gi|167130 (M95835) endochitinase [Brassica napus]

Seq. No.	191104
Contig ID	1432_4.R1039
5'-most EST	uC-gsflnu33B068d02b1
Method	BLASTX
NCBI GI	g3747050
BLAST score	425
E value	1.0e-41
Match length	106
% identity	77
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	191105
Contig ID	1432_5.R1039
5'-most EST	uC-gsronu33B159f05b1
Method	BLASTX
NCBI GI	g425194
BLAST score	617
E value	3.0e-64
Match length	147
% identity	84
NCBI Description	(L26243) heat shock protein [Spinacia oleracea] >gi|2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	191106
Contig ID	1432_6.R1039
5'-most EST	LIB3166-057-P1-K1-A5
Method	BLASTX
NCBI GI	g1076746
BLAST score	1689
E value	0.0e+00
Match length	465
% identity	91
NCBI Description	heat shock protein 70 - rice (fragment) >gi|763160|emb|CAA47948| (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	191107
Contig ID	1432_7.R1039
5'-most EST	LIB3083-024-Q1-L1-A4
Method	BLASTX
NCBI GI	g974294
BLAST score	323
E value	1.0e-29
Match length	106
% identity	60
NCBI Description	(U31309) LP6 [Pinus taeda]

Seq. No.	191108
Contig ID	1432_9.R1039
5'-most EST	LIB3083-079-Q1-L1-B10
Method	BLASTX
NCBI GI	g123620
BLAST score	1012
E value	1.0e-110
Match length	236
% identity	86
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi|100224|pir||S14950 heat shock cognate protein 70 - tomato >gi|19258|emb|CAA37971| (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]

Seq. No.	191109
Contig ID	1432_10.R1039
5'-most EST	LIB3166-029-P1-K1-F9
Method	BLASTX
NCBI GI	g1076746
BLAST score	338

E value	2.0e-31
Match length	129
% identity	61
NCBI Description	heat shock protein 70 - rice (fragment) >gi|763160|emb|CAA47948| (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	191110
Contig ID	1432_11.R1039
5'-most EST	LIB3146-010-Q1-K1-D4
Method	BLASTX
NCBI GI	g3986110
BLAST score	406
E value	1.0e-39
Match length	99
% identity	79
NCBI Description	(AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No.	191111
Contig ID	1433_1.R1039
5'-most EST	LIB3048-039-Q1-L1-E2
Method	BLASTX
NCBI GI	g2827718
BLAST score	263
E value	6.0e-23
Match length	133
% identity	50
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	191112
Contig ID	1434_1.R1039
5'-most EST	LIB3048-019-Q1-L1-A10

Seq. No.	191113
Contig ID	1434_2.R1039
5'-most EST	LIB3083-028-Q1-L1-B7
Method	BLASTX
NCBI GI	g308906
BLAST score	254
E value	8.0e-22
Match length	97
% identity	53
NCBI Description	(L18909) thioredoxin [Lilium longiflorum]

Seq. No.	191114
Contig ID	1435_1.R1039
5'-most EST	LIB3048-046-Q1-L1-F3

Seq. No.	191115
Contig ID	1440_1.R1039
5'-most EST	LIB3048-017-Q1-L1-D4
Method	BLASTX
NCBI GI	g4432866
BLAST score	254
E value	6.0e-22
Match length	117

% identity	38
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	191116
Contig ID	1441_1.R1039
5'-most EST	LIB3272-013-P1-K1-D4
Method	BLASTN
NCBI GI	g4063730
BLAST score	45
E value	9.0e-16
Match length	252
% identity	86
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	191117
Contig ID	1442_1.R1039
5'-most EST	LIB3048-053-H10T3A
Method	BLASTX
NCBI GI	g1483230
BLAST score	622
E value	9.0e-65
Match length	189
% identity	69
NCBI Description	(X99654) MADS4 protein [Betula pendula]

Seq. No.	191118
Contig ID	1444_1.R1039
5'-most EST	LIB3048-054-Q1-L1-A4

Seq. No.	191119
Contig ID	1451_1.R1039
5'-most EST	LIB3048-025-Q1-L1-F12
Method	BLASTX
NCBI GI	g4325338
BLAST score	680
E value	8.0e-72
Match length	141
% identity	87
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	191120
Contig ID	1456_1.R1039
5'-most EST	g5049550

Seq. No.	191121
Contig ID	1456_3.R1039
5'-most EST	LIB3048-033-Q1-L1-H8

Seq. No.	191122
Contig ID	1456_4.R1039
5'-most EST	g3326693
Method	BLASTX
NCBI GI	g2213583
BLAST score	534

E value	3.0e-72
Match length	211
% identity	67
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	191123
Contig ID	1457_1.R1039
5'-most EST	uC-gsronu33B036c08b1
Method	BLASTX
NCBI GI	g2772934
BLAST score	564
E value	5.0e-58
Match length	164
% identity	65
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	191124
Contig ID	1460_1.R1039
5'-most EST	uC-gsflnu33B061h12b1
Method	BLASTX
NCBI GI	g4337040
BLAST score	445
E value	4.0e-44
Match length	146
% identity	66
NCBI Description	(AF124159) molybdopterin synthase sulphurylase [Arabidopsis thaliana] >gi|4337042|gb|AAD18051| (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No.	191125
Contig ID	1460_2.R1039
5'-most EST	LIB3272-020-P1-K1-E7
Method	BLASTX
NCBI GI	g4337040
BLAST score	414
E value	1.0e-40
Match length	95
% identity	85
NCBI Description	(AF124159) molybdopterin synthase sulphurylase [Arabidopsis thaliana] >gi|4337042|gb|AAD18051| (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No.	191126
Contig ID	1463_1.R1039
5'-most EST	uC-gsflmaxxa001g08b1
Method	BLASTX
NCBI GI	g2529680
BLAST score	1512
E value	1.0e-168
Match length	360
% identity	79
NCBI Description	(AC002535) putative protein disulfide-isomerase precursor [Arabidopsis thaliana]

Seq. No.	191127
Contig ID	1463_2.R1039

5'-most EST	LIB3197-058-Q1-M1-H8
Method	BLASTX
NCBI GI	g1848212
BLAST score	460
E value	8.0e-46
Match length	163
% identity	39
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No.	191128
Contig ID	1471_1.R1039
5'-most EST	LIB3048-037-Q1-L1-E1

Seq. No.	191129
Contig ID	1472_1.R1039
5'-most EST	g5049395
Method	BLASTX
NCBI GI	g3395431
BLAST score	180
E value	7.0e-13
Match length	107
% identity	36
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	191130
Contig ID	1473_1.R1039
5'-most EST	LIB3048-025-Q1-L1-F4
Method	BLASTX
NCBI GI	g3668089
BLAST score	859
E value	3.0e-92
Match length	298
% identity	53
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	191131
Contig ID	1474_1.R1039
5'-most EST	g5045905
Method	BLASTX
NCBI GI	g3236248
BLAST score	939
E value	1.0e-101
Match length	236
% identity	78
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	191132
Contig ID	1477_1.R1039
5'-most EST	LIB3149-019-Q1-K1-E10
Method	BLASTX
NCBI GI	g4164161
BLAST score	707
E value	8.0e-75
Match length	184
% identity	72
NCBI Description	(AB015497) ethylene response sensor [Passiflora edulis]

Seq. No.	191133
Contig ID	1480_1.R1039
5'-most EST	LIB3197-021-Q1-M1-E12
Method	BLASTX
NCBI GI	g2494113
BLAST score	1689
E value	0.0e+00
Match length	403
% identity	77
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb|X92943). ESTs gb|AA042458, gb|ATTS4502, gb|N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	191134
Contig ID	1480_4.R1039
5'-most EST	LIB3197-055-Q1-M1-H7
Method	BLASTX
NCBI GI	g2494113
BLAST score	436
E value	3.0e-43
Match length	109
% identity	72
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb|X92943). ESTs gb|AA042458, gb|ATTS4502, gb|N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	191135
Contig ID	1481_1.R1039
5'-most EST	LIB3048-017-Q1-L1-H6
Method	BLASTX
NCBI GI	g231811
BLAST score	427
E value	1.0e-72
Match length	222
% identity	55
NCBI Description	CLATHRIN HEAVY CHAIN >gi|1079060|pir||S52588 clathrin heavy chain - fruit fly (Drosophila melanogaster) >gi|7722|emb|CAA78507| (Z14133) clathrin heavy chain [Drosophila melanogaster]

Seq. No.	191136
Contig ID	1482_1.R1039
5'-most EST	uC-gsflnu33B128d06b1

Seq. No.	191137
Contig ID	1482_2.R1039
5'-most EST	LIB3165-022-P1-K1-G1

Seq. No.	191138
Contig ID	1484_1.R1039
5'-most EST	LIB3048-034-Q1-L1-D9
Method	BLASTX
NCBI GI	g1173456
BLAST score	353
E value	2.0e-33
Match length	112

% identity	55
NCBI Description	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi|600750 (U15009) Sm D3 [Homo sapiens]

Seq. No.	191139
Contig ID	1487_1.R1039
5'-most EST	uC-gsflnu33B072a07b1
Method	BLASTX
NCBI GI	g2398679
BLAST score	2301
E value	0.0e+00
Match length	529
% identity	85
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	191140
Contig ID	1490_1.R1039
5'-most EST	LIB3048-030-Q1-L1-A6

Seq. No.	191141
Contig ID	1492_1.R1039
5'-most EST	LIB3048-053-Q1-L1-A11

Seq. No.	191142
Contig ID	1497_1.R1039
5'-most EST	LIB3189-034-P1-K1-F2
Method	BLASTX
NCBI GI	g4539422
BLAST score	793
E value	2.0e-93
Match length	235
% identity	72
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	191143
Contig ID	1499_1.R1039
5'-most EST	uC-gsronu33B141e12b1
Method	BLASTX
NCBI GI	g3294180
BLAST score	327
E value	9.0e-30
Match length	333
% identity	30
NCBI Description	(Z99129) dJ425C14.2 (Placental protein DIFF33 LIKE) [Homo sapiens]

Seq. No.	191144
Contig ID	1509_1.R1039
5'-most EST	uC-gsflmaxxa029a11b1
Method	BLASTX
NCBI GI	g3811007
BLAST score	606
E value	5.0e-63
Match length	122
% identity	93
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus

carota]

Seq. No.	191145
Contig ID	1510_1.R1039
5'-most EST	LIB3048-042-Q1-L1-F4
Method	BLASTX
NCBI GI	g3421090
BLAST score	1016
E value	1.0e-110
Match length	207
% identity	96
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	191146
Contig ID	1510_2.R1039
5'-most EST	LIB3196-044-P1-M1-H9
Method	BLASTX
NCBI GI	g3421090
BLAST score	1154
E value	1.0e-127
Match length	237
% identity	95
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	191147
Contig ID	1511_1.R1039
5'-most EST	LIB3048-021-Q1-L1-B10
Method	BLASTX
NCBI GI	g3115374
BLAST score	544
E value	1.0e-55
Match length	166
% identity	66
NCBI Description	(AF002016) acyl CoA oxidase homolog [Cucurbita sp.]

Seq. No.	191148
Contig ID	1516_1.R1039
5'-most EST	LIB3147-058-Q1-K1-G4
Method	BLASTX
NCBI GI	g170753
BLAST score	793
E value	1.0e-84
Match length	179
% identity	78
NCBI Description	(M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	191149
Contig ID	1516_2.R1039
5'-most EST	g5045440
Method	BLASTX
NCBI GI	g170753
BLAST score	706
E value	1.0e-74
Match length	158

% identity	78
NCBI Description	(M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No.	191150
Contig ID	1521_1.R1039
5'-most EST	LIB3048-050-Q1-L1-A1

Seq. No.	191151
Contig ID	1525_1.R1039
5'-most EST	g5045392
Method	BLASTX
NCBI GI	g2511574
BLAST score	933
E value	1.0e-101
Match length	198
% identity	93
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi|3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	191152
Contig ID	1529_1.R1039
5'-most EST	LIB3048-020-Q1-L1-A9
Method	BLASTX
NCBI GI	g2864624
BLAST score	383
E value	6.0e-37
Match length	146
% identity	26
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	191153
Contig ID	1532_1.R1039
5'-most EST	LIB3048-018-Q1-L1-E12

Seq. No.	191154
Contig ID	1533_1.R1039
5'-most EST	LIB3272-058-P1-K1-E3
Method	BLASTX
NCBI GI	g4426603
BLAST score	511
E value	1.0e-51
Match length	208
% identity	49
NCBI Description	(AF092092) AP-3 adaptor complex mu3A subunit [Homo sapiens]

Seq. No.	191155
Contig ID	1536_1.R1039
5'-most EST	LIB3135-037-Q1-K1-F10
Method	BLASTX
NCBI GI	g3892057
BLAST score	579
E value	6.0e-60
Match length	137
% identity	43
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191156
Contig ID	1538_1.R1039
5'-most EST	LIB3166-020-P1-K1-C4
Method	BLASTX
NCBI GI	g2262178
BLAST score	149
E value	1.0e-09
Match length	34
% identity	74
NCBI Description	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No.	191157
Contig ID	1545_1.R1039
5'-most EST	uC-gsflnu33B050f02b1
Method	BLASTX
NCBI GI	g2498943
BLAST score	256
E value	1.0e-21
Match length	169
% identity	32
NCBI Description	PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) >gi|2129288|pir||B64339 spermidine synthase (EC 2.5.1.16) - Methanococcus jannaschii >gi|1591033 (U67486) spermidine synthase (speE) [Methanococcus jannaschii]

Seq. No.	191158
Contig ID	1550_1.R1039
5'-most EST	LIB3048-018-Q1-L1-G10
Method	BLASTX
NCBI GI	g3461820
BLAST score	226
E value	1.0e-18
Match length	61
% identity	62
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	191159
Contig ID	1551_1.R1039
5'-most EST	LIB3135-061-Q1-K1-B11

Seq. No.	191160
Contig ID	1554_1.R1039
5'-most EST	LIB3166-027-P1-K1-C5
Method	BLASTX
NCBI GI	g4235430
BLAST score	1547
E value	1.0e-173
Match length	419
% identity	72
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No.	191161
Contig ID	1567_1.R1039
5'-most EST	LIB3048-018-Q1-L1-H5

Seq. No.	191162
Contig ID	1593_1.R1039
5'-most EST	LIB3048-019-Q1-L1-B8

Seq. No.	191163
Contig ID	1594_1.R1039
5'-most EST	LIB3048-019-Q1-L1-B9
Method	BLASTX
NCBI GI	g2618699
BLAST score	423
E value	2.0e-68
Match length	203
% identity	67
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	191164
Contig ID	1597_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C11
Method	BLASTX
NCBI GI	g3249064
BLAST score	573
E value	4.0e-59
Match length	170
% identity	65
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb|2245136 from A. thaliana chromosome 4 contig gb|Z97344. [Arabidopsis thaliana]

Seq. No.	191165
Contig ID	1598_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C12

Seq. No.	191166
Contig ID	1606_1.R1039
5'-most EST	LIB3048-019-Q1-L1-C9
Method	BLASTX
NCBI GI	g4468817
BLAST score	661
E value	2.0e-69
Match length	135
% identity	44
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	191167
Contig ID	1607_1.R1039
5'-most EST	LIB3048-019-Q1-L1-D1
Method	BLASTX
NCBI GI	g4432866
BLAST score	384
E value	4.0e-37
Match length	145
% identity	48
NCBI Description	(AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	191168
Contig ID	1608_1.R1039

5'-most EST	LIB3048-019-Q1-L1-D10
Method	BLASTX
NCBI GI	g1589913
BLAST score	810
E value	7.0e-87
Match length	189
% identity	79
NCBI Description	(U69694) ATP-sulfurylase precursor [Brassica oleracea]

Seq. No.	191169
Contig ID	1609_1.R1039
5'-most EST	LIB3166-058-P1-K1-B8
Method	BLASTX
NCBI GI	g1769903
BLAST score	529
E value	4.0e-71
Match length	231
% identity	60
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No.	191170
Contig ID	1609_2.R1039
5'-most EST	LIB3166-006-P1-K1-F1
Method	BLASTX
NCBI GI	g1769903
BLAST score	875
E value	2.0e-94
Match length	218
% identity	75
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No.	191171
Contig ID	1611_1.R1039
5'-most EST	LIB3272-049-P1-K1-A9

Seq. No.	191172
Contig ID	1612_1.R1039
5'-most EST	LIB3048-019-Q1-L1-D3
Method	BLASTX
NCBI GI	g4376203
BLAST score	468
E value	2.0e-46
Match length	189
% identity	44
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No.	191173
Contig ID	1614_1.R1039
5'-most EST	LIB3146-056-Q1-K1-D10
Method	BLASTX
NCBI GI	g3763933
BLAST score	603
E value	2.0e-62
Match length	224
% identity	58
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana]

Seq. No.	191174
Contig ID	1615_1.R1039
5'-most EST	LIB3197-048-Q1-M1-D6
Method	BLASTX
NCBI GI	g2894612
BLAST score	1529
E value	1.0e-170
Match length	351
% identity	79
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	191175
Contig ID	1622_1.R1039
5'-most EST	LIB3048-019-Q1-L1-E12
Method	BLASTX
NCBI GI	g2245070
BLAST score	210
E value	8.0e-28
Match length	95
% identity	68
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191176
Contig ID	1624_1.R1039
5'-most EST	LIB3145-016-Q1-K1-E3
Method	BLASTX
NCBI GI	g3789917
BLAST score	144
E value	7.0e-09
Match length	70
% identity	41
NCBI Description	(AF084928) erythroblast macrophage protein EMP [Homo sapiens]

Seq. No.	191177
Contig ID	1624_2.R1039
5'-most EST	g5047326
Method	BLASTX
NCBI GI	g3885336
BLAST score	240
E value	8.0e-20
Match length	143
% identity	11
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	191178
Contig ID	1630_1.R1039
5'-most EST	LIB3048-019-Q1-L1-F1
Method	BLASTX
NCBI GI	g3335375
BLAST score	457
E value	2.0e-54
Match length	133
% identity	81
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	191179
Contig ID	1642_1.R1039
5'-most EST	LIB3048-019-Q1-L1-G10

Seq. No.	191180
Contig ID	1644_1.R1039
5'-most EST	LIB3048-019-Q1-L1-G12

Seq. No.	191181
Contig ID	1647_1.R1039
5'-most EST	LIB3165-044-Q1-K1-H12
Method	BLASTX
NCBI GI	g1486472
BLAST score	1363
E value	1.0e-151
Match length	295
% identity	88
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	191182
Contig ID	1652_1.R1039
5'-most EST	uC-gsflnu33B101e11b1
Method	BLASTX
NCBI GI	g2078350
BLAST score	1708
E value	0.0e+00
Match length	440
% identity	78
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	191183
Contig ID	1654_1.R1039
5'-most EST	LIB3048-019-Q1-L1-H11
Method	BLASTX
NCBI GI	g1361973
BLAST score	407
E value	8.0e-40
Match length	144
% identity	62
NCBI Description	secA protein precursor - spinach

Seq. No.	191184
Contig ID	1665_1.R1039
5'-most EST	LIB3048-020-Q1-L1-A11

Seq. No.	191185
Contig ID	1669_1.R1039
5'-most EST	LIB3048-020-Q1-L1-A4

Seq. No.	191186
Contig ID	1671_1.R1039
5'-most EST	LIB3165-027-P1-K1-G2
Method	BLASTX
NCBI GI	g1168728
BLAST score	339

E value	1.0e-31
Match length	116
% identity	53
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi|598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	191187
Contig ID	1674_1.R1039
5'-most EST	LIB3048-049-Q1-L1-D2

Seq. No.	191188
Contig ID	1677_1.R1039
5'-most EST	LIB3048-020-Q1-L1-B12
Method	BLASTX
NCBI GI	g131276
BLAST score	953
E value	1.0e-103
Match length	182
% identity	98
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi|72704|pir||QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi|11856|emb|CAA77373| (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi|225224|prf||1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	191189
Contig ID	1679_1.R1039
5'-most EST	LIB3197-039-Q1-M1-C8
Method	BLASTX
NCBI GI	g585777
BLAST score	1047
E value	1.0e-114
Match length	193
% identity	99
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN1 >gi|453561 (L28713) Ran protein/TC4 protein [Solanum lycopersicum]

Seq. No.	191190
Contig ID	1679_2.R1039
5'-most EST	LIB3146-023-Q1-K1-H1
Method	BLASTX
NCBI GI	g2507281
BLAST score	1065
E value	1.0e-116
Match length	252
% identity	81
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi|1668706|emb|CAA66048| (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	191191
Contig ID	1679_3.R1039
5'-most EST	LIB3147-009-Q1-K1-D8
Method	BLASTX
NCBI GI	g1710008
BLAST score	302
E value	1.0e-27

Match length 79
% identity 72
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN1B >gi|1370205|emb|CAA98188| (Z73960) RAN1B [Lotus japonicus]

Seq. No. 191192
Contig ID 1683_1.R1039
5'-most EST LIB3083-107-Q1-L1-H10
Method BLASTX
NCBI GI g4510346
BLAST score 369
E value 4.0e-35
Match length 99
% identity 74
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 191193
Contig ID 1685_1.R1039
5'-most EST LIB3272-049-P1-K1-D5
Method BLASTN
NCBI GI g3128135
BLAST score 37
E value 3.0e-11
Match length 148
% identity 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No. 191194
Contig ID 1687_1.R1039
5'-most EST LIB3048-020-Q1-L1-C10
Method BLASTX
NCBI GI g3776559
BLAST score 323
E value 6.0e-30
Match length 72
% identity 81
NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi|3482933 cdc2 protein kinase homolog from A. thaliana BAC gb|AC003970. ESTs gb|Z35332 and gb|F19907 come from this gene. [Arabidopsis thaliana]

Seq. No. 191195
Contig ID 1701_1.R1039
5'-most EST LIB3048-020-Q1-L1-G8
Method BLASTX
NCBI GI g2443886
BLAST score 220
E value 1.0e-17
Match length 165
% identity 33
NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 191196
Contig ID 1706_1.R1039
5'-most EST LIB3048-022-Q1-L1-A4
Method BLASTX

NCBI GI	g2062173
BLAST score	401
E value	4.0e-39
Match length	138
% identity	59
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	191197
Contig ID	1708_1.R1039
5'-most EST	uC-gsflmaxxa001h02b1
Method	BLASTX
NCBI GI	g1346172
BLAST score	1584
E value	1.0e-177
Match length	357
% identity	88
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >gi|170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum]

Seq. No.	191198
Contig ID	1708_2.R1039
5'-most EST	uC-gsronu33B144a08b1
Method	BLASTX
NCBI GI	g1346172
BLAST score	434
E value	6.0e-43
Match length	111
% identity	77
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >gi|170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum]

Seq. No.	191199
Contig ID	1708_3.R1039
5'-most EST	uC-gsflnu33B093f12b1
Method	BLASTX
NCBI GI	g1346172
BLAST score	284
E value	3.0e-25
Match length	57
% identity	91
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >gi|170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum]

Seq. No.	191200
Contig ID	1708_4.R1039
5'-most EST	uC-gsflnu33B136a04b1
Method	BLASTX
NCBI GI	g729618
BLAST score	374
E value	1.0e-35

Match length	89
% identity	82
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP 2) >gi|82172|pir||PQ0262 luminal binding protein BLP-2 - common tobacco (fragment) >gi|100338|pir||S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment) >gi|19807|emb|CAA42661| (X60059) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	191201
Contig ID	1710_1.R1039
5'-most EST	LIB3165-047-Q1-K1-E3
Method	BLASTX
NCBI GI	g4512018
BLAST score	857
E value	3.0e-92
Match length	200
% identity	81
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	191202
Contig ID	1712_3.R1039
5'-most EST	LIB3146-001-P1-K2-C1

Seq. No.	191203
Contig ID	1716_1.R1039
5'-most EST	LIB3145-022-Q1-K1-H6
Method	BLASTX
NCBI GI	g322752
BLAST score	334
E value	5.0e-31
Match length	162
% identity	43
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi|559921|emb|CAA56570| (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	191204
Contig ID	1719_1.R1039
5'-most EST	LIB3048-020-Q1-L1-E7

Seq. No.	191205
Contig ID	1723_1.R1039
5'-most EST	LIB3048-033-Q1-L1-D1
Method	BLASTX
NCBI GI	g3355467
BLAST score	164
E value	2.0e-11
Match length	134
% identity	31
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191206
Contig ID	1732_1.R1039
5'-most EST	uC-gsronu33B147h12b1
Method	BLASTX

NCBI GI g3023751
BLAST score 444
E value 8.0e-57
Match length 175
% identity 34
NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi|1076772|pir||S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi|854626|emb|CAA60505| (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No. 191207
Contig ID 1733_1.R1039
5'-most EST LIB3048-025-Q1-L1-G2

Seq. No. 191208
Contig ID 1737_1.R1039
5'-most EST LIB3048-020-Q1-L1-G2

Seq. No. 191209
Contig ID 1747_1.R1039
5'-most EST LIB3272-030-P1-K1-A1
Method BLASTX
NCBI GI g3451147
BLAST score 808
E value 2.0e-86
Match length 227
% identity 67
NCBI Description (AJ010397) chitinase [Hevea brasiliensis]

Seq. No. 191210
Contig ID 1748_1.R1039
5'-most EST g5046327
Method BLASTX
NCBI GI g3176690
BLAST score 1829
E value 0.0e+00
Match length 450
% identity 78
NCBI Description (AC003671) Similar to ubiquitin ligase gb|D63905 from S. cerevisiae. EST gb|R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No. 191211
Contig ID 1751_1.R1039
5'-most EST uC-gsronu33B159c11b1
Method BLASTX
NCBI GI g2894599
BLAST score 775
E value 1.0e-82
Match length 223
% identity 70
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 191212
Contig ID 1751_2.R1039
5'-most EST LIB3048-036-Q1-L1-F4

Method	BLASTX
NCBI GI	g2894599
BLAST score	524
E value	2.0e-53
Match length	108
% identity	85
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	191213
Contig ID	1751_3.R1039
5'-most EST	LIB3272-048-P1-K1-E11
Method	BLASTX
NCBI GI	g2894599
BLAST score	563
E value	5.0e-58
Match length	122
% identity	81
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	191214
Contig ID	1751_4.R1039
5'-most EST	LIB3165-014-P1-K1-F4
Method	BLASTX
NCBI GI	g2894599
BLAST score	517
E value	1.0e-52
Match length	108
% identity	83
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	191215
Contig ID	1759_1.R1039
5'-most EST	LIB3048-021-Q1-L1-A11
Method	BLASTN
NCBI GI	g4220643
BLAST score	39
E value	2.0e-12
Match length	121
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	191216
Contig ID	1768_1.R1039
5'-most EST	LIB3048-021-Q1-L1-B12
Method	BLASTX
NCBI GI	g130582
BLAST score	476
E value	7.0e-48
Match length	140
% identity	64
NCBI Description	RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94 [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE] >gi|100342|pir||S04273 hypothetical protein - common tobacco >gi|20045|emb|CAA32025| (X13777) ORF [Nicotiana tabacum]

Seq. No.	191217
Contig ID	1775_1.R1039
5'-most EST	LIB3048-021-Q1-L1-C1
Method	BLASTX
NCBI GI	g2897942
BLAST score	267
E value	4.0e-23
Match length	165
% identity	37
NCBI Description	(AF003938) thioredoxin-like protein [Homo sapiens] >gi|2961254 (AF051896) thioredoxin homolog [Homo sapiens] >gi|2970689 (AF052659) thioredoxin-related protein [Homo sapiens]

Seq. No.	191218
Contig ID	1790_1.R1039
5'-most EST	LIB3048-053-Q1-L1-E10
Method	BLASTX
NCBI GI	g3377848
BLAST score	412
E value	3.0e-40
Match length	144
% identity	56
NCBI Description	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No.	191219
Contig ID	1800_1.R1039
5'-most EST	LIB3048-043-Q1-L2-B5
Method	BLASTX
NCBI GI	g99809
BLAST score	1308
E value	1.0e-145
Match length	326
% identity	72
NCBI Description	gene Bp10 protein - rape >gi|17795|emb|CAA47177| (X66608) Bplo [Brassica napus]

Seq. No.	191220
Contig ID	1808_1.R1039
5'-most EST	LIB3048-021-Q1-L1-F11
Method	BLASTX
NCBI GI	g1361311
BLAST score	171
E value	4.0e-12
Match length	73
% identity	47
NCBI Description	CMP-2-keto-3-deoxyoctulosonic acid synthetase homolog - Chlamydia trachomatis >gi|557478 (U15192) CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia trachomatis]

Seq. No.	191221
Contig ID	1809_1.R1039
5'-most EST	LIB3147-031-Q1-K1-G7
Method	BLASTX
NCBI GI	g4467145

BLAST score 618
E value 3.0e-64
Match length 140
% identity 83
NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No. 191222
Contig ID 1817_1.R1039
5'-most EST LIB3189-014-P1-K1-B9
Method BLASTX
NCBI GI g3980380
BLAST score 386
E value 3.0e-37
Match length 86
% identity 91
NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No. 191223
Contig ID 1819_1.R1039
5'-most EST LIB3048-021-Q1-L1-G11

Seq. No. 191224
Contig ID 1820_1.R1039
5'-most EST LIB3048-021-Q1-L1-G12

Seq. No. 191225
Contig ID 1820_2.R1039
5'-most EST LIB3148-038-Q1-K1-B8

Seq. No. 191226
Contig ID 1821_1.R1039
5'-most EST LIB3048-021-Q1-L1-G3
Method BLASTX
NCBI GI g4240207
BLAST score 191
E value 2.0e-14
Match length 128
% identity 38
NCBI Description (AB020666) KIAA0859 protein [Homo sapiens]

Seq. No. 191227
Contig ID 1826_1.R1039
5'-most EST LIB3272-042-P1-K1-A4
Method BLASTX
NCBI GI g4457221
BLAST score 208
E value 4.0e-16
Match length 71
% identity 58
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 191228
Contig ID 1835_1.R1039
5'-most EST LIB3048-021-Q1-L1-H9
Method BLASTX

NCBI GI	g1176658
BLAST score	351
E value	1.0e-32
Match length	157
% identity	46
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi|726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	191229
Contig ID	1841_1.R1039
5'-most EST	LIB3048-022-Q1-L1-A3

Seq. No.	191230
Contig ID	1853_2.R1039
5'-most EST	LIB3048-022-Q1-L1-B3
Method	BLASTX
NCBI GI	g2465923
BLAST score	186
E value	2.0e-14
Match length	127
% identity	16
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	191231
Contig ID	1854_1.R1039
5'-most EST	LIB3197-034-Q1-M1-E9
Method	BLASTX
NCBI GI	g584825
BLAST score	757
E value	4.0e-80
Match length	152
% identity	91
NCBI Description	B2 PROTEIN >gi|322726|pir||S32124 B2 protein - carrot >gi|297889|emb|CAA51078| (X72385) B2 protein [Daucus carota]

Seq. No.	191232
Contig ID	1885_1.R1039
5'-most EST	LIB3189-016-P1-K1-E4
Method	BLASTX
NCBI GI	g3687237
BLAST score	860
E value	2.0e-92
Match length	340
% identity	53
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	191233
Contig ID	1905_1.R1039
5'-most EST	LIB3048-022-Q1-L1-G1
Method	BLASTX
NCBI GI	g1931650
BLAST score	144
E value	6.0e-09

Match length	143
% identity	34
NCBI Description	(U95973) disease resistance protein RPM1 isolog [Arabidopsis thaliana]

Seq. No.	191234
Contig ID	1925_1.R1039
5'-most EST	uC-gsronu33B129a11b1
Method	BLASTX
NCBI GI	g4566614
BLAST score	554
E value	1.0e-56
Match length	137
% identity	78
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	191235
Contig ID	1938_1.R1039
5'-most EST	uC-gsflnu33B131c10b1
Method	BLASTX
NCBI GI	g4454051
BLAST score	449
E value	2.0e-44
Match length	164
% identity	53
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	191236
Contig ID	1940_1.R1039
5'-most EST	LIB3048-023-Q1-L1-C1

Seq. No.	191237
Contig ID	1947_1.R1039
5'-most EST	LIB3272-055-P1-K1-D4
Method	BLASTX
NCBI GI	g927428
BLAST score	414
E value	2.0e-40
Match length	121
% identity	69
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	191238
Contig ID	1950_1.R1039
5'-most EST	LIB3048-026-Q1-L1-A5
Method	BLASTX
NCBI GI	g3540200
BLAST score	217
E value	2.0e-17
Match length	84
% identity	51
NCBI Description	(AC004260) Similar to TINY [Arabidopsis thaliana]

Seq. No.	191239
Contig ID	1958_1.R1039

5'-most EST	LIB3048-023-Q1-L1-E3
Method	BLASTX
NCBI GI	g4512685
BLAST score	408
E value	1.0e-39
Match length	185
% identity	45
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi|4559325|gb|AAD22987.1|AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191240
Contig ID	1961_1.R1039
5'-most EST	uC-gsflmaxxa061e04b1
Method	BLASTX
NCBI GI	g4455199
BLAST score	419
E value	4.0e-41
Match length	110
% identity	79
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	191241
Contig ID	1965_1.R1039
5'-most EST	LIB3165-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g3193330
BLAST score	470
E value	1.0e-46
Match length	194
% identity	54
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	191242
Contig ID	1977_1.R1039
5'-most EST	g3326835
Method	BLASTX
NCBI GI	g3643608
BLAST score	303
E value	7.0e-27
Match length	233
% identity	34
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191243
Contig ID	1977_2.R1039
5'-most EST	LIB3165-023-P1-K1-B3
Method	BLASTN
NCBI GI	g4415905
BLAST score	41
E value	2.0e-13
Match length	253
% identity	79
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191244
Contig ID	1978_1.R1039
5'-most EST	LIB3166-033-P1-K1-A3

Seq. No.	191245
Contig ID	1979_1.R1039
5'-most EST	LIB3048-041-Q1-L1-B8
Method	BLASTX
NCBI GI	g3047114
BLAST score	634
E value	6.0e-66
Match length	254
% identity	48
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	191246
Contig ID	1980_1.R1039
5'-most EST	LIB3166-039-P1-K1-D6

Seq. No.	191247
Contig ID	1995_1.R1039
5'-most EST	LIB3166-030-P1-K1-B10
Method	BLASTX
NCBI GI	g2583123
BLAST score	1074
E value	1.0e-117
Match length	268
% identity	76
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	191248
Contig ID	2000_1.R1039
5'-most EST	LIB3189-018-P1-K1-C2
Method	BLASTN
NCBI GI	g4538895
BLAST score	43
E value	8.0e-15
Match length	119
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	191249
Contig ID	2005_1.R1039
5'-most EST	LIB3197-023-Q1-M1-G8

Seq. No.	191250
Contig ID	2006_1.R1039
5'-most EST	LIB3166-007-P1-K1-G12
Method	BLASTX
NCBI GI	g2058313
BLAST score	698
E value	1.0e-73
Match length	158
% identity	84
NCBI Description	(X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No.	191251
Contig ID	2006_2.R1039
5'-most EST	uC-gsflnu33B029g09b1
Method	BLASTX
NCBI GI	g2960364
BLAST score	1046
E value	1.0e-114
Match length	223
% identity	88
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	191252
Contig ID	2009_1.R1039
5'-most EST	LIB3048-024-Q1-L1-D2

Seq. No.	191253
Contig ID	2016_1.R1039
5'-most EST	LIB3189-040-P1-K1-B9

Seq. No.	191254
Contig ID	2021_1.R1039
5'-most EST	LIB3048-024-Q1-L1-E7
Method	BLASTX
NCBI GI	g1946359
BLAST score	363
E value	1.0e-34
Match length	123
% identity	57
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	191255
Contig ID	2024_1.R1039
5'-most EST	LIB3048-024-Q1-L1-F2

Seq. No.	191256
Contig ID	2026_1.R1039
5'-most EST	uC-gsronu33B166e01b2
Method	BLASTX
NCBI GI	g543905
BLAST score	1058
E value	1.0e-125
Match length	260
% identity	82
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi|347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	191257
Contig ID	2026_3.R1039
5'-most EST	LIB3147-056-Q1-K1-H4
Method	BLASTX
NCBI GI	g543905
BLAST score	515
E value	5.0e-89
Match length	194
% identity	84

NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi|347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	191258
Contig ID	2026_4.R1039
5'-most EST	LIB3272-020-P1-K1-B3
Method	BLASTX
NCBI GI	g2129772
BLAST score	299
E value	5.0e-27
Match length	90
% identity	63
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi|1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	191259
Contig ID	2027_1.R1039
5'-most EST	LIB3135-003-Q1-K1-A7
Method	BLASTX
NCBI GI	g478389
BLAST score	366
E value	5.0e-39
Match length	128
% identity	65
NCBI Description	peroxidase (EC 1.11.1.7) precursor, anionic - Japanese aspen x large-toothed aspen >gi|217997|dbj|BAA01877| (D11102) peroxidase [Populus kitakamiensis] >gi|444801|prf||1908234A anionic peroxidase [Populus kitakamiensis]

Seq. No.	191260
Contig ID	2029_1.R1039
5'-most EST	LIB3135-018-Q1-K1-C9
Method	BLASTX
NCBI GI	g300265
BLAST score	989
E value	1.0e-108
Match length	229
% identity	89
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	191261
Contig ID	2032_1.R1039
5'-most EST	LIB3048-024-Q1-L1-G5
Method	BLASTX
NCBI GI	g4530126
BLAST score	144
E value	6.0e-09
Match length	67
% identity	42
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	191262
Contig ID	2035_1.R1039

5'-most EST	LIB3145-017-Q1-K1-E1
Method	BLASTX
NCBI GI	g4337195
BLAST score	1545
E value	1.0e-172
Match length	359
% identity	83
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	191263
Contig ID	2036_1.R1039
5'-most EST	LIB3048-052-Q1-L1-A8

Seq. No.	191264
Contig ID	2042_1.R1039
5'-most EST	g5044597
Method	BLASTX
NCBI GI	g1071912
BLAST score	725
E value	9.0e-77
Match length	228
% identity	68
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi|572517|emb|CAA57344| (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	191265
Contig ID	2046_1.R1039
5'-most EST	g5049257
Method	BLASTX
NCBI GI	g4567095
BLAST score	719
E value	4.0e-76
Match length	181
% identity	72
NCBI Description	(AF129516) fertilization-independent endosperm protein [Arabidopsis thaliana]

Seq. No.	191266
Contig ID	2048_1.R1039
5'-most EST	g5046346
Method	BLASTX
NCBI GI	g4567260
BLAST score	814
E value	3.0e-87
Match length	199
% identity	76
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	191267
Contig ID	2050_1.R1039
5'-most EST	LIB3048-025-Q1-L1-A7
Method	BLASTX
NCBI GI	g1871192
BLAST score	555
E value	7.0e-57

Match length 218
% identity 62
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 191268
Contig ID 2052_1.R1039
5'-most EST LIB3048-034-Q1-L1-B2
Method BLASTX
NCBI GI g3892055
BLAST score 461
E value 5.0e-46
Match length 133
% identity 69
NCBI Description (AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No. 191269
Contig ID 2052_4.R1039
5'-most EST LIB3146-023-Q1-K1-G4

Seq. No. 191270
Contig ID 2052_6.R1039
5'-most EST LIB3147-001-Q1-K1-C4

Seq. No. 191271
Contig ID 2052_8.R1039
5'-most EST LIB3146-025-Q1-K2-F2

Seq. No. 191272
Contig ID 2053_1.R1039
5'-most EST LIB3048-025-Q1-L1-B11

Seq. No. 191273
Contig ID 2060_1.R1039
5'-most EST LIB3189-047-P1-K1-E4
Method BLASTX
NCBI GI g3617741
BLAST score 955
E value 1.0e-103
Match length 224
% identity 81
NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No. 191274
Contig ID 2062_1.R1039
5'-most EST LIB3048-025-Q1-L1-G8
Method BLASTX
NCBI GI g3763933
BLAST score 214
E value 3.0e-17
Match length 68
% identity 63
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 191275

Contig ID	2063_1.R1039
5'-most EST	LIB3048-025-Q1-L1-C1
Method	BLASTX
NCBI GI	g2495209
BLAST score	381
E value	2.0e-36
Match length	108
% identity	62
NCBI Description	HYPOTHETICAL 12.9 KD PROTEIN SLR1417 >gi|1651819|dbj|BAA16746| (D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	191276
Contig ID	2069_1.R1039
5'-most EST	LIB3048-025-Q1-L1-C4
Method	BLASTX
NCBI GI	g3738319
BLAST score	590
E value	3.0e-61
Match length	131
% identity	81
NCBI Description	(AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191277
Contig ID	2076_1.R1039
5'-most EST	LIB3272-022-P1-K1-F2
Method	BLASTX
NCBI GI	g3080424
BLAST score	1508
E value	1.0e-168
Match length	346
% identity	84
NCBI Description	(AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	191278
Contig ID	2077_1.R1039
5'-most EST	LIB3048-025-Q1-L1-D11

Seq. No.	191279
Contig ID	2078_1.R1039
5'-most EST	LIB3197-034-Q1-M1-A11
Method	BLASTX
NCBI GI	g1841464
BLAST score	317
E value	4.0e-29
Match length	61
% identity	47
NCBI Description	(Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No.	191280
Contig ID	2079_1.R1039
5'-most EST	LIB3048-025-Q1-L1-D2
Method	BLASTX
NCBI GI	g3122914
BLAST score	792
E value	2.0e-84

Match length	256
% identity	59
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi|1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	191281
Contig ID	2080_1.R1039
5'-most EST	LIB3083-015-Q1-L2-H12
Method	BLASTX
NCBI GI	g2864609
BLAST score	238
E value	4.0e-42
Match length	168
% identity	55
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi|4049337|emb|CAA22562| (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	191282
Contig ID	2087_1.R1039
5'-most EST	LIB3048-025-Q1-L1-E1

Seq. No.	191283
Contig ID	2094_1.R1039
5'-most EST	uC-gsflmaxxa001g03b1
Method	BLASTX
NCBI GI	g2739044
BLAST score	653
E value	2.0e-68
Match length	170
% identity	69
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	191284
Contig ID	2111_1.R1039
5'-most EST	LIB3048-025-Q1-L1-G1
Method	BLASTX
NCBI GI	g3953467
BLAST score	664
E value	1.0e-69
Match length	149
% identity	43
NCBI Description	(AC002328) F20N2.12 [Arabidopsis thaliana]

Seq. No.	191285
Contig ID	2118_1.R1039
5'-most EST	LIB3048-025-Q1-L1-G5

Seq. No.	191286
Contig ID	2126_1.R1039
5'-most EST	LIB3048-025-Q1-L1-H12

Seq. No.	191287
Contig ID	2128_1.R1039
5'-most EST	LIB3048-025-Q1-L1-H3

Method	BLASTX
NCBI GI	g4490330
BLAST score	2157
E value	0.0e+00
Match length	458
% identity	87
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	191288
Contig ID	2132_1.R1039
5'-most EST	LIB3189-042-P1-K1-F2
Method	BLASTX
NCBI GI	g116343
BLAST score	483
E value	5.0e-48
Match length	251
% identity	39
NCBI Description	BASIC ENDOCHITINASE PRECURSOR

Seq. No.	191289
Contig ID	2144_1.R1039
5'-most EST	LIB3048-026-Q1-L1-A8

Seq. No.	191290
Contig ID	2148_1.R1039
5'-most EST	LIB3048-026-Q1-L1-B11
Method	BLASTX
NCBI GI	g2252830
BLAST score	240
E value	3.0e-20
Match length	80
% identity	61
NCBI Description	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]

Seq. No.	191291
Contig ID	2153_1.R1039
5'-most EST	LIB3166-045-P1-K1-D12
Method	BLASTX
NCBI GI	g4115377
BLAST score	567
E value	3.0e-58
Match length	160
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	191292
Contig ID	2168_1.R1039
5'-most EST	LIB3272-022-P1-K1-D9
Method	BLASTX
NCBI GI	g1840045
BLAST score	177
E value	2.0e-12
Match length	169
% identity	30
NCBI Description	(U49082) transporter protein [Homo sapiens]

Seq. No.	191293
Contig ID	2168_2.R1039
5'-most EST	uC-gsflnu33B037b06b1

Seq. No.	191294
Contig ID	2175_1.R1039
5'-most EST	LIB3149-053-Q1-K1-D3
Method	BLASTX
NCBI GI	g3790102
BLAST score	1635
E value	0.0e+00
Match length	341
% identity	92
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	191295
Contig ID	2175_2.R1039
5'-most EST	LIB3048-026-Q1-L1-D6
Method	BLASTX
NCBI GI	g2499488
BLAST score	1012
E value	1.0e-110
Match length	206
% identity	90
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi|483547|emb|CAA83682| (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	191296
Contig ID	2183_1.R1039
5'-most EST	g3326570
Method	BLASTX
NCBI GI	g1362066
BLAST score	806
E value	5.0e-93
Match length	199
% identity	89
NCBI Description	small GTP-binding protein - garden pea >gi|871510|emb|CAA90080| (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	191297
Contig ID	2195_1.R1039
5'-most EST	LIB3048-026-Q1-L1-F3
Method	BLASTX
NCBI GI	g3033377
BLAST score	201
E value	1.0e-15
Match length	98
% identity	44
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No. 191298
Contig ID 2204_1.R1039
5'-most EST LIB3149-023-Q1-K1-E12

Seq. No. 191299
Contig ID 2208_1.R1039
5'-most EST LIB3048-026-Q1-L1-G5
Method BLASTX
NCBI GI g3687230
BLAST score 479
E value 3.0e-48
Match length 132
% identity 72
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 191300
Contig ID 2211_1.R1039
5'-most EST uC-gsflmaxxa040b01b1
Method BLASTX
NCBI GI g4388533
BLAST score 393
E value 7.0e-38
Match length 85
% identity 93
NCBI Description (Y15178) F1-ATP synthase, beta subunit [Sorghum bicolor]

Seq. No. 191301
Contig ID 2219_1.R1039
5'-most EST g5046386
Method BLASTX
NCBI GI g3219912
BLAST score 157
E value 4.0e-14
Match length 144
% identity 32
NCBI Description HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II >gi|2239244|emb|CAB10162| (Z97211) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 191302
Contig ID 2234_1.R1039
5'-most EST LIB3048-027-Q1-L1-A7
Method BLASTX
NCBI GI g3790587
BLAST score 518
E value 8.0e-53
Match length 131
% identity 73
NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No. 191303
Contig ID 2241_1.R1039
5'-most EST LIB3048-053-Q1-L1-F4
Method BLASTX
NCBI GI g4455225

BLAST score 736
E value 3.0e-78
Match length 163
% identity 78
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 191304
Contig ID 2242_1.R1039
5'-most EST g3325893
Method BLASTX
NCBI GI g3600060
BLAST score 233
E value 2.0e-21
Match length 94
% identity 59
NCBI Description (AF080120) contains similarity to protein kinases (Pfam: pkinase.hmm, score: 24.94) [Arabidopsis thaliana]

Seq. No. 191305
Contig ID 2243_1.R1039
5'-most EST LIB3272-019-P1-K1-C4

Seq. No. 191306
Contig ID 2247_1.R1039
5'-most EST LIB3048-027-Q1-L1-B8
Method BLASTX
NCBI GI g3426037
BLAST score 311
E value 2.0e-28
Match length 122
% identity 28
NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 191307
Contig ID 2248_1.R1039
5'-most EST LIB3048-027-Q1-L1-C1
Method BLASTX
NCBI GI g130828
BLAST score 394
E value 3.0e-38
Match length 122
% identity 65
NCBI Description PATHOGENESIS-RELATED PROTEIN 1C PRECURSOR (PR-1C) >gi|2119762|pir||C24620 pathogenesis-related protein 1c precursor - common tobacco >gi|19958|emb|CAA35666| (X17681) pathogenesis-related protein 1b (AA 1-168) [Nicotiana tabacum]

Seq. No. 191308
Contig ID 2249_1.R1039
5'-most EST uC-gsronu33B002e12b1
Method BLASTX
NCBI GI g1304227
BLAST score 509
E value 1.0e-51
Match length 140

% identity	64
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi|2764804|emb|CAA55293| (X78547) epoxide hydrolase [Glycine max]

Seq. No.	191309
Contig ID	2252_1.R1039
5'-most EST	LIB3189-003-P1-K1-G11
Method	BLASTX
NCBI GI	g126894
BLAST score	468
E value	9.0e-47
Match length	113
% identity	83
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi|319832|pir||DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi|167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris]

Seq. No.	191310
Contig ID	2253_1.R1039
5'-most EST	LIB3048-027-Q1-L1-C3
Method	BLASTX
NCBI GI	g1255951
BLAST score	472
E value	2.0e-47
Match length	113
% identity	78
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	191311
Contig ID	2259_1.R1039
5'-most EST	LIB3120-024-Q1-K1-B2
Method	BLASTX
NCBI GI	g2961372
BLAST score	1238
E value	1.0e-136
Match length	238
% identity	95
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi|3036817|emb|CAA18507| (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	191312
Contig ID	2259_2.R1039
5'-most EST	LIB3165-028-P1-K1-H10
Method	BLASTX
NCBI GI	g2961372
BLAST score	1274
E value	1.0e-141
Match length	249
% identity	93
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi|3036817|emb|CAA18507| (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	191313
Contig ID	2259_3.R1039
5'-most EST	LIB3149-002-P1-K2-C6
Method	BLASTX
NCBI GI	g4406816
BLAST score	189
E value	3.0e-14
Match length	38
% identity	92
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	191314
Contig ID	2267_1.R1039
5'-most EST	LIB3165-060-Q1-K1-F12
Method	BLASTX
NCBI GI	g729668
BLAST score	361
E value	3.0e-34
Match length	109
% identity	70
NCBI Description	HISTONE H1 >gi|2147479|pir||S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi|436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No.	191315
Contig ID	2288_1.R1039
5'-most EST	LIB3048-027-Q1-L1-F3
Method	BLASTX
NCBI GI	g2388585
BLAST score	388
E value	2.0e-73
Match length	215
% identity	75
NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb|U88169). [Arabidopsis thaliana]

Seq. No.	191316
Contig ID	2297_1.R1039
5'-most EST	LIB3083-006-Q1-L1-H9
Method	BLASTX
NCBI GI	g2286153
BLAST score	1527
E value	1.0e-170
Match length	331
% identity	89
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	191317
Contig ID	2297_3.R1039
5'-most EST	LIB3189-052-P1-K1-D5
Method	BLASTX
NCBI GI	g2286153
BLAST score	527
E value	7.0e-54
Match length	109
% identity	96
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 191318
Contig ID 2307_1.R1039
5'-most EST LIB3048-030-Q1-L1-D1
Method BLASTX
NCBI GI g4263709
BLAST score 202
E value 8.0e-16
Match length 48
% identity 73
NCBI Description (AC006223) unknown protein [Arabidopsis thaliana]

Seq. No. 191319
Contig ID 2309_1.R1039
5'-most EST LIB3048-029-Q1-L1-C6
Method BLASTX
NCBI GI g2316016
BLAST score 356
E value 8.0e-34
Match length 125
% identity 31
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 191320
Contig ID 2310_1.R1039
5'-most EST LIB3146-051-Q1-K1-E10

Seq. No. 191321
Contig ID 2310_3.R1039
5'-most EST LIB3048-042-Q1-L1-E12

Seq. No. 191322
Contig ID 2311_1.R1039
5'-most EST LIB3048-027-Q1-L1-H3
Method BLASTX
NCBI GI g2462756
BLAST score 443
E value 5.0e-44
Match length 136
% identity 68
NCBI Description (AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 191323
Contig ID 2316_1.R1039
5'-most EST LIB3048-027-Q1-L1-H9
Method BLASTX
NCBI GI g2213619
BLAST score 258
E value 6.0e-22
Match length 159
% identity 41
NCBI Description (AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No. 191324
Contig ID 2321_1.R1039
5'-most EST LIB3048-054-Q1-L1-F2
Method BLASTX

NCBI GI g3264767
BLAST score 258
E value 2.0e-22
Match length 138
% identity 41
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 191325
Contig ID 2322_2.R1039
5'-most EST LIB3145-046-Q1-K1-B3
Method BLASTX
NCBI GI g2648032
BLAST score 808
E value 1.0e-122
Match length 236
% identity 82
NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 191326
Contig ID 2330_1.R1039
5'-most EST uC-gsflnu33B126b09b1
Method BLASTX
NCBI GI g4580575
BLAST score 600
E value 2.0e-62
Match length 155
% identity 72
NCBI Description (AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No. 191327
Contig ID 2332_1.R1039
5'-most EST LIB3048-028-Q1-L1-B3
Method BLASTX
NCBI GI g2194118
BLAST score 202
E value 9.0e-16
Match length 97
% identity 40
NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No. 191328
Contig ID 2340_1.R1039
5'-most EST LIB3048-028-Q1-L1-C11
Method BLASTX
NCBI GI g2435511
BLAST score 292
E value 3.0e-26
Match length 83
% identity 69
NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No. 191329
Contig ID 2342_1.R1039
5'-most EST LIB3272-016-P1-K1-A2
Method BLASTX
NCBI GI g3128209

BLAST score 659
E value 4.0e-69
Match length 169
% identity 39
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 191330
Contig ID 2343_1.R1039
5'-most EST LIB3048-043-Q1-L2-C8
Method BLASTX
NCBI GI g2943792
BLAST score 1162
E value 1.0e-128
Match length 272
% identity 76
NCBI Description (AB006809) PV72 [Cucurbita sp.]

Seq. No. 191331
Contig ID 2345_1.R1039
5'-most EST LIB3197-053-Q1-M1-H5
Method BLASTX
NCBI GI g2462762
BLAST score 818
E value 2.0e-88
Match length 281
% identity 63
NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 191332
Contig ID 2345_2.R1039
5'-most EST LIB3165-048-Q1-K1-G9
Method BLASTX
NCBI GI g2462762
BLAST score 482
E value 3.0e-60
Match length 193
% identity 65
NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 191333
Contig ID 2350_1.R1039
5'-most EST LIB3048-028-Q1-L1-D10
Method BLASTX
NCBI GI g4337189
BLAST score 662
E value 2.0e-69
Match length 187
% identity 70
NCBI Description (AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 191334
Contig ID 2351_1.R1039
5'-most EST LIB3272-045-P1-K1-D1
Method BLASTX

NCBI GI	g1199778
BLAST score	566
E value	4.0e-58
Match length	170
% identity	67
NCBI Description	(D83225) peroxidase [Populus nigra]

Seq. No.	191335
Contig ID	2351_2.R1039
5'-most EST	uC-gsronu33B171e12b1
Method	BLASTX
NCBI GI	g1279654
BLAST score	971
E value	1.0e-105
Match length	268
% identity	74
NCBI Description	(X97351) peroxidase [Populus balsamifera subsp. trichocarpa]

Seq. No.	191336
Contig ID	2353_1.R1039
5'-most EST	LIB3048-039-Q1-L1-E10

Seq. No.	191337
Contig ID	2354_1.R1039
5'-most EST	LIB3120-024-Q1-K1-A4
Method	BLASTX
NCBI GI	g2244792
BLAST score	1832
E value	0.0e+00
Match length	406
% identity	83
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	191338
Contig ID	2358_1.R1039
5'-most EST	LIB3048-052-Q1-L1-A11
Method	BLASTN
NCBI GI	g1658192
BLAST score	39
E value	2.0e-12
Match length	171
% identity	81
NCBI Description	Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51 (CYP51) mRNA, complete cds

Seq. No.	191339
Contig ID	2359_1.R1039
5'-most EST	LIB3120-043-P1-K1-F11
Method	BLASTX
NCBI GI	g3128168
BLAST score	286
E value	2.0e-25
Match length	112
% identity	47
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 191340
Contig ID 2376_1.R1039
5'-most EST LIB3048-036-Q1-L1-F3

Seq. No. 191341
Contig ID 2377_1.R1039
5'-most EST LIB3048-040-Q1-L1-A7

Seq. No. 191342
Contig ID 2377_2.R1039
5'-most EST LIB3272-002-P1-K1-G8

Seq. No. 191343
Contig ID 2383_1.R1039
5'-most EST LIB3083-114-Q1-L1-E9
Method BLASTX
NCBI GI g3204101
BLAST score 144
E value 1.0e-08
Match length 108
% identity 31
NCBI Description (AJ006760) hypothetical protein [Cicer arietinum]

Seq. No. 191344
Contig ID 2386_1.R1039
5'-most EST LIB3146-030-Q1-K1-E10
Method BLASTX
NCBI GI g1408460
BLAST score 616
E value 4.0e-64
Match length 191
% identity 65
NCBI Description (U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No. 191345
Contig ID 2391_1.R1039
5'-most EST LIB3048-028-Q1-L1-G9
Method BLASTX
NCBI GI g1666096
BLAST score 271
E value 6.0e-24
Match length 103
% identity 53
NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No. 191346
Contig ID 2396_1.R1039
5'-most EST LIB3147-023-Q1-K1-A5
Method BLASTX
NCBI GI g1173223
BLAST score 713
E value 3.0e-75
Match length 159
% identity 87
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi|454848 (L28831) ribosomal

protein S11 [Glycine max]

Seq. No.	191347
Contig ID	2396_2.R1039
5'-most EST	LIB3147-022-Q1-K1-F2
Method	BLASTX
NCBI GI	g1173223
BLAST score	718
E value	8.0e-76
Match length	159
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi|454848 (L28831) ribosomal protein S11 [Glycine max]

Seq. No.	191348
Contig ID	2396_3.R1039
5'-most EST	uC-gsronu33B107d09b1
Method	BLASTX
NCBI GI	g1173223
BLAST score	480
E value	3.0e-48
Match length	99
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi|454848 (L28831) ribosomal protein S11 [Glycine max]

Seq. No.	191349
Contig ID	2409_1.R1039
5'-most EST	LIB3048-029-Q1-L1-A4

Seq. No.	191350
Contig ID	2423_1.R1039
5'-most EST	LIB3048-029-Q1-L1-B6
Method	BLASTX
NCBI GI	g3482933
BLAST score	375
E value	1.0e-50
Match length	144
% identity	70
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	191351
Contig ID	2428_1.R1039
5'-most EST	LIB3048-030-Q1-L1-B12
Method	BLASTX
NCBI GI	g398966
BLAST score	419
E value	4.0e-41
Match length	90
% identity	90
NCBI Description	4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16) >gi|541937|pir||PQ0772 4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL1B) - soybean (fragment) >gi|18520|emb|CAA49576| (X69955) 4-coumarate--CoA ligase [Glycine max]

Seq. No.	191352
Contig ID	2429_1.R1039
5'-most EST	LIB3135-008-Q1-K1-A3
Method	BLASTX
NCBI GI	g3746069
BLAST score	167
E value	2.0e-11
Match length	134
% identity	31
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	191353
Contig ID	2445_1.R1039
5'-most EST	LIB3272-020-P1-K1-H10
Method	BLASTX
NCBI GI	g3551954
BLAST score	480
E value	5.0e-48
Match length	217
% identity	43
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	191354
Contig ID	2446_1.R1039
5'-most EST	LIB3146-028-Q1-K1-A5
Method	BLASTX
NCBI GI	g3033400
BLAST score	1207
E value	1.0e-144
Match length	326
% identity	81
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	191355
Contig ID	2446_2.R1039
5'-most EST	uC-gsflmaxxa091g10b1
Method	BLASTX
NCBI GI	g4539423
BLAST score	597
E value	9.0e-62
Match length	151
% identity	83
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	191356
Contig ID	2457_1.R1039
5'-most EST	uC-gsflnu33B143e01b1
Method	BLASTX
NCBI GI	g2281631
BLAST score	364
E value	2.0e-34
Match length	223
% identity	43

NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	191357
Contig ID	2457_2.R1039
5'-most EST	LIB3149-029-Q1-K1-F9
Method	BLASTX
NCBI GI	g2467088
BLAST score	279
E value	1.0e-24
Match length	98
% identity	59
NCBI Description	(AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No.	191358
Contig ID	2458_1.R1039
5'-most EST	LIB3272-001-P1-K1-E6
Method	BLASTX
NCBI GI	g4510346
BLAST score	518
E value	1.0e-75
Match length	185
% identity	75
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191359
Contig ID	2470_1.R1039
5'-most EST	LIB3048-029-Q1-L1-F6
Method	BLASTX
NCBI GI	g1491615
BLAST score	300
E value	3.0e-36
Match length	173
% identity	53
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	191360
Contig ID	2475_1.R1039
5'-most EST	LIB3048-037-Q1-L1-C7
Method	BLASTX
NCBI GI	g3335341
BLAST score	171
E value	4.0e-12
Match length	41
% identity	85
NCBI Description	(AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No.	191361
Contig ID	2476_1.R1039
5'-most EST	LIB3048-029-Q1-L1-G11
Method	BLASTX
NCBI GI	g3337352
BLAST score	690
E value	2.0e-72
Match length	331
% identity	50

NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	191362
Contig ID	2477_1.R1039
5'-most EST	LIB3083-022-Q1-L1-D3
Method	BLASTX
NCBI GI	g3236238
BLAST score	762
E value	7.0e-81
Match length	285
% identity	59
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi|4519792|dbj|BAA75744.1| (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	191363
Contig ID	2482_1.R1039
5'-most EST	LIB3048-029-Q1-L1-G8
Method	BLASTX
NCBI GI	g2275204
BLAST score	215
E value	3.0e-17
Match length	122
% identity	39
NCBI Description	(AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No.	191364
Contig ID	2483_1.R1039
5'-most EST	g5048195
Method	BLASTX
NCBI GI	g3135274
BLAST score	830
E value	6.0e-89
Match length	292
% identity	55
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	191365
Contig ID	2484_1.R1039
5'-most EST	LIB3197-040-Q1-M1-E3
Method	BLASTX
NCBI GI	g2832623
BLAST score	531
E value	4.0e-54
Match length	134
% identity	73
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	191366
Contig ID	2491_1.R1039
5'-most EST	LIB3166-013-P1-K1-C2

Seq. No. 191367

Contig ID	2493_1.R1039
5'-most EST	LIB3048-051-Q1-L1-D4

Seq. No.	191368
Contig ID	2494_1.R1039
5'-most EST	LIB3048-039-Q1-L1-F5

Seq. No.	191369
Contig ID	2506_1.R1039
5'-most EST	g5050125
Method	BLASTX
NCBI GI	g3183217
BLAST score	294
E value	3.0e-26
Match length	157
% identity	39
NCBI Description	HYPOTHETICAL PROTEIN KIAA0103 >gi|285943|dbj|BAA03493| (D14659) KIAA0103 [Homo sapiens]

Seq. No.	191370
Contig ID	2513_1.R1039
5'-most EST	LIB3048-046-Q1-L1-H7

Seq. No.	191371
Contig ID	2516_1.R1039
5'-most EST	LIB3197-049-Q1-M1-A12
Method	BLASTX
NCBI GI	g4239845
BLAST score	812
E value	1.0e-113
Match length	229
% identity	89
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	191372
Contig ID	2516_2.R1039
5'-most EST	LIB3083-001-Q1-L2-B2
Method	BLASTX
NCBI GI	g4239845
BLAST score	558
E value	3.0e-57
Match length	143
% identity	76
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	191373
Contig ID	2516_4.R1039
5'-most EST	LIB3166-007-P1-K1-H11
Method	BLASTX
NCBI GI	g2224927
BLAST score	210
E value	2.0e-36
Match length	143
% identity	72
NCBI Description	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No.	191374
Contig ID	2517_1.R1039
5'-most EST	LIB3048-034-Q1-L1-B3

Seq. No.	191375
Contig ID	2521_1.R1039
5'-most EST	g5046242
Method	BLASTN
NCBI GI	g2996011
BLAST score	244
E value	1.0e-134
Match length	864
% identity	82
NCBI Description	Leavenworthia crassa cytosolic phosphoglucose isomerase mRNA, complete cds

Seq. No.	191376
Contig ID	2522_1.R1039
5'-most EST	LIB3166-043-P1-K1-B4
Method	BLASTX
NCBI GI	g4220533
BLAST score	692
E value	7.0e-73
Match length	220
% identity	65
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	191377
Contig ID	2525_1.R1039
5'-most EST	LIB3146-019-Q1-K1-C11
Method	BLASTX
NCBI GI	g1703380
BLAST score	932
E value	1.0e-101
Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR >gi|1132483|dbj|BAA04607| (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	191378
Contig ID	2525_2.R1039
5'-most EST	uC-gsflnu33B088a07b1
Method	BLASTX
NCBI GI	g4056469
BLAST score	928
E value	1.0e-100
Match length	180
% identity	99
NCBI Description	(AC005990) Strong similarity to gb|M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb|Z25826, gb|R90191, gb|N65697, gb|AA713150, gb|T46332, gb|AA040967, gb|AA712956, gb|T46403, gb|T46050, gb|AI100391 and gb|Z25043 come from t

Seq. No.	191379
Contig ID	2525_4.R1039

5'-most EST	LIB3189-015-P1-K1-G11
Method	BLASTX
NCBI GI	g1703380
BLAST score	932
E value	1.0e-101
Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR >gi|1132483|dbj|BAA04607| (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	191380
Contig ID	2525_5.R1039
5'-most EST	g5047018
Method	BLASTX
NCBI GI	g1703380
BLAST score	919
E value	2.0e-99
Match length	181
% identity	97
NCBI Description	ADP-RIBOSYLATION FACTOR >gi|1132483|dbj|BAA04607| (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	191381
Contig ID	2525_6.R1039
5'-most EST	LIB3083-089-Q1-L1-D12
Method	BLASTX
NCBI GI	g1703380
BLAST score	685
E value	7.0e-72
Match length	177
% identity	69
NCBI Description	ADP-RIBOSYLATION FACTOR >gi|1132483|dbj|BAA04607| (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	191382
Contig ID	2525_8.R1039
5'-most EST	LIB3189-041-P1-K1-E11
Method	BLASTX
NCBI GI	g1703375
BLAST score	430
E value	2.0e-51
Match length	112
% identity	87
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|965483|dbj|BAA08259| (D45420) DcARF1 [Daucus carota]

Seq. No.	191383
Contig ID	2525_9.R1039
5'-most EST	LIB3083-076-Q1-L1-B2
Method	BLASTX
NCBI GI	g1703375
BLAST score	585
E value	1.0e-60
Match length	115
% identity	98
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|965483|dbj|BAA08259| (D45420) DcARF1 [Daucus carota]

Seq. No.	191384
Contig ID	2525_10.R1039
5'-most EST	uC-gsflmaxxa041f11b1
Method	BLASTX
NCBI GI	g543841
BLAST score	929
E value	1.0e-100
Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|322518|pir||S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi|166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi|2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	191385
Contig ID	2525_11.R1039
5'-most EST	uC-gsflnu33B130c03b1
Method	BLASTX
NCBI GI	g2689631
BLAST score	805
E value	4.0e-86
Match length	156
% identity	100
NCBI Description	(AF022389) ADP-ribosylation factor [Vigna unguiculata]

Seq. No.	191386
Contig ID	2525_12.R1039
5'-most EST	uC-gsronu33B132b02b1
Method	BLASTX
NCBI GI	g4056469
BLAST score	615
E value	3.0e-64
Match length	120
% identity	100
NCBI Description	(AC005990) Strong similarity to gb|M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb|Z25826, gb|R90191, gb|N65697, gb|AA713150, gb|T46332, gb|AA040967, gb|AA712956, gb|T46403, gb|T46050, gb|AI100391 and gb|Z25043 come from t

Seq. No.	191387
Contig ID	2525_13.R1039
5'-most EST	LIB3120-011-Q1-K1-G1
Method	BLASTX
NCBI GI	g1703375
BLAST score	336
E value	8.0e-34
Match length	89
% identity	92
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|965483|dbj|BAA08259| (D45420) DcARF1 [Daucus carota]

Seq. No.	191388
Contig ID	2525_14.R1039
5'-most EST	LIB3272-017-P1-K1-D6

Method	BLASTX
NCBI GI	g4056469
BLAST score	564
E value	3.0e-58
Match length	113
% identity	96
NCBI Description	(AC005990) Strong similarity to gb|M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb|Z25826, gb|R90191, gb|N65697, gb|AA713150, gb|T46332, gb|AA040967, gb|AA712956, gb|T46403, gb|T46050, gb|AI100391 and gb|Z25043 come from t

Seq. No.	191389
Contig ID	2525_15.R1039
5'-most EST	LIB3189-052-P1-K1-B9
Method	BLASTX
NCBI GI	g2689631
BLAST score	400
E value	1.0e-90
Match length	181
% identity	93
NCBI Description	(AF022389) ADP-ribosylation factor [Vigna unguiculata]

Seq. No.	191390
Contig ID	2525_18.R1039
5'-most EST	LIB3145-050-Q1-K1-D7
Method	BLASTX
NCBI GI	g1703375
BLAST score	466
E value	9.0e-47
Match length	90
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi|965483|dbj|BAA08259| (D45420) DcARF1 [Daucus carota]

Seq. No.	191391
Contig ID	2525_22.R1039
5'-most EST	uC-gsronu33B077f12b1
Method	BLASTX
NCBI GI	g2129946
BLAST score	358
E value	4.0e-34
Match length	71
% identity	100
NCBI Description	ADP-ribosylation factor homolog GTP-binding protein NTGB1 - common tobacco (fragment) >gi|1184987 (U46927) NTGB1 [Nicotiana tabacum]

Seq. No.	191392
Contig ID	2525_23.R1039
5'-most EST	uC-gsronu33B144g04b1
Method	BLASTX
NCBI GI	g2689631
BLAST score	285
E value	1.0e-25
Match length	58
% identity	100

NCBI Description	(AF022389) ADP-ribosylation factor [Vigna unguiculata]
Seq. No.	191393
Contig ID	2537_1.R1039
5'-most EST	uC-gsflmaxxa005c09b1
Seq. No.	191394
Contig ID	2537_2.R1039
5'-most EST	LIB3189-041-P1-K1-A6
Method	BLASTX
NCBI GI	g2244806
BLAST score	595
E value	4.0e-61
Match length	356
% identity	40
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	191395
Contig ID	2537_3.R1039
5'-most EST	LIB3165-017-P1-K1-B7
Seq. No.	191396
Contig ID	2537_4.R1039
5'-most EST	uC-gsronu33B116d04b1
Method	BLASTX
NCBI GI	g3786001
BLAST score	867
E value	4.0e-93
Match length	205
% identity	78
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	191397
Contig ID	2543_1.R1039
5'-most EST	LIB3048-033-Q1-L1-G2
Method	BLASTX
NCBI GI	g2944180
BLAST score	157
E value	1.0e-18
Match length	79
% identity	56
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]
Seq. No.	191398
Contig ID	2554_1.R1039
5'-most EST	LIB3165-022-P1-K1-C12
Method	BLASTX
NCBI GI	g231610
BLAST score	846
E value	7.0e-91
Match length	240
% identity	72
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi|67880|pir||PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi|19785|emb|CAA45152| (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No.	191399
Contig ID	2556_1.R1039
5'-most EST	uC-gsflmaxxa090d08b1
Method	BLASTX
NCBI GI	g3929333
BLAST score	466
E value	3.0e-46
Match length	227
% identity	44
NCBI Description	CYTOCHROME P450 76B1 (7-ETHOXYCOUMARIN O-DEETHYLASE) (ECOD) (PHENYLUREA DEALKYLASE) >gi|2370230|emb|CAA71054| (Y09920) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq. No.	191400
Contig ID	2558_1.R1039
5'-most EST	LIB3048-030-Q1-L1-F3
Method	BLASTX
NCBI GI	g4531442
BLAST score	683
E value	5.0e-72
Match length	172
% identity	77
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191401
Contig ID	2560_1.R1039
5'-most EST	LIB3048-030-Q1-L1-F5
Method	BLASTX
NCBI GI	g4038056
BLAST score	154
E value	1.0e-18
Match length	121
% identity	44
NCBI Description	(AC005897) putative transposon [Arabidopsis thaliana]

Seq. No.	191402
Contig ID	2571_1.R1039
5'-most EST	LIB3048-030-Q1-L1-G5
Method	BLASTX
NCBI GI	g1351856
BLAST score	587
E value	1.0e-60
Match length	122
% identity	92
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi|868003|dbj|BAA06108| (D29629) aconitase [Cucurbita sp.]

Seq. No.	191403
Contig ID	2586_1.R1039
5'-most EST	LIB3048-036-Q1-L1-A2
Method	BLASTX
NCBI GI	g4239845
BLAST score	632
E value	1.0e-65

Match length	274
% identity	50
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	191404
Contig ID	2596_1.R1039
5'-most EST	LIB3048-042-Q1-L1-D7
Method	BLASTX
NCBI GI	g3297816
BLAST score	576
E value	2.0e-59
Match length	160
% identity	70
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	191405
Contig ID	2600_1.R1039
5'-most EST	LIB3048-031-Q1-L1-B11
Method	BLASTX
NCBI GI	g3152559
BLAST score	626
E value	5.0e-65
Match length	182
% identity	65
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	191406
Contig ID	2608_1.R1039
5'-most EST	LIB3166-024-P1-K1-B2
Method	BLASTX
NCBI GI	g2959767
BLAST score	429
E value	2.0e-42
Match length	114
% identity	75
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi|3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	191407
Contig ID	2612_2.R1039
5'-most EST	LIB3048-032-Q1-L1-C12
Method	BLASTX
NCBI GI	g3426043
BLAST score	745
E value	4.0e-79
Match length	237
% identity	63
NCBI Description	(AC005168) putative choline kinase [Arabidopsis thaliana]

Seq. No.	191408
Contig ID	2614_1.R1039
5'-most EST	LIB3272-011-P1-K1-C12
Method	BLASTX
NCBI GI	g3094012

BLAST score	367
E value	6.0e-35
Match length	75
% identity	87
NCBI Description	(AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No.	191409
Contig ID	2614_2.R1039
5'-most EST	g5049461
Method	BLASTX
NCBI GI	g117988
BLAST score	573
E value	5.0e-59
Match length	111
% identity	95
NCBI Description	CYTOCHROME C >gi|65503|pir||CCCN cytochrome c - sea-island cotton

Seq. No.	191410
Contig ID	2614_4.R1039
5'-most EST	LIB3147-040-Q1-K1-E6
Method	BLASTX
NCBI GI	g117952
BLAST score	571
E value	6.0e-59
Match length	111
% identity	94
NCBI Description	CYTOCHROME C >gi|65504|pir||CCAB cytochrome c - China jute

Seq. No.	191411
Contig ID	2624_1.R1039
5'-most EST	LIB3048-031-Q1-L1-D12

Seq. No.	191412
Contig ID	2637_1.R1039
5'-most EST	uC-gsflnu33B107d12b1

Seq. No.	191413
Contig ID	2638_1.R1039
5'-most EST	LIB3083-052-Q1-L1-F8
Method	BLASTX
NCBI GI	g4191778
BLAST score	549
E value	6.0e-59
Match length	180
% identity	67
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	191414
Contig ID	2641_1.R1039
5'-most EST	LIB3048-031-Q1-L1-F1

Seq. No.	191415
Contig ID	2643_1.R1039
5'-most EST	g3326354
Method	BLASTX

NCBI GI	g1906830
BLAST score	1193
E value	1.0e-131
Match length	290
% identity	80
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	191416
Contig ID	2646_1.R1039
5'-most EST	LIB3048-031-Q1-L1-F5
Method	BLASTX
NCBI GI	g1742951
BLAST score	194
E value	8.0e-15
Match length	45
% identity	89
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	191417
Contig ID	2657_1.R1039
5'-most EST	LIB3048-047-Q1-L1-F8
Method	BLASTX
NCBI GI	g1710401
BLAST score	1009
E value	1.0e-110
Match length	210
% identity	88
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi|1044912|emb|CAA63194| (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	191418
Contig ID	2663_1.R1039
5'-most EST	LIB3048-052-Q1-L1-G5
Method	BLASTN
NCBI GI	g167336
BLAST score	145
E value	9.0e-76
Match length	333
% identity	86
NCBI Description	Gossypium hirsutum Lea4-A gene, complete CDS

Seq. No.	191419
Contig ID	2668_1.R1039
5'-most EST	LIB3048-031-Q1-L1-H5
Method	BLASTX
NCBI GI	g3928083
BLAST score	322
E value	8.0e-30
Match length	117
% identity	53
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	191420
Contig ID	2670_1.R1039
5'-most EST	g5048769

Seq. No.	191421
Contig ID	2677_1.R1039
5'-most EST	LIB3165-053-Q1-K1-G1
Method	BLASTX
NCBI GI	g232031
BLAST score	613
E value	2.0e-63
Match length	222
% identity	57
NCBI Description	ELONGATION FACTOR 1 BETA' >gi|322851|pir||S29224 translation elongation factor eEF-1 beta' chain - rice >gi|218161|dbj|BAA02253| (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	191422
Contig ID	2691_1.R1039
5'-most EST	LIB3048-034-Q1-L1-C1

Seq. No.	191423
Contig ID	2696_1.R1039
5'-most EST	LIB3048-054-Q1-L1-C7
Method	BLASTX
NCBI GI	g3025188
BLAST score	293
E value	2.0e-26
Match length	85
% identity	61
NCBI Description	HYPOTHETICAL 11.9 KD PROTEIN SLR1846 >gi|1652154|dbj|BAA17078| (D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	191424
Contig ID	2697_1.R1039
5'-most EST	LIB3165-004-P1-K1-A1
Method	BLASTX
NCBI GI	g3746060
BLAST score	370
E value	4.0e-35
Match length	121
% identity	61
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.	191425
Contig ID	2704_1.R1039
5'-most EST	LIB3048-032-Q1-L1-C9

Seq. No.	191426
Contig ID	2709_1.R1039
5'-most EST	LIB3165-057-P1-K1-D10
Method	BLASTX
NCBI GI	g1931640
BLAST score	463
E value	3.0e-46
Match length	124
% identity	67
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis

thaliana]

Seq. No.	191427
Contig ID	2710_1.R1039
5'-most EST	LIB3272-052-P1-K1-E11
Method	BLASTX
NCBI GI	g4539292
BLAST score	461
E value	7.0e-46
Match length	95
% identity	88
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	191428
Contig ID	2724_1.R1039
5'-most EST	LIB3197-017-P1-M1-A10
Method	BLASTX
NCBI GI	g1174162
BLAST score	799
E value	2.0e-85
Match length	160
% identity	88
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi|3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	191429
Contig ID	2730_1.R1039
5'-most EST	LIB3048-042-Q1-L1-E9

Seq. No.	191430
Contig ID	2736_1.R1039
5'-most EST	LIB3048-032-Q1-L1-G10
Method	BLASTX
NCBI GI	g1929056
BLAST score	462
E value	2.0e-46
Match length	103
% identity	85
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	191431
Contig ID	2744_1.R1039
5'-most EST	LIB3197-016-P1-M1-H6
Method	BLASTX
NCBI GI	g1168256
BLAST score	523
E value	7.0e-54
Match length	118
% identity	84
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi|693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi|3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	191432
Contig ID	2749_1.R1039
5'-most EST	LIB3048-039-Q1-L1-E1
Method	BLASTX
NCBI GI	g2624383
BLAST score	386
E value	1.0e-62
Match length	143
% identity	78
NCBI Description	(Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]

Seq. No.	191433
Contig ID	2765_1.R1039
5'-most EST	LIB3189-052-P1-K1-H11
Method	BLASTX
NCBI GI	g2129955
BLAST score	462
E value	3.0e-46
Match length	120
% identity	68
NCBI Description	photoassimilate-responsive protein PAR-1b precursor - common tobacco >gi|871487|emb|CAA58731| (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No.	191434
Contig ID	2790_1.R1039
5'-most EST	LIB3048-033-Q1-L1-D5
Method	BLASTX
NCBI GI	g3702321
BLAST score	735
E value	4.0e-78
Match length	174
% identity	42
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	191435
Contig ID	2791_1.R1039
5'-most EST	LIB3189-032-P1-K1-A2
Method	BLASTX
NCBI GI	g4220481
BLAST score	153
E value	5.0e-17
Match length	107
% identity	45
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	191436
Contig ID	2796_1.R1039
5'-most EST	LIB3149-007-Q1-K1-A12
Method	BLASTX
NCBI GI	g1850546
BLAST score	830
E value	6.0e-89
Match length	254

% identity	69
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	191437
Contig ID	2796_2.R1039
5'-most EST	uC-gsflmaxxa038f04b1
Method	BLASTX
NCBI GI	g4107099
BLAST score	214
E value	4.0e-17
Match length	65
% identity	66
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi|4156245|dbj|BAA37112| (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	191438
Contig ID	2796_3.R1039
5'-most EST	uC-gsronu33B032e04b1
Method	BLASTX
NCBI GI	g1850546
BLAST score	310
E value	2.0e-28
Match length	124
% identity	59
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	191439
Contig ID	2796_4.R1039
5'-most EST	uC-gsronu33B057b11b1
Method	BLASTN
NCBI GI	g899121
BLAST score	43
E value	6.0e-15
Match length	91
% identity	87
NCBI Description	Arabidopsis thaliana syntaxin homologue mRNA, complete cds

Seq. No.	191440
Contig ID	2797_1.R1039
5'-most EST	uC-gsflmaxxa048a07b1
Method	BLASTX
NCBI GI	g2129578
BLAST score	773
E value	2.0e-82
Match length	211
% identity	75
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi|928932|emb|CAA89205| (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi|1585435|prf||2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	191441
Contig ID	2802_1.R1039

5'-most EST	LIB3048-033-Q1-L1-E6
Seq. No.	191442
Contig ID	2804_1.R1039
5'-most EST	LIB3083-113-Q1-L1-A7
Method	BLASTX
NCBI GI	g2813966
BLAST score	218
E value	3.0e-17
Match length	227
% identity	30
NCBI Description	(Z97053) placental protein Diff33 [Homo sapiens] >gi|4545219|gb|AAD22448.1| (AF112227) TDE homolog [Homo sapiens]
Seq. No.	191443
Contig ID	2804_2.R1039
5'-most EST	g3326165
Seq. No.	191444
Contig ID	2809_2.R1039
5'-most EST	LIB3048-033-Q1-L1-F4
Method	BLASTX
NCBI GI	g3288823
BLAST score	728
E value	6.0e-77
Match length	202
% identity	70
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]
Seq. No.	191445
Contig ID	2817_1.R1039
5'-most EST	LIB3048-036-Q1-L1-D8
Seq. No.	191446
Contig ID	2819_1.R1039
5'-most EST	LIB3048-033-Q1-L1-G11
Method	BLASTX
NCBI GI	g2997591
BLAST score	1384
E value	1.0e-153
Match length	362
% identity	75
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
Seq. No.	191447
Contig ID	2834_1.R1039
5'-most EST	LIB3145-008-Q1-K1-H7
Seq. No.	191448
Contig ID	2837_1.R1039
5'-most EST	LIB3145-034-Q1-K1-H12
Seq. No.	191449
Contig ID	2850_1.R1039
5'-most EST	LIB3048-039-Q1-L1-G4

Method	BLASTX
NCBI GI	g4455317
BLAST score	175
E value	1.0e-12
Match length	123
% identity	12
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	191450
Contig ID	2856_1.R1039
5'-most EST	LIB3048-034-Q1-L1-B7

Seq. No.	191451
Contig ID	2858_1.R1039
5'-most EST	uC-gsronu33B146g10b1
Method	BLASTX
NCBI GI	g4432860
BLAST score	793
E value	1.0e-84
Match length	262
% identity	16
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	191452
Contig ID	2866_1.R1039
5'-most EST	LIB3048-034-Q1-L1-C5
Method	BLASTX
NCBI GI	g3560264
BLAST score	168
E value	2.0e-11
Match length	102
% identity	38
NCBI Description	(AL031535) sol1 family protein [Schizosaccharomyces pombe]

Seq. No.	191453
Contig ID	2870_1.R1039
5'-most EST	LIB3048-034-Q1-L1-C9
Method	BLASTN
NCBI GI	g217844
BLAST score	41
E value	9.0e-14
Match length	97
% identity	86
NCBI Description	A.thaliana ATS1 gene for glycerol-3-phosphate acyltransferase

Seq. No.	191454
Contig ID	2888_1.R1039
5'-most EST	LIB3048-034-Q1-L1-F6
Method	BLASTX
NCBI GI	g3297816
BLAST score	577
E value	1.0e-59
Match length	141
% identity	80

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 191455
Contig ID 2907_1.R1039
5'-most EST LIB3048-034-Q1-L1-G4
Method BLASTX
NCBI GI g2129759
BLAST score 500
E value 1.0e-50
Match length 132
% identity 77
NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi|1143392|emb|CAA90941| (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No. 191456
Contig ID 2927_1.R1039
5'-most EST LIB3197-028-Q1-M1-E5
Method BLASTX
NCBI GI g4033424
BLAST score 626
E value 3.0e-65
Match length 162
% identity 74
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi|2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No. 191457
Contig ID 2930_1.R1039
5'-most EST LIB3196-034-P1-M1-H7
Method BLASTX
NCBI GI g464707
BLAST score 692
E value 9.0e-73
Match length 152
% identity 88
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi|480908|pir||S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi|405613|emb|CAA80684| (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi|434343|emb|CAA82273| (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi|434345|emb|CAA82274| (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi|434906|emb|CAA82275| (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi|2505871|emb|CAA72909| (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi|3287678 (AC003979) Match to ribosomal S18 gene mRNA gb|Z28701, DNA gb|Z23165 from A. thaliana. ESTs gb|T21121, gb|Z17755, gb|R64776 and gb|R30430 come from this gene. [Arabidopsis thaliana] >gi|4538910|emb|CAB39647.1| (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 191458
Contig ID 2930_2.R1039
5'-most EST uC-gsflnu33B028g09b1
Method BLASTX

NCBI GI	g464707
BLAST score	692
E value	8.0e-73
Match length	152
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi|480908|pir||S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi|405613|emb|CAA80684| (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi|434343|emb|CAA82273| (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi|434345|emb|CAA82274| (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi|434906|emb|CAA82275| (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi|2505871|emb|CAA72909| (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi|3287678 (AC003979) Match to ribosomal S18 gene mRNA gb|Z28701, DNA gb|Z23165 from A. thaliana. ESTs gb|T21121, gb|Z17755, gb|R64776 and gb|R30430 come from this gene. [Arabidopsis thaliana] >gi|4538910|emb|CAB39647.1| (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	191459
Contig ID	2930_3.R1039
5'-most EST	uC-gsflnu33B101h11b1
Method	BLASTX
NCBI GI	g464707
BLAST score	678
E value	2.0e-71
Match length	137
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi|480908|pir||S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi|405613|emb|CAA80684| (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi|434343|emb|CAA82273| (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi|434345|emb|CAA82274| (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi|434906|emb|CAA82275| (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi|2505871|emb|CAA72909| (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi|3287678 (AC003979) Match to ribosomal S18 gene mRNA gb|Z28701, DNA gb|Z23165 from A. thaliana. ESTs gb|T21121, gb|Z17755, gb|R64776 and gb|R30430 come from this gene. [Arabidopsis thaliana] >gi|4538910|emb|CAB39647.1| (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	191460
Contig ID	2939_1.R1039
5'-most EST	LIB3272-053-P1-K1-A5
Method	BLASTX
NCBI GI	g3913996
BLAST score	440
E value	2.0e-43
Match length	125
% identity	70
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi|2208927|dbj|BAA20482| (D85610) ATP-dependent protease

Lon [Spinacia oleracea]

Seq. No.	191461
Contig ID	2942_1.R1039
5'-most EST	LIB3048-035-Q1-L1-B8

Seq. No.	191462
Contig ID	2946_1.R1039
5'-most EST	LIB3197-045-Q1-M1-H1

Seq. No.	191463
Contig ID	2948_1.R1039
5'-most EST	LIB3048-035-Q1-L1-C2
Method	BLASTX
NCBI GI	g3559816
BLAST score	932
E value	1.0e-101
Match length	224
% identity	80
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	191464
Contig ID	2951_1.R1039
5'-most EST	LIB3048-042-Q1-L1-B12
Method	BLASTX
NCBI GI	g3445238
BLAST score	158
E value	1.0e-10
Match length	45
% identity	78
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana] >gi|3451059|emb|CAA20455.1| (AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	191465
Contig ID	2953_1.R1039
5'-most EST	LIB3048-050-Q1-L1-B5
Method	BLASTX
NCBI GI	g3367522
BLAST score	399
E value	7.0e-39
Match length	120
% identity	65
NCBI Description	(AC004392) EST gb|T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	191466
Contig ID	2958_1.R1039
5'-most EST	LIB3197-010-P1-M1-H5
Method	BLASTX
NCBI GI	g2104959
BLAST score	474
E value	2.0e-47
Match length	109
% identity	79
NCBI Description	(U96925) immunophilin [Vicia faba]

Seq. No.	191467
Contig ID	2958_2.R1039
5'-most EST	LIB3166-021-P1-K1-G5
Method	BLASTX
NCBI GI	g2507421
BLAST score	543
E value	2.0e-55
Match length	113
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191468
Contig ID	2958_3.R1039
5'-most EST	uC-gsflnu33B085c07b1
Method	BLASTX
NCBI GI	g2507421
BLAST score	542
E value	2.0e-55
Match length	113
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191469
Contig ID	2958_4.R1039
5'-most EST	LIB3145-037-Q1-K1-D6
Method	BLASTX
NCBI GI	g2507421
BLAST score	467
E value	1.0e-46
Match length	97
% identity	92
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191470
Contig ID	2958_5.R1039
5'-most EST	uC-gsronu33B143e05b1
Method	BLASTX
NCBI GI	g3334346
BLAST score	430
E value	2.0e-45
Match length	112
% identity	88
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|2852445|dbj|BAA24697| (AB003378) SUI1 homolog [Salix bakko]

Seq. No.	191471
Contig ID	2958_6.R1039

5'-most EST	LIB3135-035-Q1-K1-D4
Method	BLASTX
NCBI GI	g462195
BLAST score	482
E value	3.0e-48
Match length	113
% identity	84
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi|100682|pir||S21636 GOS2 protein - rice >gi|20238|emb|CAA36190| (X51910) GOS2 [Oryza sativa] >gi|3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	191472
Contig ID	2958_7.R1039
5'-most EST	LIB3147-050-Q1-K1-F5
Method	BLASTX
NCBI GI	g2507421
BLAST score	543
E value	2.0e-55
Match length	113
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191473
Contig ID	2958_9.R1039
5'-most EST	LIB3083-091-Q1-L1-A3
Method	BLASTX
NCBI GI	g2507421
BLAST score	538
E value	6.0e-55
Match length	113
% identity	92
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191474
Contig ID	2958_10.R1039
5'-most EST	LIB3146-046-Q1-K1-B7
Method	BLASTX
NCBI GI	g462195
BLAST score	293
E value	9.0e-29
Match length	100
% identity	71
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi|100682|pir||S21636 GOS2 protein - rice >gi|20238|emb|CAA36190| (X51910) GOS2 [Oryza sativa] >gi|3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	191475

Contig ID	2958_11.R1039
5'-most EST	uC-gsronu33B106a08b2
Method	BLASTX
NCBI GI	g2507421
BLAST score	336
E value	4.0e-46
Match length	116
% identity	91
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi|1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi|4490709|emb|CAB38843.1| (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	191476
Contig ID	2962_1.R1039
5'-most EST	uC-gsflnu33B085b08b1
Method	BLASTX
NCBI GI	g2342736
BLAST score	147
E value	3.0e-09
Match length	140
% identity	33
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	191477
Contig ID	2973_1.R1039
5'-most EST	LIB3048-042-Q1-L1-E4
Method	BLASTX
NCBI GI	g4262228
BLAST score	381
E value	1.0e-36
Match length	135
% identity	32
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	191478
Contig ID	2985_1.R1039
5'-most EST	uC-gsflmaxxa001d09b1
Method	BLASTX
NCBI GI	g4138109
BLAST score	781
E value	2.0e-83
Match length	209
% identity	75
NCBI Description	(AJ006414) spermidine synthase [Lycopersicon esculentum]

Seq. No.	191479
Contig ID	2987_1.R1039
5'-most EST	LIB3048-041-Q1-L1-F12

Seq. No.	191480
Contig ID	2988_1.R1039
5'-most EST	uC-gsronu33B153g10b2

Seq. No.	191481
Contig ID	2989_1.R1039

5'-most EST	uC-gsronu33B016g10b1
Method	BLASTX
NCBI GI	g3650032
BLAST score	274
E value	5.0e-24
Match length	60
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	191482
Contig ID	3000_1.R1039
5'-most EST	LIB3048-046-Q1-L1-D8

Seq. No.	191483
Contig ID	3011_1.R1039
5'-most EST	LIB3048-036-Q1-L1-A1

Seq. No.	191484
Contig ID	3015_1.R1039
5'-most EST	LIB3048-043-Q1-L1-F7
Method	BLASTX
NCBI GI	g3551425
BLAST score	196
E value	1.0e-14
Match length	182
% identity	32
NCBI Description	(AB015291) pyrrolidone carboxyl peptidase [Pyrococcus furiosus]

Seq. No.	191485
Contig ID	3017_1.R1039
5'-most EST	LIB3048-036-Q1-L1-A5
Method	BLASTX
NCBI GI	g3063465
BLAST score	266
E value	4.0e-27
Match length	137
% identity	56
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	191486
Contig ID	3019_1.R1039
5'-most EST	LIB3148-013-Q1-K1-D11
Method	BLASTX
NCBI GI	g586339
BLAST score	427
E value	7.0e-42
Match length	137
% identity	58
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi|626794|pir||S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi|536615|emb|CAA85185| (Z36091) ORF YBR222c [Saccharomyces cerevisiae]

Seq. No.	191487
Contig ID	3019_2.R1039

5'-most EST	LIB3048-036-Q1-L1-A7
Method	BLASTX
NCBI GI	g586339
BLAST score	155
E value	4.0e-21
Match length	95
% identity	53
NCBI Description	PEROXISOMAL-COENZYME A SYNTHETASE >gi|626794|pir||S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi|536615|emb|CAA85185| (Z36091) ORF YBR222c [Saccharomyces cerevisiae]

Seq. No.	191488
Contig ID	3030_1.R1039
5'-most EST	LIB3120-054-P1-K1-F7
Method	BLASTX
NCBI GI	g4006887
BLAST score	491
E value	1.0e-49
Match length	113
% identity	76
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	191489
Contig ID	3046_1.R1039
5'-most EST	LIB3048-036-Q1-L1-D5

Seq. No.	191490
Contig ID	3052_1.R1039
5'-most EST	uC-gsronu33B103e05b1
Method	BLASTX
NCBI GI	g416758
BLAST score	1881
E value	0.0e+00
Match length	483
% identity	72
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi|166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi|445120|prf||1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	191491
Contig ID	3081_1.R1039
5'-most EST	g3325734
Method	BLASTX
NCBI GI	g1709449
BLAST score	664
E value	1.0e-69
Match length	159
% identity	81
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi|1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No.	191492
Contig ID	3081_2.R1039
5'-most EST	LIB3165-033-P1-K1-F8

Method	BLASTX
NCBI GI	g2829869
BLAST score	1702
E value	0.0e+00
Match length	368
% identity	85
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	191493
Contig ID	3081_3.R1039
5'-most EST	uC-gsronu33B155b04b2
Method	BLASTX
NCBI GI	g1709446
BLAST score	382
E value	1.0e-36
Match length	92
% identity	80
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi|2117533|pir||JC4358 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi|710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	191494
Contig ID	3081_4.R1039
5'-most EST	uC-gsronu33B129a08b1
Method	BLASTN
NCBI GI	g710399
BLAST score	33
E value	6.0e-09
Match length	73
% identity	86
NCBI Description	Arabidopsis thaliana pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	191495
Contig ID	3090_1.R1039
5'-most EST	LIB3189-002-P1-K1-G9
Method	BLASTX
NCBI GI	g1421730
BLAST score	745
E value	6.0e-79
Match length	211
% identity	67
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	191496
Contig ID	3093_1.R1039
5'-most EST	LIB3083-107-Q1-L1-E5
Method	BLASTX
NCBI GI	g799177
BLAST score	635
E value	1.0e-65
Match length	536

% identity	22
NCBI Description	(U22055) 100 kDa coactivator [Homo sapiens]

Seq. No.	191497
Contig ID	3104_1.R1039
5'-most EST	uC-gsronu33B109f07b1
Method	BLASTX
NCBI GI	g1871194
BLAST score	162
E value	5.0e-11
Match length	94
% identity	48
NCBI Description	(U90439) DNA binding protein isolog [Arabidopsis thaliana] >gi|2335092 (AC002339) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	191498
Contig ID	3142_1.R1039
5'-most EST	LIB3189-043-P1-K1-B1
Method	BLASTX
NCBI GI	g3914430
BLAST score	1267
E value	1.0e-140
Match length	272
% identity	88
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi|2285800|dbj|BAA21650| (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No.	191499
Contig ID	3165_2.R1039
5'-most EST	LIB3048-037-Q1-L1-H11

Seq. No.	191500
Contig ID	3166_1.R1039
5'-most EST	LIB3048-043-Q1-L1-B8
Method	BLASTN
NCBI GI	g2351064
BLAST score	56
E value	5.0e-22
Match length	791
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	191501
Contig ID	3172_1.R1039
5'-most EST	LIB3048-038-Q1-L1-A10

Seq. No.	191502
Contig ID	3173_1.R1039
5'-most EST	g5046118
Method	BLASTX
NCBI GI	g1172555
BLAST score	764
E value	2.0e-81

Match length	170
% identity	84
NCBI Description	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi|629720|pir||S46936 34K porin - potato >gi|1076682|pir||A55364 porin (clone pPOM-34) - potato mitochondrion >gi|516166|emb|CAA56599| (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No.	191503
Contig ID	3173_2.R1039
5'-most EST	LIB3149-047-Q1-K1-A5
Method	BLASTN
NCBI GI	g4006940
BLAST score	34
E value	2.0e-09
Match length	70
% identity	87
NCBI Description	Arabidopsis thaliana mRNA for voltage-dependent anion-selective channel protein

Seq. No.	191504
Contig ID	3173_3.R1039
5'-most EST	LIB3272-032-P1-K1-D6
Method	BLASTX
NCBI GI	g1172555
BLAST score	477
E value	5.0e-48
Match length	105
% identity	87
NCBI Description	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi|629720|pir||S46936 34K porin - potato >gi|1076682|pir||A55364 porin (clone pPOM-34) - potato mitochondrion >gi|516166|emb|CAA56599| (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No.	191505
Contig ID	3179_1.R1039
5'-most EST	LIB3048-038-Q1-L1-A6
Method	BLASTX
NCBI GI	g2465923
BLAST score	154
E value	9.0e-10
Match length	143
% identity	43
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	191506
Contig ID	3181_1.R1039
5'-most EST	LIB3147-040-Q1-K1-G9
Method	BLASTX
NCBI GI	g1351722
BLAST score	240
E value	5.0e-20
Match length	125

% identity	41
NCBI Description	HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi|1122371|emb|CAA92386| (Z68198) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	191507
Contig ID	3188_1.R1039
5'-most EST	LIB3189-053-P1-K1-G2
Method	BLASTX
NCBI GI	g3152576
BLAST score	360
E value	4.0e-34
Match length	102
% identity	69
NCBI Description	(AC002986) Similar to liver-specific transport protein gb|L27651 from Rattus norviegicus. [Arabidopsis thaliana]
Seq. No.	191508
Contig ID	3210_2.R1039
5'-most EST	LIB3048-038-Q1-L1-D2
Seq. No.	191509
Contig ID	3211_1.R1039
5'-most EST	LIB3165-022-P1-K1-A4
Seq. No.	191510
Contig ID	3216_1.R1039
5'-most EST	LIB3166-019-P1-K1-G1
Method	BLASTX
NCBI GI	g4220537
BLAST score	400
E value	9.0e-39
Match length	109
% identity	74
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
Seq. No.	191511
Contig ID	3237_1.R1039
5'-most EST	g5047307
Method	BLASTX
NCBI GI	g2832623
BLAST score	352
E value	4.0e-33
Match length	211
% identity	40
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
Seq. No.	191512
Contig ID	3239_1.R1039
5'-most EST	LIB3048-038-Q1-L1-G2
Seq. No.	191513
Contig ID	3261_1.R1039
5'-most EST	LIB3272-007-P1-K1-F7
Method	BLASTX
NCBI GI	g4309889

BLAST score	161
E value	9.0e-11
Match length	137
% identity	31
NCBI Description	(AC004983) similar to PID:g3877944 [Homo sapiens]

Seq. No.	191514
Contig ID	3262_1.R1039
5'-most EST	LIB3048-039-Q1-L1-A2
Method	BLASTX
NCBI GI	g3461820
BLAST score	588
E value	1.0e-60
Match length	176
% identity	66
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	191515
Contig ID	3264_1.R1039
5'-most EST	LIB3048-039-Q1-L1-A4
Method	BLASTX
NCBI GI	g4210451
BLAST score	160
E value	1.0e-10
Match length	66
% identity	56
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No.	191516
Contig ID	3271_1.R1039
5'-most EST	g3326656
Method	BLASTX
NCBI GI	g2499710
BLAST score	418
E value	8.0e-41
Match length	116
% identity	73
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi|1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No.	191517
Contig ID	3271_2.R1039
5'-most EST	LIB3165-022-P1-K1-B7
Method	BLASTN
NCBI GI	g1438074
BLAST score	619
E value	0.0e+00
Match length	1750
% identity	84
NCBI Description	Ricinus communis phospholipase D mRNA, complete cds

Seq. No.	191518
Contig ID	3271_3.R1039
5'-most EST	LIB3147-037-Q1-K1-F5
Method	BLASTX
NCBI GI	g2499710

BLAST score 3010
E value 0.0e+00
Match length 621
% identity 88
NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi|1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 191519
Contig ID 3276_1.R1039
5'-most EST g5047241
Method BLASTX
NCBI GI g2052383
BLAST score 1202
E value 1.0e-132
Match length 244
% identity 85
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]

Seq. No. 191520
Contig ID 3280_1.R1039
5'-most EST LIB3048-039-Q1-L1-C1
Method BLASTX
NCBI GI g3342913
BLAST score 419
E value 2.0e-83
Match length 381
% identity 46
NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]

Seq. No. 191521
Contig ID 3288_1.R1039
5'-most EST uC-gsronu33B168d03b1

Seq. No. 191522
Contig ID 3291_1.R1039
5'-most EST LIB3048-039-Q1-L1-E3
Method BLASTX
NCBI GI g2618721
BLAST score 811
E value 1.0e-86
Match length 226
% identity 73
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 191523
Contig ID 3291_2.R1039
5'-most EST LIB3147-013-Q1-K1-C12
Method BLASTX
NCBI GI g2618721
BLAST score 411
E value 1.0e-44
Match length 107
% identity 87
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 191524

Contig ID	3332_1.R1039
5'-most EST	LIB3048-055-Q1-L1-E8
Method	BLASTX
NCBI GI	g4008037
BLAST score	250
E value	2.0e-21
Match length	131
% identity	44
NCBI Description	(AF104925) 2-oxoglutarate-dependent dioxygenase [Solanum chacoense]

Seq. No.	191525
Contig ID	3346_2.R1039
5'-most EST	LIB3148-058-Q1-K1-C12
Method	BLASTN
NCBI GI	g4455189
BLAST score	38
E value	9.0e-12
Match length	90
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSAII project)

Seq. No.	191526
Contig ID	3347_1.R1039
5'-most EST	LIB3048-040-Q1-L1-A1
Method	BLASTX
NCBI GI	g629561
BLAST score	407
E value	2.0e-47
Match length	262
% identity	43
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi|479047|emb|CAA55654| (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	191527
Contig ID	3353_1.R1039
5'-most EST	LIB3048-053-Q1-L1-C5
Method	BLASTN
NCBI GI	g1865678
BLAST score	40
E value	4.0e-13
Match length	72
% identity	89
NCBI Description	A.thaliana ATB2 gene

Seq. No.	191528
Contig ID	3353_2.R1039
5'-most EST	uC-gsflmaxxa001g10b1
Method	BLASTN
NCBI GI	g1865678
BLAST score	48
E value	7.0e-18
Match length	68
% identity	93
NCBI Description	A.thaliana ATB2 gene

Seq. No.	191529
Contig ID	3364_1.R1039
5'-most EST	LIB3146-022-Q1-K1-A1
Method	BLASTX
NCBI GI	g3281851
BLAST score	317
E value	7.0e-29
Match length	142
% identity	38
NCBI Description	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]

Seq. No.	191530
Contig ID	3397_1.R1039
5'-most EST	uC-gsronu33B156a08b1
Method	BLASTX
NCBI GI	g4160579
BLAST score	196
E value	1.0e-14
Match length	137
% identity	32
NCBI Description	(AL035218) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	191531
Contig ID	3399_1.R1039
5'-most EST	LIB3048-040-Q1-L1-F2
Method	BLASTX
NCBI GI	g1381676
BLAST score	259
E value	3.0e-22
Match length	57
% identity	89
NCBI Description	(U58853) small GTP-binding protein [Glycine max]

Seq. No.	191532
Contig ID	3416_1.R1039
5'-most EST	LIB3048-040-Q1-L1-H2
Method	BLASTX
NCBI GI	g3269287
BLAST score	359
E value	6.0e-34
Match length	195
% identity	43
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	191533
Contig ID	3440_1.R1039
5'-most EST	LIB3048-054-Q1-L1-B7
Method	BLASTX
NCBI GI	g2944187
BLAST score	124
E value	8.0e-11
Match length	119
% identity	39
NCBI Description	(AF011336) putative E1-E2 ATPase [Mus musculus]

Seq. No.	191534
Contig ID	3444_1.R1039
5'-most EST	LIB3048-041-Q1-L1-C11
Method	BLASTX
NCBI GI	g2499553
BLAST score	493
E value	1.0e-54
Match length	134
% identity	77
NCBI Description	CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi|629524|pir||S39058 probable deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi|442529|bbs|139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa] [Arabidopsis thaliana]

Seq. No.	191535
Contig ID	3456_1.R1039
5'-most EST	LIB3048-041-Q1-L1-D12
Method	BLASTX
NCBI GI	g629592
BLAST score	302
E value	3.0e-27
Match length	125
% identity	50
NCBI Description	hypothetical protein - rape

Seq. No.	191536
Contig ID	3468_1.R1039
5'-most EST	LIB3048-052-Q1-L1-C8

Seq. No.	191537
Contig ID	3474_1.R1039
5'-most EST	LIB3048-041-Q1-L1-F10

Seq. No.	191538
Contig ID	3489_1.R1039
5'-most EST	g3326032

Seq. No.	191539
Contig ID	3489_2.R1039
5'-most EST	uC-gsflmaxxa088e01b1

Seq. No.	191540
Contig ID	3498_1.R1039
5'-most EST	g5048105
Method	BLASTX
NCBI GI	g2833375
BLAST score	356
E value	2.0e-33
Match length	71
% identity	93
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi|533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No.	191541
Contig ID	3498_2.R1039
5'-most EST	LIB3166-016-P1-K1-G9
Method	BLASTX
NCBI GI	g2833375
BLAST score	353
E value	2.0e-33
Match length	71
% identity	92
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi|533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	191542
Contig ID	3498_3.R1039
5'-most EST	uC-gsronu33B179g11b1
Method	BLASTX
NCBI GI	g2833375
BLAST score	176
E value	1.0e-12
Match length	39
% identity	87
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi|533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	191543
Contig ID	3498_5.R1039
5'-most EST	LIB3048-041-Q1-L1-H4
Method	BLASTX
NCBI GI	g4204281
BLAST score	257
E value	6.0e-22
Match length	75
% identity	65
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	191544
Contig ID	3498_6.R1039
5'-most EST	LIB3148-030-Q1-K1-D3
Method	BLASTX
NCBI GI	g2833375
BLAST score	187
E value	4.0e-14
Match length	39
% identity	92
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10) (RP10) (ABC10) >gi|533690 (U12133) RNA polymerase II subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

Seq. No.	191545
Contig ID	3501_1.R1039
5'-most EST	LIB3135-060-Q1-K1-F2
Method	BLASTX
NCBI GI	g3643607
BLAST score	342
E value	3.0e-32
Match length	87
% identity	74
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	191546
Contig ID	3516_1.R1039
5'-most EST	LIB3048-042-Q1-L1-B10
Method	BLASTX
NCBI GI	g2052508
BLAST score	815
E value	2.0e-87
Match length	219
% identity	70
NCBI Description	(U95759) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No.	191547
Contig ID	3537_1.R1039
5'-most EST	LIB3083-050-Q1-L1-C5

Seq. No.	191548
Contig ID	3550_1.R1039
5'-most EST	LIB3083-063-Q1-L1-G11
Method	BLASTX
NCBI GI	g462013
BLAST score	1600
E value	1.0e-179
Match length	381
% identity	83
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi|542022|pir||S39558 HSP90 homolog - Madagascar periwinkle >gi|348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	191549
Contig ID	3550_2.R1039
5'-most EST	g5050493
Method	BLASTX
NCBI GI	g462013
BLAST score	475
E value	2.0e-47
Match length	133
% identity	71
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi|542022|pir||S39558 HSP90 homolog - Madagascar periwinkle >gi|348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No.	191550

Contig ID	3561_1.R1039
5'-most EST	LIB3048-042-Q1-L1-G10
Method	BLASTX
NCBI GI	g3377803
BLAST score	480
E value	4.0e-48
Match length	139
% identity	75
NCBI Description	(AF075597) Similar to (p)ppGpp synthetase; T2H3.9 [Arabidopsis thaliana]

Seq. No.	191551
Contig ID	3562_1.R1039
5'-most EST	uC-gsronu33b112e10b1
Method	BLASTX
NCBI GI	g3335366
BLAST score	343
E value	6.0e-32
Match length	102
% identity	66
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	191552
Contig ID	3565_1.R1039
5'-most EST	LIB3272-011-P1-K1-A10
Method	BLASTN
NCBI GI	g3212102
BLAST score	53
E value	8.0e-21
Match length	129
% identity	85
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	191553
Contig ID	3572_1.R1039
5'-most EST	LIB3048-042-Q1-L1-H2
Method	BLASTX
NCBI GI	g4239845
BLAST score	507
E value	6.0e-51
Match length	238
% identity	45
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	191554
Contig ID	3615_1.R1039
5'-most EST	LIB3197-041-Q1-M1-B7
Method	BLASTN
NCBI GI	g3309242
BLAST score	213
E value	1.0e-116
Match length	421
% identity	88
NCBI Description	Citrus limon aconitase-iron regulated protein 1 (IRP1) mRNA, complete cds

Seq. No.	191555
Contig ID	3640_1.R1039
5'-most EST	LIB3272-001-P1-K1-F3
Method	BLASTX
NCBI GI	g4204303
BLAST score	772
E value	3.0e-82
Match length	186
% identity	76
NCBI Description	(AC003027) lcl|prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	191556
Contig ID	3657_1.R1039
5'-most EST	LIB3272-005-P1-K1-H6
Method	BLASTX
NCBI GI	g1418990
BLAST score	248
E value	4.0e-21
Match length	73
% identity	59
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	191557
Contig ID	3693_1.R1039
5'-most EST	g5044578
Method	BLASTX
NCBI GI	g1730635
BLAST score	162
E value	1.0e-10
Match length	102
% identity	37
NCBI Description	HYPOTHETICAL 40.7 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION >gi|2132777|pir||S60917 probable membrane protein YNL264c - yeast (Saccharomyces cerevisiae) >gi|1045245|emb|CAA63233| (X92494) ORF N0815 [Saccharomyces cerevisiae] >gi|1302321|emb|CAA96171| (Z71540) ORF YNL264c [Saccharomyces cerevisiae]

Seq. No.	191558
Contig ID	3705_1.R1039
5'-most EST	LIB3048-055-Q1-L1-C4

Seq. No.	191559
Contig ID	3720_1.R1039
5'-most EST	LIB3197-041-Q1-M1-H3
Method	BLASTX
NCBI GI	g82175
BLAST score	1270
E value	1.0e-140
Match length	281
% identity	88
NCBI Description	luminal binding protein BLP-5 - common tobacco

Seq. No.	191560
Contig ID	3720_2.R1039
5'-most EST	uC-gsflmaxxa070d03b1

Method	BLASTX
NCBI GI	g729623
BLAST score	983
E value	1.0e-107
Match length	221
% identity	88
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP 78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 5) (BIP 5) >gi|100340|pir||S21880 heat shock protein BiP homolog blp5 - common tobacco >gi|19813|emb|CAA42660| (X60058) luminal binding protein (BiP) [Nicotiana tabacum]

Seq. No.	191561
Contig ID	3723_1.R1039
5'-most EST	LIB3083-082-Q1-L1-C4

Seq. No.	191562
Contig ID	3729_1.R1039
5'-most EST	LIB3048-046-Q1-L1-B10
Method	BLASTX
NCBI GI	g1946364
BLAST score	283
E value	2.0e-25
Match length	105
% identity	45
NCBI Description	(U93215) lipase isolog [Arabidopsis thaliana]

Seq. No.	191563
Contig ID	3742_1.R1039
5'-most EST	g3326231
Method	BLASTX
NCBI GI	g1498731
BLAST score	353
E value	2.0e-35
Match length	175
% identity	49
NCBI Description	(U64806) pathogenesis-related protein PR1 [Brassica napus]

Seq. No.	191564
Contig ID	3744_1.R1039
5'-most EST	g5047845
Method	BLASTX
NCBI GI	g4454026
BLAST score	437
E value	5.0e-43
Match length	184
% identity	52
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	191565
Contig ID	3744_2.R1039
5'-most EST	LIB3197-024-Q1-M1-E9
Method	BLASTX
NCBI GI	g4454026
BLAST score	373
E value	1.0e-35
Match length	166

% identity	48
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.	191566
Contig ID	3749_1.R1039
5'-most EST	LIB3048-046-Q1-L1-D1
Method	BLASTX
NCBI GI	g396384
BLAST score	167
E value	1.0e-16
Match length	92
% identity	54
NCBI Description	(U00006) No definition line found [Escherichia coli]

Seq. No.	191567
Contig ID	3778_1.R1039
5'-most EST	LIB3048-046-Q1-L1-G10
Method	BLASTN
NCBI GI	g4519191
BLAST score	36
E value	1.0e-10
Match length	100
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	191568
Contig ID	3783_1.R1039
5'-most EST	LIB3048-046-Q1-L1-G5
Method	BLASTX
NCBI GI	g4572674
BLAST score	359
E value	7.0e-34
Match length	193
% identity	45
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	191569
Contig ID	3805_1.R1039
5'-most EST	LIB3048-047-Q1-L1-A6
Method	BLASTX
NCBI GI	g2880043
BLAST score	411
E value	5.0e-40
Match length	200
% identity	42
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	191570
Contig ID	3827_1.R1039
5'-most EST	LIB3135-023-Q1-K1-C12
Method	BLASTX
NCBI GI	g136057
BLAST score	1035
E value	1.0e-113
Match length	250

% identity	79
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi|99499|pir||A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi|556171 (J04121) triosephosphate isomerase [Coptis japonica]
Seq. No.	191571
Contig ID	3827_2.R1039
5'-most EST	uC-gsflnu33B071a04b1
Seq. No.	191572
Contig ID	3827_3.R1039
5'-most EST	LIB3135-038-Q1-K1-H1
Method	BLASTX
NCBI GI	g2829899
BLAST score	344
E value	5.0e-32
Match length	157
% identity	44
NCBI Description	(AC002311) similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana]
Seq. No.	191573
Contig ID	3829_1.R1039
5'-most EST	LIB3048-047-Q1-L1-C8
Method	BLASTX
NCBI GI	g2244851
BLAST score	529
E value	8.0e-54
Match length	237
% identity	45
NCBI Description	(Z97337) amine oxidase [Arabidopsis thaliana]
Seq. No.	191574
Contig ID	3852_1.R1039
5'-most EST	LIB3165-011-P1-K1-E11
Method	BLASTX
NCBI GI	g3608495
BLAST score	319
E value	3.0e-29
Match length	93
% identity	69
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi|4510351|gb|AAD21440.1| (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]
Seq. No.	191575
Contig ID	3859_1.R1039
5'-most EST	LIB3272-034-P1-K1-E1
Seq. No.	191576
Contig ID	3897_1.R1039
5'-most EST	g3326166
Method	BLASTX
NCBI GI	g3355626
BLAST score	530

E value	7.0e-54
Match length	174
% identity	61
NCBI Description	(Y09204) histidinol-phosphate aminotransferase [Nicotiana tabacum]

Seq. No.	191577
Contig ID	3916_1.R1039
5'-most EST	g3326524
Method	BLASTX
NCBI GI	g3514097
BLAST score	728
E value	1.0e-141
Match length	419
% identity	62
NCBI Description	(AF084260) signalosome subunit 2 [Homo sapiens] >gi|3639069|gb|AAC36309.1| (AF087688) alien-like protein [Mus musculus]

Seq. No.	191578
Contig ID	3955_1.R1039
5'-most EST	LIB3048-048-Q1-L1-G5
Method	BLASTX
NCBI GI	g4239845
BLAST score	583
E value	3.0e-60
Match length	213
% identity	57
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	191579
Contig ID	3974_1.R1039
5'-most EST	g5049429
Method	BLASTX
NCBI GI	g3821793
BLAST score	1429
E value	1.0e-159
Match length	333
% identity	85
NCBI Description	(Y11526) casein kinase II alpha subunit [Zea mays]

Seq. No.	191580
Contig ID	3974_2.R1039
5'-most EST	uC-gsflnu33B016a12b1
Method	BLASTX
NCBI GI	g125271
BLAST score	616
E value	6.0e-64
Match length	141
% identity	82
NCBI Description	CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) >gi|100860|pir||S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi|3318993|pdb|1A6O| Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi|22117|emb|CAA43659| (X61387) casein kinase II alpha subunit [Zea mays]

Seq. No. 191581

Contig ID	3979_1.R1039
5'-most EST	g5044717
Method	BLASTX
NCBI GI	g133940
BLAST score	477
E value	7.0e-81
Match length	192
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	191582
Contig ID	3979_2.R1039
5'-most EST	g5048193
Method	BLASTX
NCBI GI	g133940
BLAST score	428
E value	6.0e-42
Match length	108
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	191583
Contig ID	3979_3.R1039
5'-most EST	LIB3189-002-P1-K1-E10
Method	BLASTX
NCBI GI	g133940
BLAST score	429
E value	4.0e-76
Match length	208
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	191584
Contig ID	3991_1.R1039
5'-most EST	LIB3048-053-Q1-L1-E5
Method	BLASTX
NCBI GI	g4105697
BLAST score	535
E value	9.0e-55
Match length	129
% identity	73
NCBI Description	(AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	191585
Contig ID	4006_1.R1039
5'-most EST	LIB3048-049-Q1-L1-D4
Method	BLASTX
NCBI GI	g3522938

BLAST score	211
E value	1.0e-16
Match length	119
% identity	37
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]

Seq. No.	191586
Contig ID	4013_1.R1039
5'-most EST	LIB3166-024-P1-K1-D11

Seq. No.	191587
Contig ID	4013_2.R1039
5'-most EST	uC-gsronu33B080h12b1

Seq. No.	191588
Contig ID	4082_1.R1039
5'-most EST	uC-gsflnu33B139e01b1
Method	BLASTX
NCBI GI	g1841468
BLAST score	841
E value	2.0e-90
Match length	178
% identity	88
NCBI Description	(Y10990) Tyrosyl-tRNA synthetase [Nicotiana tabacum]

Seq. No.	191589
Contig ID	4091_1.R1039
5'-most EST	LIB3048-050-Q1-L1-D10
Method	BLASTX
NCBI GI	g3033377
BLAST score	232
E value	2.0e-35
Match length	233
% identity	37
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	191590
Contig ID	4114_1.R1039
5'-most EST	LIB3165-012-P1-K1-G8
Method	BLASTX
NCBI GI	g4468979
BLAST score	277
E value	3.0e-24
Match length	125
% identity	48
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	191591
Contig ID	4123_1.R1039
5'-most EST	LIB3189-047-P1-K1-E7
Method	BLASTX
NCBI GI	g3789911
BLAST score	425
E value	2.0e-41
Match length	194
% identity	43

NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No. 191592
Contig ID 4123_2.R1039
5'-most EST uC-gsronu33B113e08b1
Method BLASTX
NCBI GI g3789911
BLAST score 235
E value 1.0e-19
Match length 95
% identity 48
NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No. 191593
Contig ID 4195_1.R1039
5'-most EST LIB3189-052-P1-K1-B3

Seq. No. 191594
Contig ID 4213_1.R1039
5'-most EST LIB3048-051-Q1-L1-H6
Method BLASTX
NCBI GI g3297816
BLAST score 238
E value 4.0e-20
Match length 63
% identity 73
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 191595
Contig ID 4238_1.R1039
5'-most EST LIB3165-002-Q1-K1-A8
Method BLASTN
NCBI GI g4519194
BLAST score 47
E value 3.0e-17
Match length 259
% identity 80
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No. 191596
Contig ID 4238_2.R1039
5'-most EST LIB3048-052-Q1-L1-C1

Seq. No. 191597
Contig ID 4262_1.R1039
5'-most EST LIB3166-050-P1-K1-D6

Seq. No. 191598
Contig ID 4263_1.R1039
5'-most EST LIB3048-054-Q1-L1-C3

Seq. No. 191599
Contig ID 4268_1.R1039
5'-most EST uC-gsronu33B156f02b1

Method	BLASTX
NCBI GI	g3482926
BLAST score	235
E value	2.0e-19
Match length	155
% identity	36
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi|1143445 [Arabidopsis thaliana]

Seq. No.	191600
Contig ID	4276_1.R1039
5'-most EST	g5048679
Method	BLASTX
NCBI GI	g2829927
BLAST score	667
E value	9.0e-70
Match length	367
% identity	46
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	191601
Contig ID	4284_1.R1039
5'-most EST	LIB3145-050-Q1-K1-A10
Method	BLASTX
NCBI GI	g4006827
BLAST score	1651
E value	0.0e+00
Match length	399
% identity	78
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	191602
Contig ID	4307_1.R1039
5'-most EST	uC-gsronu33B127b02b1
Method	BLASTX
NCBI GI	g399046
BLAST score	222
E value	7.0e-33
Match length	118
% identity	58
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi|99657|pir||S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi|16164|emb|CAA41497| (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	191603
Contig ID	4346_1.R1039
5'-most EST	LIB3272-043-P1-K1-D3
Method	BLASTX
NCBI GI	g4490332
BLAST score	558
E value	3.0e-57
Match length	168
% identity	66

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 191604
Contig ID 4349_1.R1039
5'-most EST LIB3166-027-P1-K1-A7
Method BLASTX
NCBI GI g3766368
BLAST score 220
E value 7.0e-18
Match length 106
% identity 47
NCBI Description (AL031907) putative trascription factor, ccr4-associated factor homolog [Schizosaccharomyces pombe]

Seq. No. 191605
Contig ID 4396_1.R1039
5'-most EST g5049533
Method BLASTX
NCBI GI g3894178
BLAST score 659
E value 6.0e-69
Match length 202
% identity 65
NCBI Description (AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 191606
Contig ID 4396_2.R1039
5'-most EST LIB3048-054-Q1-L1-A5

Seq. No. 191607
Contig ID 4397_1.R1039
5'-most EST LIB3272-019-P1-K1-G8
Method BLASTX
NCBI GI g1084461
BLAST score 354
E value 4.0e-33
Match length 112
% identity 62
NCBI Description RCc3 protein - rice >gi|786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 191608
Contig ID 4397_2.R1039
5'-most EST uC-gsflnu33B028e04b1
Method BLASTX
NCBI GI g629597
BLAST score 342
E value 6.0e-32
Match length 80
% identity 79
NCBI Description proline-rich protein - rape >gi|545029|bbs|142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]

Seq. No. 191609
Contig ID 4397_3.R1039
5'-most EST uC-gsflnu33B013g03b1

Method	BLASTX
NCBI GI	g1084461
BLAST score	363
E value	2.0e-34
Match length	89
% identity	73
NCBI Description	RCc3 protein - rice >gi|786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	191610
Contig ID	4397_4.R1039
5'-most EST	LIB3147-008-Q1-K1-C12
Method	BLASTX
NCBI GI	g1199772
BLAST score	416
E value	4.0e-40
Match length	219
% identity	69
NCBI Description	(D83226) extensin like protein [Populus nigra] >gi|1199774|dbj|BAA11855| (D83227) extensin like protein [Populus nigra]

Seq. No.	191611
Contig ID	4397_6.R1039
5'-most EST	LIB3149-020-Q1-K1-C8

Seq. No.	191612
Contig ID	4397_7.R1039
5'-most EST	LIB3149-051-Q1-K1-C2
Method	BLASTX
NCBI GI	g629597
BLAST score	277
E value	2.0e-24
Match length	62
% identity	79
NCBI Description	proline-rich protein - rape >gi|545029|bbs|142669 (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]

Seq. No.	191613
Contig ID	4398_1.R1039
5'-most EST	LIB3165-040-Q1-K1-D11
Method	BLASTX
NCBI GI	g2980770
BLAST score	1345
E value	1.0e-149
Match length	335
% identity	78
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	191614
Contig ID	4398_2.R1039
5'-most EST	uC-gsflnu33B107d10b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	4.0e-10
Match length	35

% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	191615
Contig ID	4398_3.R1039
5'-most EST	g5046609
Method	BLASTX
NCBI GI	g2980770
BLAST score	771
E value	4.0e-82
Match length	236
% identity	66
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	191616
Contig ID	4398_4.R1039
5'-most EST	LIB3272-033-P1-K1-F9

Seq. No.	191617
Contig ID	4401_1.R1039
5'-most EST	LIB3048-054-Q1-L1-B1

Seq. No.	191618
Contig ID	4436_1.R1039
5'-most EST	LIB3197-029-Q1-M1-G10
Method	BLASTX
NCBI GI	g3341681
BLAST score	590
E value	9.0e-83
Match length	171
% identity	89
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	191619
Contig ID	4444_1.R1039
5'-most EST	LIB3166-039-P1-K1-B9
Method	BLASTX
NCBI GI	g417103
BLAST score	632
E value	4.0e-66
Match length	126
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi|282871|pir||S24346 histone H3.3-like protein - Arabidopsis thaliana >gi|16324|emb|CAA42957| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|404825|emb|CAA42958| (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi|488563 (U09458) histone H3.2 [Medicago sativa] >gi|488567 (U09460) histone H3.2 [Medicago sativa] >gi|488569 (U09461) histone H3.2 [Medicago sativa] >gi|488575 (U09464) histone H3.2 [Medicago sativa] >gi|488577 (U09465) histone H3.2 [Medicago sativa] >gi|510911|emb|CAA56153| (X79714) histone H3 [Lolium temulentum] >gi|1435157|emb|CAA58445| (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi|2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi|3273350|dbj|BAA31218| (AB015760) histone H3 [Nicotiana tabacum] >gi|3885890 (AF093633) histone H3 [Oryza sativa] >gi|4038469|gb|AAC97380| (AF109910) histone H3 [Porteresia coarctata] >gi|4490754|emb|CAB38916.1| (AL035708) histone H3.3 [Arabidopsis thaliana] >gi|4490755|emb|CAB38917.1| (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	191620
Contig ID	4444_2.R1039
5'-most EST	LIB3145-015-Q1-K1-D9
Method	BLASTN
NCBI GI	g2558943
BLAST score	66
E value	2.0e-28
Match length	133
% identity	88
NCBI Description	Gossypium hirsutum histone 3 mRNA, complete cds

Seq. No.	191621
Contig ID	4446_1.R1039
5'-most EST	LIB3165-022-P1-K1-C10
Method	BLASTX
NCBI GI	g2924521
BLAST score	185
E value	2.0e-13
Match length	129
% identity	40
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	191622
Contig ID	4449_1.R1039
5'-most EST	LIB3146-048-Q1-K1-C6
Method	BLASTX
NCBI GI	g1001955
BLAST score	887
E value	9.0e-96
Match length	216
% identity	80
NCBI Description	(U19099) unknown protein [Lycopersicon chilense]

Seq. No.	191623
Contig ID	4459_1.R1039
5'-most EST	LIB3148-045-Q1-K1-G8
Method	BLASTX
NCBI GI	g2492782
BLAST score	511
E value	6.0e-52
Match length	134
% identity	70
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi|504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	191624
Contig ID	4469_1.R1039
5'-most EST	LIB3048-054-Q1-L1-G9
Method	BLASTX

NCBI GI	g285741
BLAST score	221
E value	1.0e-17
Match length	166
% identity	36
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	191625
Contig ID	4474_1.R1039
5'-most EST	LIB3120-011-Q1-K1-G2
Method	BLASTX
NCBI GI	g3337361
BLAST score	2067
E value	0.0e+00
Match length	516
% identity	71
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	191626
Contig ID	4566_1.R1039
5'-most EST	LIB3189-007-P1-K1-E9
Method	BLASTX
NCBI GI	g4544399
BLAST score	1732
E value	0.0e+00
Match length	486
% identity	65
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	191627
Contig ID	4566_2.R1039
5'-most EST	g5044405
Method	BLASTX
NCBI GI	g4115364
BLAST score	427
E value	7.0e-42
Match length	110
% identity	70
NCBI Description	(AC005957) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	191628
Contig ID	4566_3.R1039
5'-most EST	g5046200
Method	BLASTX
NCBI GI	g4544399
BLAST score	475
E value	1.0e-47
Match length	179
% identity	49
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	191629
Contig ID	4566_5.R1039
5'-most EST	LIB3197-044-Q1-M1-G11

Method	BLASTX
NCBI GI	g3142289
BLAST score	316
E value	2.0e-33
Match length	121
% identity	64
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb|U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	191630
Contig ID	4568_1.R1039
5'-most EST	g5045284
Method	BLASTX
NCBI GI	g1903364
BLAST score	519
E value	9.0e-53
Match length	158
% identity	66
NCBI Description	(AC000104) EST gb|T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No.	191631
Contig ID	4569_1.R1039
5'-most EST	LIB3189-014-P1-K1-F12
Method	BLASTX
NCBI GI	g4098323
BLAST score	2095
E value	0.0e+00
Match length	428
% identity	91
NCBI Description	(U76746) beta-tubulin 3 [Triticum aestivum]

Seq. No.	191632
Contig ID	4569_2.R1039
5'-most EST	LIB3083-051-Q1-L1-E12
Method	BLASTN
NCBI GI	g170059
BLAST score	137
E value	1.0e-70
Match length	652
% identity	82
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete cds

Seq. No.	191633
Contig ID	4572_1.R1039
5'-most EST	LIB3083-001-Q1-L1-D11

Seq. No.	191634
Contig ID	4577_1.R1039
5'-most EST	LIB3083-002-Q1-L1-F9

Seq. No.	191635
Contig ID	4578_1.R1039
5'-most EST	LIB3083-053-Q1-L1-D2

Seq. No.	191636

Contig ID	4579_1.R1039
5'-most EST	LIB3145-033-Q1-K1-A6
Method	BLASTX
NCBI GI	g3212877
BLAST score	1162
E value	1.0e-127
Match length	276
% identity	78
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	191637
Contig ID	4579_2.R1039
5'-most EST	LIB3146-008-Q1-K1-A7
Method	BLASTX
NCBI GI	g3264769
BLAST score	297
E value	1.0e-26
Match length	74
% identity	73
NCBI Description	(AF071894) late embryogenesis-like protein [Prunus armeniaca]

Seq. No.	191638
Contig ID	4581_1.R1039
5'-most EST	LIB3083-001-Q1-L1-G10

Seq. No.	191639
Contig ID	4586_1.R1039
5'-most EST	LIB3165-038-Q1-K1-E11
Method	BLASTX
NCBI GI	g4056568
BLAST score	286
E value	2.0e-25
Match length	116
% identity	17
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	191640
Contig ID	4588_1.R1039
5'-most EST	LIB3083-119-Q1-L1-C12
Method	BLASTX
NCBI GI	g2244833
BLAST score	277
E value	5.0e-24
Match length	270
% identity	19
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	191641
Contig ID	4590_1.R1039
5'-most EST	uC-gsflnu33B004f07b1
Method	BLASTX
NCBI GI	g2129473
BLAST score	410
E value	1.0e-39
Match length	194
% identity	48

NCBI Description	arabinogalactan-like protein - loblolly pine >gi|607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	191642
Contig ID	4592_1.R1039
5'-most EST	uC-gsflmaxxa098d03b1
Method	BLASTX
NCBI GI	g2829909
BLAST score	165
E value	6.0e-11
Match length	133
% identity	45
NCBI Description	(AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	191643
Contig ID	4593_1.R1039
5'-most EST	LIB3272-032-P1-K1-A7
Method	BLASTX
NCBI GI	g3894194
BLAST score	372
E value	3.0e-35
Match length	167
% identity	49
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	191644
Contig ID	4594_1.R1039
5'-most EST	LIB3272-047-P1-K1-D11
Method	BLASTX
NCBI GI	g4006829
BLAST score	238
E value	7.0e-20
Match length	97
% identity	53
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	191645
Contig ID	4595_1.R1039
5'-most EST	LIB3196-039-P1-M1-A10
Method	BLASTX
NCBI GI	g131772
BLAST score	580
E value	9.0e-60
Match length	139
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi|82723|pir||A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No.	191646
Contig ID	4595_2.R1039
5'-most EST	LIB3147-019-Q1-K1-H8
Method	BLASTX
NCBI GI	g131772
BLAST score	580
E value	1.0e-59

Match length	139
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi|82723|pir||A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No.	191647
Contig ID	4595_3.R1039
5'-most EST	uC-gsflnu33B006a04b1
Method	BLASTX
NCBI GI	g131773
BLAST score	564
E value	5.0e-58
Match length	139
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi|82724|pir||B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	191648
Contig ID	4595_4.R1039
5'-most EST	LIB3120-010-Q1-K1-H7
Method	BLASTX
NCBI GI	g131772
BLAST score	251
E value	2.0e-48
Match length	139
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi|82723|pir||A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No.	191649
Contig ID	4597_1.R1039
5'-most EST	uC-gsronu33B139e10b1
Method	BLASTX
NCBI GI	g1086249
BLAST score	501
E value	9.0e-51
Match length	153
% identity	59
NCBI Description	subtilisin-like protease - Alnus glutinosa >gi|757522|emb|CAA59964| (X85975) subtilisin-like protease [Alnus glutinosa]

Seq. No.	191650
Contig ID	4601_1.R1039
5'-most EST	LIB3135-029-Q1-K1-F8
Method	BLASTX
NCBI GI	g2760330
BLAST score	541
E value	3.0e-55
Match length	133
% identity	75
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No. 191651

Contig ID	4603_1.R1039
5'-most EST	LIB3083-001-Q1-L2-C1

Seq. No.	191652
Contig ID	4607_1.R1039
5'-most EST	LIB3083-095-Q1-L1-G1
Method	BLASTX
NCBI GI	g1076387
BLAST score	541
E value	4.0e-55
Match length	146
% identity	70
NCBI Description	protein kinase homolog - Arabidopsis thaliana >gi|717180|emb|CAA55866| (X79279) protein kinase homologous to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]

Seq. No.	191653
Contig ID	4608_1.R1039
5'-most EST	LIB3083-027-Q1-L1-D3
Method	BLASTX
NCBI GI	g130720
BLAST score	453
E value	8.0e-45
Match length	177
% identity	49
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi|101508|pir||A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi|172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi|500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	191654
Contig ID	4608_2.R1039
5'-most EST	LIB3146-023-Q1-K1-B2
Method	BLASTX
NCBI GI	g2414624
BLAST score	252
E value	2.0e-21
Match length	78
% identity	60
NCBI Description	(Z99259) ATP synthase subunit [Schizosaccharomyces pombe]

Seq. No.	191655
Contig ID	4611_1.R1039
5'-most EST	LIB3083-001-Q1-L2-D1

Seq. No.	191656
Contig ID	4612_1.R1039
5'-most EST	LIB3189-041-P1-K1-E10
Method	BLASTX
NCBI GI	g4337175
BLAST score	513
E value	7.0e-52
Match length	165
% identity	62

NCBI Description	(AC006416) ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	191657
Contig ID	4614_1.R1039
5'-most EST	LIB3083-073-Q1-L1-F11
Method	BLASTX
NCBI GI	g2347208
BLAST score	596
E value	9.0e-62
Match length	193
% identity	59
NCBI Description	(AC002338) APG protein isolog [Arabidopsis thaliana]

Seq. No.	191658
Contig ID	4616_1.R1039
5'-most EST	LIB3083-001-Q1-L2-E2

Seq. No.	191659
Contig ID	4617_1.R1039
5'-most EST	LIB3189-018-P1-K1-H4
Method	BLASTX
NCBI GI	g4544412
BLAST score	548
E value	1.0e-55
Match length	380
% identity	35
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191660
Contig ID	4622_1.R1039
5'-most EST	g5048305
Method	BLASTX
NCBI GI	g731097
BLAST score	357
E value	1.0e-33
Match length	145
% identity	51
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi|1083086|pir||A55910 subunit D vacuolar H(+)-ATPase - bovine >gi|517446 (U11927) vacuolar H-ATPase subunit D [Bos gaurus]

Seq. No.	191661
Contig ID	4622_2.R1039
5'-most EST	uC-gsronu33B143c08b1
Method	BLASTX
NCBI GI	g4097094
BLAST score	624
E value	1.0e-64
Match length	261
% identity	53
NCBI Description	(U45447) vacuolar proton-ATPase subunit D [Oryctolagus cuniculus]

Seq. No. 191662
Contig ID 4622_4.R1039
5'-most EST g5048637
Method BLASTX
NCBI GI g2493133
BLAST score 157
E value 2.0e-10
Match length 85
% identity 46
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi|2183244 (AF002134) Vma8p [Candida albicans]

Seq. No. 191663
Contig ID 4623_2.R1039
5'-most EST LIB3083-070-Q1-L1-D11

Seq. No. 191664
Contig ID 4625_1.R1039
5'-most EST LIB3197-002-P1-M1-B3
Method BLASTX
NCBI GI g2832625
BLAST score 1320
E value 1.0e-146
Match length 339
% identity 72
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 191665
Contig ID 4626_1.R1039
5'-most EST LIB3083-001-Q1-L2-F2
Method BLASTX
NCBI GI g2494620
BLAST score 277
E value 1.0e-24
Match length 71
% identity 68
NCBI Description SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN >gi|975319 (U31902) succinate dehydrogenase iron-sulfur protein subunit [Paracoccus denitrificans]

Seq. No. 191666
Contig ID 4635_1.R1039
5'-most EST g5045734
Method BLASTX
NCBI GI g586076
BLAST score 1641
E value 0.0e+00
Match length 429
% identity 95
NCBI Description TUBULIN BETA-1 CHAIN >gi|486734|pir||S35142 tubulin beta chain - white lupine >gi|402636|emb|CAA49736| (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 191667
Contig ID 4636_1.R1039
5'-most EST LIB3083-001-Q1-L2-G5
Method BLASTX

NCBI GI	g4544464
BLAST score	192
E value	5.0e-31
Match length	379
% identity	32
NCBI Description	(AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	191668
Contig ID	4636_2.R1039
5'-most EST	g5045373
Method	BLASTX
NCBI GI	g4544464
BLAST score	328
E value	5.0e-30
Match length	298
% identity	35
NCBI Description	(AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	191669
Contig ID	4639_1.R1039
5'-most EST	LIB3147-033-Q1-K1-C9
Method	BLASTX
NCBI GI	g3193303
BLAST score	264
E value	1.0e-22
Match length	108
% identity	47
NCBI Description	(AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No.	191670
Contig ID	4641_1.R1039
5'-most EST	LIB3083-109-Q1-L1-F1
Method	BLASTN
NCBI GI	g2267582
BLAST score	65
E value	4.0e-28
Match length	116
% identity	94
NCBI Description	Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, complete cds

Seq. No.	191671
Contig ID	4642_1.R1039
5'-most EST	uC-gsronu33B099f03b1
Method	BLASTX
NCBI GI	g2827699
BLAST score	149
E value	1.0e-09
Match length	129
% identity	36
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	191672
Contig ID	4643_1.R1039
5'-most EST	LIB3083-052-Q1-L1-D11
Method	BLASTX
NCBI GI	g2244896
BLAST score	214
E value	4.0e-17
Match length	147
% identity	37
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	191673
Contig ID	4650_1.R1039
5'-most EST	LIB3147-044-Q1-K1-A2
Method	BLASTX
NCBI GI	g2829899
BLAST score	355
E value	3.0e-33
Match length	153
% identity	46
NCBI Description	(AC002311) similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana]

Seq. No.	191674
Contig ID	4650_2.R1039
5'-most EST	uC-gsflnu33B111b06b1
Method	BLASTN
NCBI GI	g433664
BLAST score	62
E value	3.0e-26
Match length	154
% identity	89
NCBI Description	A.thaliana for Sec61 beta-subunit homolog

Seq. No.	191675
Contig ID	4652_1.R1039
5'-most EST	g5045271
Method	BLASTX
NCBI GI	g4510344
BLAST score	182
E value	3.0e-13
Match length	109
% identity	42
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191676
Contig ID	4657_1.R1039
5'-most EST	uC-gsronu33B129b06b1
Method	BLASTX
NCBI GI	g417360
BLAST score	372
E value	2.0e-35
Match length	133
% identity	53
NCBI Description	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2

>gi|2131280|pir||S67767 high mobility group-like protein NHP2 - yeast (Saccharomyces cerevisiae)
>gi|666101|emb|CAA40885| (X57714) high mobility group-like nuclear protein 2 [Saccharomyces cerevisiae]
>gi|1429348|emb|CAA67483| (X99000) high-mobility-group-like protein [Saccharomyces cerevisiae]
>gi|1431346|emb|CAA98786| (Z74256) ORF YDL208w [Saccharomyces cerevisiae]

Seq. No.	191677
Contig ID	4661_1.R1039
5'-most EST	LIB3145-008-Q1-K1-C10
Method	BLASTX
NCBI GI	g2827139
BLAST score	1977
E value	0.0e+00
Match length	444
% identity	83
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi|4049343|emb|CAA22568| (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	191678
Contig ID	4662_1.R1039
5'-most EST	LIB3083-067-Q1-L1-A10
Method	BLASTX
NCBI GI	g135406
BLAST score	1099
E value	1.0e-120
Match length	226
% identity	91
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi|99768|pir||A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi|166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi|166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	191679
Contig ID	4664_1.R1039
5'-most EST	g5046883
Method	BLASTX
NCBI GI	g1805617
BLAST score	209
E value	9.0e-33
Match length	104
% identity	69
NCBI Description	(D49704) OSH44 transcript; homeobox gene [Oryza sativa]

Seq. No.	191680
Contig ID	4664_2.R1039
5'-most EST	g5046124
Method	BLASTX
NCBI GI	g4098246
BLAST score	842
E value	1.0e-90
Match length	176
% identity	91

NCBI Description	(U76410) homeobox 2 protein [Lycopersicon esculentum]

Seq. No.	191681
Contig ID	4665_1.R1039
5'-most EST	uC-gsflnu33B083c04b1
Method	BLASTX
NCBI GI	g3269288
BLAST score	792
E value	2.0e-84
Match length	203
% identity	76
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	191682
Contig ID	4666_1.R1039
5'-most EST	LIB3083-002-Q1-L1-B3
Method	BLASTX
NCBI GI	g2129932
BLAST score	656
E value	6.0e-69
Match length	120
% identity	95
NCBI Description	myb-related transcription factor TMH1 - tomato >gi|1167486|emb|CAA64615| (X95297) transcription factor [Lycopersicon esculentum]

Seq. No.	191683
Contig ID	4667_1.R1039
5'-most EST	LIB3083-002-Q1-L1-B4

Seq. No.	191684
Contig ID	4668_1.R1039
5'-most EST	LIB3120-060-Q1-K1-C8
Method	BLASTX
NCBI GI	g4580523
BLAST score	713
E value	3.0e-75
Match length	190
% identity	73
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	191685
Contig ID	4669_1.R1039
5'-most EST	LIB3083-079-Q1-L1-E9
Method	BLASTN
NCBI GI	g4580522
BLAST score	47
E value	5.0e-17
Match length	262
% identity	85
NCBI Description	Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial cds

Seq. No.	191686
Contig ID	4671_1.R1039
5'-most EST	LIB3145-045-Q1-K1-F11
Method	BLASTX

NCBI GI	g2270994
BLAST score	819
E value	9.0e-88
Match length	219
% identity	66
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	191687
Contig ID	4672_1.R1039
5'-most EST	LIB3148-013-Q1-K1-A11
Method	BLASTX
NCBI GI	g3914535
BLAST score	873
E value	6.0e-94
Match length	206
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi|2791948|emb|CAA11283| (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	191688
Contig ID	4672_2.R1039
5'-most EST	LIB3149-034-Q1-K1-B9
Method	BLASTX
NCBI GI	g3914535
BLAST score	213
E value	5.0e-34
Match length	95
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi|2791948|emb|CAA11283| (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	191689
Contig ID	4672_3.R1039
5'-most EST	LIB3148-039-Q1-K1-H11
Method	BLASTX
NCBI GI	g3914535
BLAST score	337
E value	2.0e-31
Match length	80
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi|2791948|emb|CAA11283| (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	191690
Contig ID	4672_4.R1039
5'-most EST	LIB3147-041-Q1-K1-A10
Method	BLASTX
NCBI GI	g3914535
BLAST score	445
E value	3.0e-87
Match length	194
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L13A >gi|2791948|emb|CAA11283| (AJ223363) ribosomal protein L13a [Lupinus luteus]

Seq. No.	191691
Contig ID	4673_1.R1039

5'-most EST	LIB3165-021-P1-K1-C1
Method	BLASTX
NCBI GI	g2244917
BLAST score	143
E value	7.0e-09
Match length	77
% identity	43
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191692
Contig ID	4677_1.R1039
5'-most EST	LIB3083-002-Q1-L1-C2
Method	BLASTX
NCBI GI	g3702964
BLAST score	781
E value	3.0e-83
Match length	188
% identity	79
NCBI Description	(AF079485) rac GTP binding protein Arac10 [Arabidopsis thaliana]

Seq. No.	191693
Contig ID	4682_1.R1039
5'-most EST	LIB3145-015-Q1-K1-C4
Method	BLASTX
NCBI GI	g266567
BLAST score	361
E value	2.0e-63
Match length	277
% identity	51
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi|421956|pir||S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi|21493|emb|CAA46990| (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	191694
Contig ID	4682_2.R1039
5'-most EST	LIB3166-032-P1-K1-C12

Seq. No.	191695
Contig ID	4683_1.R1039
5'-most EST	LIB3083-072-Q1-L1-H6
Method	BLASTX
NCBI GI	g3868758
BLAST score	1066
E value	1.0e-160
Match length	420
% identity	67
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	191696
Contig ID	4683_7.R1039
5'-most EST	LIB3196-054-P1-M1-E7
Method	BLASTX
NCBI GI	g2160158

BLAST score 197
E value 3.0e-15
Match length 48
% identity 77
NCBI Description (AC000132) Similar to elongation factor 1-gamma (gb|EF1G_XENLA). ESTs gb|T20564,gb|T45940,gb|T04527 come from this gene. [Arabidopsis thaliana]

Seq. No. 191697
Contig ID 4690_1.R1039
5'-most EST uC-gsflnu33B012e01b1

Seq. No. 191698
Contig ID 4690_2.R1039
5'-most EST LIB3083-056-Q1-L1-C4

Seq. No. 191699
Contig ID 4691_1.R1039
5'-most EST g5048763

Seq. No. 191700
Contig ID 4693_1.R1039
5'-most EST uC-gsflnu33B130a10b1
Method BLASTX
NCBI GI g3158476
BLAST score 1307
E value 1.0e-145
Match length 285
% identity 87
NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 191701
Contig ID 4693_2.R1039
5'-most EST uC-gsflnu33B083f05b1
Method BLASTX
NCBI GI g886100
BLAST score 700
E value 9.0e-74
Match length 154
% identity 86
NCBI Description (U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No. 191702
Contig ID 4693_3.R1039
5'-most EST uC-gsronu33B136a09b1
Method BLASTX
NCBI GI g21699
BLAST score 152
E value 1.0e-09
Match length 35
% identity 77
NCBI Description (X66013) cathepsin B [Triticum aestivum]

Seq. No. 191703
Contig ID 4693_4.R1039

5'-most EST	LIB3120-027-Q1-K1-G2
Method	BLASTX
NCBI GI	g3158476
BLAST score	656
E value	7.0e-69
Match length	145
% identity	86
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	191704
Contig ID	4693_5.R1039
5'-most EST	LIB3120-007-Q1-K1-B5
Method	BLASTX
NCBI GI	g3158476
BLAST score	436
E value	6.0e-43
Match length	93
% identity	87
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	191705
Contig ID	4693_7.R1039
5'-most EST	LIB3135-012-Q1-K1-H8
Method	BLASTX
NCBI GI	g1657948
BLAST score	411
E value	5.0e-40
Match length	89
% identity	88
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	191706
Contig ID	4694_1.R1039
5'-most EST	g5049873
Method	BLASTX
NCBI GI	g4538975
BLAST score	318
E value	6.0e-29
Match length	109
% identity	61
NCBI Description	(AL049487) putative protein [Arabidopsis thaliana]

Seq. No.	191707
Contig ID	4697_1.R1039
5'-most EST	uC-gsronu33b112a07b1

Seq. No.	191708
Contig ID	4698_1.R1039
5'-most EST	LIB3189-013-P1-K1-H8
Method	BLASTX
NCBI GI	g4454014
BLAST score	347
E value	2.0e-32
Match length	173
% identity	46
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	191709
Contig ID	4699_1.R1039
5'-most EST	g5047982
Seq. No.	191710
Contig ID	4700_1.R1039
5'-most EST	LIB3120-022-Q1-K1-D4
Seq. No.	191711
Contig ID	4702_1.R1039
5'-most EST	LIB3083-002-Q1-L1-E5
Seq. No.	191712
Contig ID	4703_1.R1039
5'-most EST	LIB3083-108-Q1-L1-D3
Method	BLASTX
NCBI GI	g730030
BLAST score	151
E value	4.0e-09
Match length	228
% identity	9
NCBI Description	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA] >gi|161804 (M87306) micronuclear linker histone polyprotein [Tetrahymena thermophila]
Seq. No.	191713
Contig ID	4703_2.R1039
5'-most EST	LIB3083-078-Q1-L1-C7
Method	BLASTN
NCBI GI	g1143223
BLAST score	163
E value	3.0e-86
Match length	730
% identity	53
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.	191714
Contig ID	4703_3.R1039
5'-most EST	LIB3083-060-Q1-L1-H7
Method	BLASTN
NCBI GI	g1143223
BLAST score	267
E value	1.0e-148
Match length	865
% identity	50
NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.	191715
Contig ID	4703_5.R1039
5'-most EST	LIB3083-028-Q1-L1-G7
Method	BLASTN
NCBI GI	g1143223
BLAST score	192
E value	1.0e-103
Match length	496
% identity	38

NCBI Description	Gossypium barbadense FbLate-2 gene, complete cds
Seq. No.	191716
Contig ID	4705_1.R1039
5'-most EST	g5049642
Method	BLASTX
NCBI GI	g2058282
BLAST score	708
E value	1.0e-74
Match length	164
% identity	80
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	191717
Contig ID	4705_2.R1039
5'-most EST	uC-gsflnu33B037e03b1
Method	BLASTX
NCBI GI	g2058282
BLAST score	259
E value	5.0e-22
Match length	66
% identity	70
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	191718
Contig ID	4705_3.R1039
5'-most EST	LIB3083-002-Q1-L1-E8
Method	BLASTX
NCBI GI	g2058282
BLAST score	651
E value	7.0e-68
Match length	156
% identity	77
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]
Seq. No.	191719
Contig ID	4707_1.R1039
5'-most EST	LIB3083-002-Q1-L1-F1
Seq. No.	191720
Contig ID	4711_1.R1039
5'-most EST	uC-gsflnu33B108c08b1
Method	BLASTX
NCBI GI	g4490737
BLAST score	337
E value	1.0e-31
Match length	97
% identity	41
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	191721
Contig ID	4713_1.R1039
5'-most EST	LIB3083-002-Q1-L1-F7
Method	BLASTX
NCBI GI	g1169012
BLAST score	343
E value	3.0e-32

Match length	101
% identity	70
NCBI Description	COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1) >gi|402685 (L24437) regulatory protein [Arabidopsis thaliana]

Seq. No.	191722
Contig ID	4716_1.R1039
5'-most EST	LIB3145-002-P1-K1-E1
Method	BLASTX
NCBI GI	g266945
BLAST score	845
E value	1.0e-90
Match length	190
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi|100065|pir||S19978 ribosomal protein L9 - garden pea >gi|20727|emb|CAA46273| (X65155) GA [Pisum sativum] >gi|1279645|emb|CAA65987| (X97322) ribosomal protein L9 [Pisum sativum]

Seq. No.	191723
Contig ID	4716_2.R1039
5'-most EST	g5047192
Method	BLASTX
NCBI GI	g266945
BLAST score	844
E value	1.0e-90
Match length	194
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi|100065|pir||S19978 ribosomal protein L9 - garden pea >gi|20727|emb|CAA46273| (X65155) GA [Pisum sativum] >gi|1279645|emb|CAA65987| (X97322) ribosomal protein L9 [Pisum sativum]

Seq. No.	191724
Contig ID	4716_3.R1039
5'-most EST	LIB3189-034-P1-K1-H7
Method	BLASTX
NCBI GI	g4539405
BLAST score	799
E value	3.0e-85
Match length	194
% identity	81
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	191725
Contig ID	4726_1.R1039
5'-most EST	LIB3083-103-Q1-L1-D11
Method	BLASTX
NCBI GI	g4006886
BLAST score	557
E value	2.0e-57
Match length	122
% identity	81
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	191726
Contig ID	4728_1.R1039
5'-most EST	g5050159
Method	BLASTX
NCBI GI	g2695711
BLAST score	626
E value	4.0e-65
Match length	134
% identity	84
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	191727
Contig ID	4728_2.R1039
5'-most EST	LIB3135-051-Q1-K1-A8
Method	BLASTX
NCBI GI	g2695711
BLAST score	246
E value	9.0e-21
Match length	52
% identity	81
NCBI Description	(AJ001370) cytochome b5 [Olea europaea]

Seq. No.	191728
Contig ID	4729_1.R1039
5'-most EST	LIB3149-033-Q1-K1-D10
Method	BLASTX
NCBI GI	g1353157
BLAST score	252
E value	2.0e-21
Match length	177
% identity	31
NCBI Description	HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II >gi|3878900|emb|CAA86774| (Z46794) similar to vacuolar biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from this gene; cDNA EST EMBL:D34974 comes from this gene [Caenorhabditis elegans]

Seq. No.	191729
Contig ID	4731_1.R1039
5'-most EST	LIB3083-002-Q1-L1-H2
Method	BLASTX
NCBI GI	g1808656
BLAST score	358
E value	6.0e-34
Match length	78
% identity	82
NCBI Description	(Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No.	191730
Contig ID	4733_1.R1039
5'-most EST	LIB3083-002-Q1-L1-H4
Method	BLASTX
NCBI GI	g114420
BLAST score	2373
E value	0.0e+00
Match length	518

% identity	91
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi|100882|pir||S11491 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - maize >gi|22173|emb|CAA38140| (X54233) ATPase F1 subunit protein [Zea mays] >gi|897618 (M36087) F-1-ATPase subunit 2 [Zea mays]

Seq. No.	191731
Contig ID	4733_3.R1039
5'-most EST	LIB3165-006-P1-K1-D11
Method	BLASTX
NCBI GI	g231586
BLAST score	274
E value	4.0e-24
Match length	57
% identity	95
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi|82027|pir||S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi|18831|emb|CAA41401| (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	191732
Contig ID	4733_4.R1039
5'-most EST	LIB3145-007-Q1-K1-F6
Method	BLASTX
NCBI GI	g231586
BLAST score	513
E value	5.0e-52
Match length	107
% identity	95
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi|82027|pir||S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi|18831|emb|CAA41401| (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	191733
Contig ID	4735_1.R1039
5'-most EST	g5046872
Method	BLASTX
NCBI GI	g3395436
BLAST score	393
E value	5.0e-46
Match length	175
% identity	53
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	191734
Contig ID	4739_1.R1039
5'-most EST	LIB3197-047-Q1-M1-B3
Method	BLASTX
NCBI GI	g3213227
BLAST score	291
E value	9.0e-26
Match length	200

% identity	32
NCBI Description	(AF035209) putative v-SNARE Vti1a [Mus musculus] >gi|3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No.	191735
Contig ID	4739_2.R1039
5'-most EST	LIB3083-028-Q1-L1-G6
Method	BLASTX
NCBI GI	g3213227
BLAST score	151
E value	8.0e-10
Match length	90
% identity	32
NCBI Description	(AF035209) putative v-SNARE Vti1a [Mus musculus] >gi|3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No.	191736
Contig ID	4742_1.R1039
5'-most EST	uC-gsflmaxxa047c02b1
Method	BLASTX
NCBI GI	g2459429
BLAST score	800
E value	3.0e-85
Match length	201
% identity	71
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	191737
Contig ID	4743_1.R1039
5'-most EST	LIB3083-101-Q1-L1-E7
Method	BLASTX
NCBI GI	g4510383
BLAST score	342
E value	5.0e-32
Match length	112
% identity	64
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	191738
Contig ID	4747_1.R1039
5'-most EST	LIB3149-056-Q1-K1-F8

Seq. No.	191739
Contig ID	4748_1.R1039
5'-most EST	LIB3083-006-Q1-L1-B12
Method	BLASTX
NCBI GI	g2760332
BLAST score	193
E value	6.0e-15
Match length	77
% identity	29
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	191740
Contig ID	4750_1.R1039
5'-most EST	uC-gsflnu33B140c11b1
Method	BLASTX

NCBI GI g643469
BLAST score 808
E value 2.0e-86
Match length 253
% identity 61
NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 191741
Contig ID 4751_1.R1039
5'-most EST LIB3083-006-Q1-L1-B5
Method BLASTX
NCBI GI g4512659
BLAST score 422
E value 2.0e-41
Match length 176
% identity 54
NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana] >gi|4544465|gb|AAD22372.1|AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No. 191742
Contig ID 4753_1.R1039
5'-most EST LIB3272-017-P1-K1-F1
Method BLASTX
NCBI GI g4538911
BLAST score 350
E value 2.0e-49
Match length 259
% identity 46
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 191743
Contig ID 4755_1.R1039
5'-most EST uC-gsronu33B004a10b1
Method BLASTX
NCBI GI g3341693
BLAST score 152
E value 1.0e-09
Match length 79
% identity 39
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 191744
Contig ID 4763_1.R1039
5'-most EST g5050297
Method BLASTX
NCBI GI g2961384
BLAST score 703
E value 4.0e-74
Match length 223
% identity 57
NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 191745
Contig ID 4764_1.R1039
5'-most EST LIB3145-017-Q1-K1-A3

Method	BLASTX
NCBI GI	g3367534
BLAST score	1177
E value	1.0e-129
Match length	265
% identity	84
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb|U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	191746
Contig ID	4764_2.R1039
5'-most EST	LIB3197-021-Q1-M1-E3
Method	BLASTX
NCBI GI	g3367534
BLAST score	383
E value	4.0e-63
Match length	151
% identity	80
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb|U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	191747
Contig ID	4764_3.R1039
5'-most EST	LIB3147-058-Q1-K1-C11
Method	BLASTX
NCBI GI	g4567286
BLAST score	514
E value	3.0e-60
Match length	141
% identity	82
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	191748
Contig ID	4764_4.R1039
5'-most EST	uC-gsronu33B060f11b1
Method	BLASTX
NCBI GI	g3367534
BLAST score	662
E value	1.0e-69
Match length	160
% identity	81
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb|U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	191749
Contig ID	4766_1.R1039
5'-most EST	g5049446
Method	BLASTX
NCBI GI	g1076621
BLAST score	555
E value	9.0e-57
Match length	132
% identity	77

NCBI Description	cytochrome b5 - common tobacco >gi|296386|emb|CAA50575| (X71441) cytochrome b5 [Nicotiana tabacum]

Seq. No.	191750
Contig ID	4766_2.R1039
5'-most EST	uC-gsronu33B038g02b1
Method	BLASTX
NCBI GI	g1076621
BLAST score	615
E value	1.0e-63
Match length	132
% identity	85
NCBI Description	cytochrome b5 - common tobacco >gi|296386|emb|CAA50575| (X71441) cytochrome b5 [Nicotiana tabacum]

Seq. No.	191751
Contig ID	4768_1.R1039
5'-most EST	LIB3146-020-Q1-K1-G9
Method	BLASTX
NCBI GI	g2055384
BLAST score	224
E value	7.0e-18
Match length	84
% identity	26
NCBI Description	(U69633) cold-stress inducible protein [Solanum tuberosum]

Seq. No.	191752
Contig ID	4768_2.R1039
5'-most EST	uC-gsronu33B089e10b1
Method	BLASTN
NCBI GI	g2865522
BLAST score	42
E value	3.0e-14
Match length	106
% identity	85
NCBI Description	Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA, complete cds

Seq. No.	191753
Contig ID	4770_1.R1039
5'-most EST	LIB3083-064-Q1-L1-E3
Method	BLASTX
NCBI GI	g4262186
BLAST score	716
E value	7.0e-76
Match length	173
% identity	77
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	191754
Contig ID	4772_1.R1039
5'-most EST	LIB3083-006-Q1-L1-D4
Method	BLASTX
NCBI GI	g2739366
BLAST score	175
E value	1.0e-12

Match length 90
% identity 39
NCBI Description (AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No. 191755
Contig ID 4773_1.R1039
5'-most EST g5050672
Method BLASTX
NCBI GI g2842490
BLAST score 386
E value 4.0e-37
Match length 174
% identity 50
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 191756
Contig ID 4778_1.R1039
5'-most EST g3326237
Method BLASTX
NCBI GI g584794
BLAST score 668
E value 6.0e-70
Match length 226
% identity 62
NCBI Description PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
>gi|282953|pir||A41779 H+-transporting ATPase (EC 3.6.1.35)
- curled-leaved tobacco >gi|170289 (M80489) plasma membrane
H+ ATPase [Nicotiana plumbaginifolia]

Seq. No. 191757
Contig ID 4778_3.R1039
5'-most EST LIB3083-021-Q1-L1-B2
Method BLASTX
NCBI GI g218179
BLAST score 300
E value 8.0e-42
Match length 122
% identity 75
NCBI Description (D10207) H-ATPase [Oryza sativa] >gi|444339|prf||1906387A H
ATPase [Oryza sativa]

Seq. No. 191758
Contig ID 4780_1.R1039
5'-most EST LIB3272-021-P1-K1-G9

Seq. No. 191759
Contig ID 4786_1.R1039
5'-most EST g5046537
Method BLASTX
NCBI GI g2511689
BLAST score 1177
E value 1.0e-129
Match length 319
% identity 68
NCBI Description (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No. 191760

Contig ID	4787_1.R1039
5'-most EST	LIB3083-006-Q1-L1-E8
Method	BLASTX
NCBI GI	g4455194
BLAST score	307
E value	5.0e-28
Match length	70
% identity	80
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	191761
Contig ID	4790_1.R1039
5'-most EST	LIB3083-015-Q1-L2-G4

Seq. No.	191762
Contig ID	4791_1.R1039
5'-most EST	LIB3166-008-P1-K1-H2
Method	BLASTX
NCBI GI	g3549667
BLAST score	578
E value	8.0e-60
Match length	138
% identity	79
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	191763
Contig ID	4792_1.R1039
5'-most EST	LIB3083-079-Q1-L1-A1
Method	BLASTN
NCBI GI	g2980787
BLAST score	39
E value	3.0e-12
Match length	75
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	191764
Contig ID	4792_2.R1039
5'-most EST	uC-gsflnu33B093c01b1
Method	BLASTN
NCBI GI	g2980787
BLAST score	35
E value	6.0e-10
Match length	75
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	191765
Contig ID	4793_1.R1039
5'-most EST	g5044575
Method	BLASTX
NCBI GI	g3851636
BLAST score	837
E value	9.0e-90

Match length	190
% identity	84
NCBI Description	(AF098519) unknown [Avicennia marina] >gi|4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	191766
Contig ID	4793_2.R1039
5'-most EST	LIB3197-013-P1-M1-G9
Method	BLASTX
NCBI GI	g3851636
BLAST score	834
E value	1.0e-89
Match length	190
% identity	83
NCBI Description	(AF098519) unknown [Avicennia marina] >gi|4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	191767
Contig ID	4793_3.R1039
5'-most EST	LIB3272-048-P1-K1-E6
Method	BLASTX
NCBI GI	g3851636
BLAST score	841
E value	3.0e-90
Match length	190
% identity	84
NCBI Description	(AF098519) unknown [Avicennia marina] >gi|4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	191768
Contig ID	4793_5.R1039
5'-most EST	uC-gsronu33B036h04b1
Method	BLASTX
NCBI GI	g3851636
BLAST score	311
E value	2.0e-28
Match length	74
% identity	80
NCBI Description	(AF098519) unknown [Avicennia marina] >gi|4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	191769
Contig ID	4795_1.R1039
5'-most EST	LIB3083-082-Q1-L1-E4
Method	BLASTX
NCBI GI	g2098709
BLAST score	1727
E value	0.0e+00
Match length	424
% identity	76
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	191770
Contig ID	4797_1.R1039
5'-most EST	LIB3197-060-Q1-M1-A2
Method	BLASTX
NCBI GI	g586076

BLAST score	2198
E value	0.0e+00
Match length	432
% identity	96
NCBI Description	TUBULIN BETA-1 CHAIN >gi|486734|pir||S35142 tubulin beta chain - white lupine >gi|402636|emb|CAA49736| (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	191771
Contig ID	4797_2.R1039
5'-most EST	LIB3189-030-P1-K1-F4
Method	BLASTX
NCBI GI	g2827753
BLAST score	523
E value	4.0e-53
Match length	100
% identity	99
NCBI Description	TUBULIN BETA CHAIN >gi|1490665 (U64029) beta-tubulin 1 [Daucus carota]

Seq. No.	191772
Contig ID	4797_3.R1039
5'-most EST	LIB3197-021-Q1-M1-D9
Method	BLASTX
NCBI GI	g586076
BLAST score	715
E value	8.0e-76
Match length	139
% identity	91
NCBI Description	TUBULIN BETA-1 CHAIN >gi|486734|pir||S35142 tubulin beta chain - white lupine >gi|402636|emb|CAA49736| (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No.	191773
Contig ID	4801_1.R1039
5'-most EST	g5048386
Method	BLASTX
NCBI GI	g2270994
BLAST score	234
E value	4.0e-40
Match length	146
% identity	55
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	191774
Contig ID	4802_1.R1039
5'-most EST	g5045500
Method	BLASTX
NCBI GI	g2494299
BLAST score	698
E value	1.0e-73
Match length	221
% identity	67
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi|1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	191775
Contig ID	4807_1.R1039
5'-most EST	g5047333
Method	BLASTX
NCBI GI	g4091008
BLAST score	678
E value	3.0e-71
Match length	230
% identity	58
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	191776
Contig ID	4810_1.R1039
5'-most EST	LIB3083-006-Q1-L1-G8
Method	BLASTX
NCBI GI	g3786005
BLAST score	547
E value	7.0e-59
Match length	172
% identity	39
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	191777
Contig ID	4815_1.R1039
5'-most EST	LIB3083-104-Q1-L1-D5
Method	BLASTX
NCBI GI	g1076315
BLAST score	332
E value	7.0e-31
Match length	174
% identity	42
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi|853719|emb|CAA60793| (X87367) CYP90 protein [Arabidopsis thaliana] >gi|871988|emb|CAA60794| (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	191778
Contig ID	4816_1.R1039
5'-most EST	LIB3083-056-Q1-L1-E7
Method	BLASTX
NCBI GI	g1542941
BLAST score	360
E value	8.0e-34
Match length	111
% identity	71
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	191779
Contig ID	4816_3.R1039
5'-most EST	LIB3147-042-Q1-K1-D1
Method	BLASTX
NCBI GI	g4262226
BLAST score	253
E value	2.0e-21
Match length	171
% identity	44

NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.	191780
Contig ID	4818_1.R1039
5'-most EST	uC-gsronu33B031d12b1
Method	BLASTX
NCBI GI	g4539389
BLAST score	403
E value	2.0e-39
Match length	138
% identity	64
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]
Seq. No.	191781
Contig ID	4824_1.R1039
5'-most EST	g5044863
Method	BLASTX
NCBI GI	g4006890
BLAST score	787
E value	6.0e-84
Match length	182
% identity	80
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]
Seq. No.	191782
Contig ID	4824_2.R1039
5'-most EST	uC-gsronu33B124h01b1
Method	BLASTX
NCBI GI	g4006890
BLAST score	818
E value	1.0e-87
Match length	179
% identity	87
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]
Seq. No.	191783
Contig ID	4824_3.R1039
5'-most EST	LIB3149-035-Q1-K1-H5
Method	BLASTX
NCBI GI	g4006890
BLAST score	540
E value	3.0e-55
Match length	105
% identity	90
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]
Seq. No.	191784
Contig ID	4827_1.R1039
5'-most EST	LIB3165-013-P1-K1-E4
Method	BLASTX
NCBI GI	g2642448
BLAST score	256
E value	2.0e-22
Match length	163

% identity	15
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi|3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191785
Contig ID	4830_1.R1039
5'-most EST	g5048067
Method	BLASTX
NCBI GI	g3128175
BLAST score	181
E value	7.0e-13
Match length	100
% identity	39
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	191786
Contig ID	4831_1.R1039
5'-most EST	uC-gsflnu33B112d03b1
Method	BLASTX
NCBI GI	g2245066
BLAST score	780
E value	3.0e-83
Match length	196
% identity	69
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	191787
Contig ID	4839_1.R1039
5'-most EST	uC-gsflnu33B008f12b1
Method	BLASTX
NCBI GI	g1174448
BLAST score	713
E value	4.0e-75
Match length	233
% identity	61
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi|547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	191788
Contig ID	4839_2.R1039
5'-most EST	LIB3196-049-P1-M1-C10
Method	BLASTX
NCBI GI	g1174448
BLAST score	328
E value	2.0e-30
Match length	121
% identity	58
NCBI Description	TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi|547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No.	191789
Contig ID	4840_1.R1039

5'-most EST	LIB3083-007-Q1-L1-E3
Method	BLASTX
NCBI GI	g3175990
BLAST score	862
E value	7.0e-93
Match length	212
% identity	76
NCBI Description	(AJ005836) GDP dissociation inhibitor [Cicer arietinum]

Seq. No.	191790
Contig ID	4842_1.R1039
5'-most EST	LIB3145-015-Q1-K1-A11

Seq. No.	191791
Contig ID	4845_1.R1039
5'-most EST	LIB3083-113-Q1-L1-E8

Seq. No.	191792
Contig ID	4847_1.R1039
5'-most EST	uC-gsronu33B077g11b1
Method	BLASTX
NCBI GI	g1632831
BLAST score	666
E value	7.0e-70
Match length	142
% identity	92
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	191793
Contig ID	4847_2.R1039
5'-most EST	LIB3148-022-Q1-K1-F3
Method	BLASTX
NCBI GI	g1632831
BLAST score	147
E value	4.0e-10
Match length	41
% identity	71
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	191794
Contig ID	4849_1.R1039
5'-most EST	LIB3083-099-Q1-L1-E6
Method	BLASTX
NCBI GI	g2129473
BLAST score	407
E value	2.0e-39
Match length	197
% identity	46
NCBI Description	arabinogalactan-like protein - loblolly pine >gi|607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	191795
Contig ID	4850_1.R1039
5'-most EST	LIB3083-007-Q1-L1-D12
Method	BLASTX
NCBI GI	g3335359
BLAST score	586

E value	3.0e-63
Match length	149
% identity	81
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	191796
Contig ID	4852_1.R1039
5'-most EST	uC-gsronu33B166a10b2
Method	BLASTX
NCBI GI	g3482974
BLAST score	928
E value	1.0e-100
Match length	214
% identity	84
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	191797
Contig ID	4855_1.R1039
5'-most EST	LIB3083-007-Q1-L1-D7
Method	BLASTX
NCBI GI	g4455234
BLAST score	301
E value	1.0e-30
Match length	141
% identity	52
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	191798
Contig ID	4860_1.R1039
5'-most EST	g5049822
Method	BLASTX
NCBI GI	g3608141
BLAST score	171
E value	1.0e-11
Match length	149
% identity	38
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	191799
Contig ID	4869_1.R1039
5'-most EST	LIB3145-052-Q1-K1-G8
Method	BLASTX
NCBI GI	g2129597
BLAST score	689
E value	1.0e-72
Match length	142
% identity	92
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi|1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi|1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	191800
Contig ID	4870_1.R1039
5'-most EST	LIB3083-007-Q1-L1-F10
Method	BLASTX

NCBI GI	g3695388
BLAST score	248
E value	9.0e-21
Match length	91
% identity	48
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	191801
Contig ID	4871_1.R1039
5'-most EST	LIB3083-090-Q1-L1-A9
Method	BLASTX
NCBI GI	g3885328
BLAST score	647
E value	2.0e-67
Match length	277
% identity	47
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	191802
Contig ID	4873_1.R1039
5'-most EST	uC-gsflnu33B072d12b1
Method	BLASTX
NCBI GI	g1346735
BLAST score	2455
E value	0.0e+00
Match length	553
% identity	84
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi|1076562|pir||S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi|474170|emb|CAA49995| (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No.	191803
Contig ID	4873_2.R1039
5'-most EST	LIB3147-027-Q1-K1-F8
Method	BLASTX
NCBI GI	g1346735
BLAST score	323
E value	9.0e-30
Match length	100
% identity	64
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi|1076562|pir||S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi|474170|emb|CAA49995| (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No.	191804
Contig ID	4873_3.R1039
5'-most EST	LIB3145-050-Q1-K1-C6
Method	BLASTX
NCBI GI	g1346735
BLAST score	405
E value	2.0e-39
Match length	117

% identity	68
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi|1076562|pir||S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi|474170|emb|CAA49995| (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No.	191805
Contig ID	4874_1.R1039
5'-most EST	LIB3120-019-Q1-K1-F11
Method	BLASTX
NCBI GI	g1706958
BLAST score	1191
E value	1.0e-131
Match length	293
% identity	77
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	191806
Contig ID	4875_1.R1039
5'-most EST	LIB3120-024-Q1-K1-C4

Seq. No.	191807
Contig ID	4885_1.R1039
5'-most EST	uC-gsflnu33B062h04b1
Method	BLASTX
NCBI GI	g4539330
BLAST score	244
E value	2.0e-20
Match length	147
% identity	41
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	191808
Contig ID	4886_1.R1039
5'-most EST	LIB3145-055-Q1-K1-A9
Method	BLASTX
NCBI GI	g3212116
BLAST score	290
E value	9.0e-26
Match length	127
% identity	46
NCBI Description	(Y17393) prefoldin subunit 2 [Mus musculus]

Seq. No.	191809
Contig ID	4888_1.R1039
5'-most EST	uC-gsflnu33B084a04b1

Seq. No.	191810
Contig ID	4890_1.R1039
5'-most EST	LIB3083-027-Q1-L1-A3
Method	BLASTX
NCBI GI	g481762
BLAST score	371
E value	5.0e-35
Match length	347

% identity	31
NCBI Description	beta-adaptin 1 - fruit fly (Drosophila melanogaster) >gi|434902|emb|CAA53509| (X75910) beta-adaptin Drosophila 1 [Drosophila melanogaster]

Seq. No.	191811
Contig ID	4892_1.R1039
5'-most EST	LIB3083-060-Q1-L1-A1
Method	BLASTX
NCBI GI	g1370196
BLAST score	750
E value	1.0e-79
Match length	175
% identity	85
NCBI Description	(Z73947) RAB8D [Lotus japonicus]

Seq. No.	191812
Contig ID	4895_1.R1039
5'-most EST	g5044921
Method	BLASTX
NCBI GI	g2642443
BLAST score	965
E value	1.0e-104
Match length	509
% identity	39
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	191813
Contig ID	4896_1.R1039
5'-most EST	LIB3189-018-P1-K1-D1

Seq. No.	191814
Contig ID	4896_2.R1039
5'-most EST	LIB3083-007-Q1-L1-H8

Seq. No.	191815
Contig ID	4898_1.R1039
5'-most EST	LIB3083-008-Q1-L1-A10
Method	BLASTX
NCBI GI	g133872
BLAST score	1582
E value	1.0e-177
Match length	392
% identity	82
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi|282838|pir||S26494 ribosomal protein S1, chloroplast - spinach >gi|322404|pir||A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi|18060|emb|CAA46927| (X66135) ribosomal protein S1 [Spinacia oleracea] >gi|170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	191816
Contig ID	4899_1.R1039
5'-most EST	LIB3146-042-Q1-K1-A8
Method	BLASTX
NCBI GI	g2341041

BLAST score	222
E value	7.0e-39
Match length	141
% identity	62
NCBI Description	(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb|AF047976). EST gb|W43451 comes from this gene. [Arabidopsis thaliana] >gi|3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No.	191817
Contig ID	4901_1.R1039
5'-most EST	g5050632
Method	BLASTX
NCBI GI	g2190547
BLAST score	595
E value	1.0e-61
Match length	201
% identity	57
NCBI Description	(AC001229) ESTs gb|T43256,gb|46316,gb|N64930,gb|AA395255,gb|AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	191818
Contig ID	4906_1.R1039
5'-most EST	LIB3197-020-Q1-M1-G6
Method	BLASTX
NCBI GI	g4512671
BLAST score	179
E value	1.0e-12
Match length	45
% identity	71
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	191819
Contig ID	4906_2.R1039
5'-most EST	g5048108
Method	BLASTX
NCBI GI	g4512671
BLAST score	131
E value	2.0e-10
Match length	37
% identity	86
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	191820
Contig ID	4906_3.R1039
5'-most EST	LIB3197-007-P1-M1-H4
Method	BLASTX
NCBI GI	g4512671
BLAST score	377
E value	1.0e-35
Match length	110
% identity	65
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	191821
Contig ID	4907_1.R1039

5'-most EST	g3326072
Method	BLASTX
NCBI GI	g4234941
BLAST score	700
E value	1.0e-84
Match length	201
% identity	83
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	191822
Contig ID	4910_1.R1039
5'-most EST	uC-gsflmaxxa119a02b1
Method	BLASTX
NCBI GI	g2497753
BLAST score	376
E value	1.0e-35
Match length	123
% identity	55
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi|1321915|emb|CAA65477| (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	191823
Contig ID	4910_2.R1039
5'-most EST	LIB3146-012-Q1-K1-A1
Method	BLASTX
NCBI GI	g2497753
BLAST score	176
E value	4.0e-24
Match length	124
% identity	50
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi|1321915|emb|CAA65477| (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	191824
Contig ID	4911_1.R1039
5'-most EST	LIB3083-008-Q1-L1-D12
Method	BLASTX
NCBI GI	g2213602
BLAST score	310
E value	5.0e-28
Match length	152
% identity	49
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	191825
Contig ID	4914_1.R1039
5'-most EST	uC-gsflnu33B135d05b1
Method	BLASTX
NCBI GI	g2129613
BLAST score	164
E value	2.0e-11
Match length	116
% identity	43
NCBI Description	homeotic protein BEL1 - Arabidopsis thaliana >gi|1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No.	191826
Contig ID	4917_1.R1039
5'-most EST	LIB3083-079-Q1-L1-C10
Method	BLASTX
NCBI GI	g1171577
BLAST score	313
E value	2.0e-28
Match length	174
% identity	36
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	191827
Contig ID	4919_1.R1039
5'-most EST	g5049026
Method	BLASTX
NCBI GI	g4006848
BLAST score	361
E value	3.0e-34
Match length	141
% identity	52
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	191828
Contig ID	4921_1.R1039
5'-most EST	LIB3272-020-P1-K1-A10
Method	BLASTX
NCBI GI	g1657948
BLAST score	621
E value	1.0e-64
Match length	128
% identity	91
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	191829
Contig ID	4921_2.R1039
5'-most EST	uC-gsronu33B038e07b1
Method	BLASTX
NCBI GI	g1657948
BLAST score	1117
E value	1.0e-122
Match length	257
% identity	82
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	191830
Contig ID	4922_1.R1039
5'-most EST	uC-gsronu33B036e02b1
Method	BLASTX
NCBI GI	g1408471
BLAST score	631
E value	2.0e-65
Match length	139
% identity	83
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	191831
Contig ID	4922_4.R1039
5'-most EST	LIB3149-055-Q1-K1-B5
Method	BLASTX
NCBI GI	g1408471
BLAST score	158
E value	1.0e-10
Match length	39
% identity	82
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	191832
Contig ID	4922_5.R1039
5'-most EST	LIB3147-023-Q1-K1-E7
Method	BLASTX
NCBI GI	g1408471
BLAST score	484
E value	1.0e-48
Match length	141
% identity	67
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi|3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	191833
Contig ID	4923_1.R1039
5'-most EST	LIB3083-076-Q1-L1-F1
Method	BLASTX
NCBI GI	g1729980
BLAST score	531
E value	4.0e-54
Match length	117
% identity	79
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi|2129751|pir||S71175 thaumatin-like protein - Arabidopsis thaliana >gi|536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi|1094863|prf||2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	191834
Contig ID	4926_1.R1039
5'-most EST	LIB3146-043-Q1-K1-C1
Method	BLASTX
NCBI GI	g4490727
BLAST score	145
E value	7.0e-09
Match length	209
% identity	15
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	191835
Contig ID	4928_1.R1039

5'-most EST	LIB3083-008-Q1-L1-H9
Method	BLASTX
NCBI GI	g3212854
BLAST score	548
E value	5.0e-64
Match length	257
% identity	59
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	191836
Contig ID	4932_1.R1039
5'-most EST	LIB3146-057-Q1-K1-H6
Method	BLASTX
NCBI GI	g3927831
BLAST score	512
E value	5.0e-52
Match length	137
% identity	73
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	191837
Contig ID	4934_1.R1039
5'-most EST	LIB3147-013-Q1-K1-G12

Seq. No.	191838
Contig ID	4934_2.R1039
5'-most EST	LIB3189-005-P1-K1-D9

Seq. No.	191839
Contig ID	4935_1.R1039
5'-most EST	LIB3145-015-Q1-K1-F6

Seq. No.	191840
Contig ID	4936_1.R1039
5'-most EST	LIB3083-009-Q1-L1-F11

Seq. No.	191841
Contig ID	4939_1.R1039
5'-most EST	g5048134
Method	BLASTN
NCBI GI	g16504
BLAST score	192
E value	1.0e-103
Match length	548
% identity	84
NCBI Description	Arabidopsis thaliana rpII gene for RNA polymerase large subunit (EC 2.7.7.6)

Seq. No.	191842
Contig ID	4943_1.R1039
5'-most EST	LIB3083-009-Q1-L1-G5

Seq. No.	191843
Contig ID	4947_1.R1039
5'-most EST	uC-gsflmaxxa026e02b1
Method	BLASTX

NCBI GI	g3114903
BLAST score	1250
E value	1.0e-138
Match length	308
% identity	79
NCBI Description	(AJ005805) pcberl [Populus balsamifera subsp. trichocarpa]

Seq. No.	191844
Contig ID	4947_2.R1039
5'-most EST	LIB3189-041-P1-K1-G12
Method	BLASTX
NCBI GI	g2935416
BLAST score	650
E value	3.0e-68
Match length	157
% identity	80
NCBI Description	(AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No.	191845
Contig ID	4949_1.R1039
5'-most EST	uC-gsflmaxxa096f10b1
Method	BLASTX
NCBI GI	g3859606
BLAST score	687
E value	2.0e-72
Match length	185
% identity	70
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	191846
Contig ID	4949_2.R1039
5'-most EST	LIB3145-042-Q1-K1-A6
Method	BLASTX
NCBI GI	g3859606
BLAST score	510
E value	1.0e-51
Match length	156
% identity	65
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	191847
Contig ID	4957_1.R1039
5'-most EST	g5046619
Method	BLASTX
NCBI GI	g4204575
BLAST score	306
E value	3.0e-34
Match length	120
% identity	65
NCBI Description	(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No.	191848
Contig ID	4957_2.R1039
5'-most EST	LIB3146-003-P1-K1-A4
Method	BLASTX

NCBI GI	g4204575
BLAST score	411
E value	4.0e-40
Match length	127
% identity	63
NCBI Description	(AF098510) cytochrome b5 DIF-F [Petunia x hybrida]

Seq. No.	191849
Contig ID	4960_1.R1039
5'-most EST	LIB3189-014-P1-K1-H8
Method	BLASTN
NCBI GI	g3421113
BLAST score	107
E value	9.0e-53
Match length	503
% identity	80
NCBI Description	Arabidopsis thaliana 20S proteasome beta subunit PBD2 (PBD2) mRNA, complete cds

Seq. No.	191850
Contig ID	4961_1.R1039
5'-most EST	g5045502
Method	BLASTX
NCBI GI	g3881507
BLAST score	336
E value	6.0e-39
Match length	145
% identity	52
NCBI Description	(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	191851
Contig ID	4963_1.R1039
5'-most EST	uC-gsronu33B158h02b2
Method	BLASTX
NCBI GI	g2961300
BLAST score	492
E value	2.0e-49
Match length	112
% identity	85
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	191852
Contig ID	4963_2.R1039
5'-most EST	LIB3147-057-Q1-K1-H6
Method	BLASTN
NCBI GI	g2961299
BLAST score	69
E value	2.0e-30
Match length	341
% identity	80
NCBI Description	Cicer arietinum mRNA for ribosomal protein L24

Seq. No.	191853
Contig ID	4963_3.R1039
5'-most EST	LIB3149-030-Q1-K1-A11
Method	BLASTX

NCBI GI	g2961300
BLAST score	236
E value	2.0e-37
Match length	111
% identity	77
NCBI Description	(AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No.	191854
Contig ID	4964_1.R1039
5'-most EST	LIB3083-051-Q1-L1-B8
Method	BLASTX
NCBI GI	g4263771
BLAST score	149
E value	2.0e-09
Match length	150
% identity	28
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	191855
Contig ID	4968_1.R1039
5'-most EST	LIB3083-101-Q1-L1-E6
Method	BLASTX
NCBI GI	g3327868
BLAST score	193
E value	1.0e-14
Match length	171
% identity	37
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	191856
Contig ID	4971_1.R1039
5'-most EST	uC-gsflmaxxa048h09b1
Method	BLASTX
NCBI GI	g4115377
BLAST score	1799
E value	0.0e+00
Match length	421
% identity	78
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	191857
Contig ID	4973_1.R1039
5'-most EST	LIB3083-078-Q1-L1-F1

Seq. No.	191858
Contig ID	4981_1.R1039
5'-most EST	LIB3145-005-Q1-K1-G5
Method	BLASTX
NCBI GI	g2285792
BLAST score	397
E value	2.0e-48
Match length	157
% identity	66
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi|3287503|dbj|BAA31224| (AB015748) cyanase [Arabidopsis

thaliana]

Seq. No.	191859
Contig ID	4982_1.R1039
5'-most EST	LIB3083-010-Q1-L1-F1

Seq. No.	191860
Contig ID	4984_1.R1039
5'-most EST	LIB3135-008-Q1-K1-G7
Method	BLASTX
NCBI GI	g3548810
BLAST score	619
E value	8.0e-64
Match length	401
% identity	40
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	191861
Contig ID	4984_2.R1039
5'-most EST	LIB3166-019-P1-K1-C4
Method	BLASTX
NCBI GI	g2541876
BLAST score	446
E value	8.0e-44
Match length	290
% identity	38
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	191862
Contig ID	4985_1.R1039
5'-most EST	g3326661
Method	BLASTX
NCBI GI	g4490342
BLAST score	416
E value	1.0e-59
Match length	261
% identity	57
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	191863
Contig ID	4996_1.R1039
5'-most EST	LIB3083-010-Q1-L1-H1
Method	BLASTX
NCBI GI	g4262226
BLAST score	291
E value	4.0e-26
Match length	101
% identity	57
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	191864
Contig ID	5010_1.R1039
5'-most EST	LIB3083-107-Q1-L1-A10
Method	BLASTX
NCBI GI	g1917019

BLAST score	988
E value	1.0e-107
Match length	248
% identity	79
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	191865
Contig ID	5010_2.R1039
5'-most EST	uC-gsflnu33B129h01b1
Method	BLASTX
NCBI GI	g3123271
BLAST score	527
E value	6.0e-54
Match length	105
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi|2224751|emb|CAA74381| (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	191866
Contig ID	5011_1.R1039
5'-most EST	uC-gsflnu33B084b12b1
Method	BLASTX
NCBI GI	g1915974
BLAST score	1381
E value	1.0e-153
Match length	327
% identity	83
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi|2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	191867
Contig ID	5011_2.R1039
5'-most EST	uC-gsronu33B101c02b1
Method	BLASTX
NCBI GI	g585973
BLAST score	585
E value	1.0e-60
Match length	135
% identity	87
NCBI Description	FRUCTOKINASE >gi|626018|pir||S39997 fructokinase (EC 2.7.1.4) - potato >gi|297015|emb|CAA78283| (Z12823) fructokinase [Solanum tuberosum] >gi|1095321|prf||2108342A fructokinase [Solanum tuberosum]

Seq. No.	191868
Contig ID	5025_1.R1039
5'-most EST	g5048743
Method	BLASTX
NCBI GI	g1495251
BLAST score	278
E value	2.0e-24
Match length	122
% identity	53
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	191869
Contig ID	5026_1.R1039

5'-most EST	LIB3197-026-Q1-M1-F9
Method	BLASTN
NCBI GI	g3046851
BLAST score	35
E value	1.0e-09
Match length	138
% identity	45
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	191870
Contig ID	5026_3.R1039
5'-most EST	LIB3165-019-P1-K1-B1

Seq. No.	191871
Contig ID	5027_1.R1039
5'-most EST	uC-gsflmaxxa038c11b1
Method	BLASTX
NCBI GI	g2765837
BLAST score	254
E value	2.0e-21
Match length	88
% identity	68
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	191872
Contig ID	5028_1.R1039
5'-most EST	LIB3272-051-P1-K1-B11
Method	BLASTX
NCBI GI	g1815759
BLAST score	272
E value	1.0e-23
Match length	158
% identity	39
NCBI Description	(U85499) pollen-specific protein [Phalaris coerulescens]

Seq. No.	191873
Contig ID	5028_2.R1039
5'-most EST	LIB3083-114-Q1-L1-A8
Method	BLASTX
NCBI GI	g125887
BLAST score	193
E value	4.0e-20
Match length	151
% identity	40
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi|82092|pir||S04765 LAT52 protein precursor - tomato >gi|295812|emb|CAA33854| (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	191874
Contig ID	5028_3.R1039
5'-most EST	uC-gsflnu33B050e07b1
Method	BLASTX
NCBI GI	g125887
BLAST score	158
E value	8.0e-13

Match length	116
% identity	41
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi|82092|pir||S04765 LAT52 protein precursor - tomato >gi|295812|emb|CAA33854| (X15855) LAT52 [Lycopersicon esculentum]

Seq. No.	191875
Contig ID	5028_4.R1039
5'-most EST	LIB3272-010-P1-K1-E6

Seq. No.	191876
Contig ID	5028_6.R1039
5'-most EST	uC-gsronu33B047f03b1
Method	BLASTX
NCBI GI	g1815759
BLAST score	192
E value	3.0e-14
Match length	90
% identity	39
NCBI Description	(U85499) pollen-specific protein [Phalaris coerulescens]

Seq. No.	191877
Contig ID	5028_7.R1039
5'-most EST	LIB3146-033-Q1-K1-B1

Seq. No.	191878
Contig ID	5029_1.R1039
5'-most EST	g5046976
Method	BLASTX
NCBI GI	g4097579
BLAST score	914
E value	9.0e-99
Match length	193
% identity	88
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	191879
Contig ID	5029_2.R1039
5'-most EST	uC-gsronu33B021a04b1
Method	BLASTX
NCBI GI	g4097579
BLAST score	601
E value	2.0e-62
Match length	124
% identity	89
NCBI Description	(U64922) NTGP1 [Nicotiana tabacum]

Seq. No.	191880
Contig ID	5033_1.R1039
5'-most EST	LIB3083-011-Q1-L1-G12

Seq. No.	191881
Contig ID	5035_1.R1039
5'-most EST	LIB3272-023-P1-K1-G6
Method	BLASTX
NCBI GI	g4558659

BLAST score	603
E value	1.0e-62
Match length	145
% identity	73
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	191882
Contig ID	5042_1.R1039
5'-most EST	uC-gsflnu33B109b08b1
Method	BLASTX
NCBI GI	g4406372
BLAST score	175
E value	2.0e-12
Match length	40
% identity	82
NCBI Description	(AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No.	191883
Contig ID	5043_1.R1039
5'-most EST	LIB3083-012-Q1-L1-A4

Seq. No.	191884
Contig ID	5051_1.R1039
5'-most EST	LIB3083-012-Q1-L1-B2
Method	BLASTX
NCBI GI	g3047117
BLAST score	689
E value	1.0e-72
Match length	140
% identity	92
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	191885
Contig ID	5052_1.R1039
5'-most EST	LIB3189-053-P1-K1-B5
Method	BLASTN
NCBI GI	g3643588
BLAST score	35
E value	4.0e-10
Match length	55
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191886
Contig ID	5054_1.R1039
5'-most EST	LIB3197-021-Q1-M1-B1
Method	BLASTX
NCBI GI	g3176098
BLAST score	602
E value	2.0e-62
Match length	180
% identity	40
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	191887
Contig ID	5055_1.R1039
5'-most EST	LIB3083-012-Q1-L1-B7
Method	BLASTX
NCBI GI	g2244910
BLAST score	153
E value	3.0e-10
Match length	34
% identity	85
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	191888
Contig ID	5063_1.R1039
5'-most EST	LIB3135-008-Q1-K1-H8
Method	BLASTX
NCBI GI	g3925363
BLAST score	1016
E value	1.0e-111
Match length	310
% identity	64
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	191889
Contig ID	5069_1.R1039
5'-most EST	g5049652
Method	BLASTX
NCBI GI	g1651828
BLAST score	751
E value	2.0e-83
Match length	273
% identity	63
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	191890
Contig ID	5071_1.R1039
5'-most EST	LIB3083-012-Q1-L1-D3
Method	BLASTX
NCBI GI	g4490733
BLAST score	1106
E value	1.0e-121
Match length	335
% identity	64
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	191891
Contig ID	5074_1.R1039
5'-most EST	LIB3083-015-Q1-L2-C5
Method	BLASTX
NCBI GI	g1351856
BLAST score	828
E value	5.0e-89
Match length	188
% identity	85
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi|868003|dbj|BAA06108| (D29629) aconitase [Cucurbita sp.]

Seq. No.	191892
Contig ID	5082_1.R1039
5'-most EST	LIB3135-060-Q1-K1-H7
Method	BLASTX
NCBI GI	g4467147
BLAST score	810
E value	1.0e-86
Match length	204
% identity	77
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	191893
Contig ID	5085_1.R1039
5'-most EST	LIB3149-047-Q1-K1-D7

Seq. No.	191894
Contig ID	5086_1.R1039
5'-most EST	LIB3083-012-Q1-L1-E7
Method	BLASTX
NCBI GI	g169363
BLAST score	200
E value	2.0e-15
Match length	59
% identity	54
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	191895
Contig ID	5092_1.R1039
5'-most EST	LIB3165-047-Q1-K1-B4
Method	BLASTX
NCBI GI	g3559814
BLAST score	1973
E value	0.0e+00
Match length	716
% identity	82
NCBI Description	(Y15781) transketolase 1 [Capsicum annuum]

Seq. No.	191896
Contig ID	5092_2.R1039
5'-most EST	uC-gsronu33B136e05b1
Method	BLASTN
NCBI GI	g4263694
BLAST score	42
E value	3.0e-14
Match length	194
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191897
Contig ID	5094_1.R1039
5'-most EST	LIB3083-012-Q1-L1-F4
Method	BLASTX
NCBI GI	g3033380
BLAST score	816
E value	1.0e-126
Match length	288

% identity	81
NCBI Description	(AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No.	191898
Contig ID	5099_1.R1039
5'-most EST	uC-gsflnu33B075c02b1
Method	BLASTN
NCBI GI	g3033373
BLAST score	44
E value	4.0e-15
Match length	337
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	191899
Contig ID	5100_1.R1039
5'-most EST	uC-gsflmaxxa039f09b1
Method	BLASTX
NCBI GI	g2388689
BLAST score	1047
E value	1.0e-114
Match length	348
% identity	62
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	191900
Contig ID	5100_2.R1039
5'-most EST	LIB3146-038-P1-K1-C12
Method	BLASTX
NCBI GI	g2388689
BLAST score	528
E value	1.0e-53
Match length	128
% identity	79
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	191901
Contig ID	5100_3.R1039
5'-most EST	LIB3272-006-P1-K1-B7
Method	BLASTX
NCBI GI	g2388689
BLAST score	185
E value	1.0e-13
Match length	61
% identity	66
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	191902
Contig ID	5106_1.R1039
5'-most EST	LIB3083-012-Q1-L1-G5
Method	BLASTX
NCBI GI	g2244861
BLAST score	272
E value	6.0e-24
Match length	105

% identity	58
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	191903
Contig ID	5107_1.R1039
5'-most EST	LIB3165-032-P1-K1-D5
Method	BLASTX
NCBI GI	g2924325
BLAST score	307
E value	5.0e-28
Match length	70
% identity	80
NCBI Description	(Z93765) hypothetical protein [Malus domestica]

Seq. No.	191904
Contig ID	5109_1.R1039
5'-most EST	LIB3083-012-Q1-L1-G8
Method	BLASTX
NCBI GI	g1173200
BLAST score	154
E value	4.0e-10
Match length	48
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S14

Seq. No.	191905
Contig ID	5110_1.R1039
5'-most EST	uC-gsronu33B049h12b1
Method	BLASTN
NCBI GI	g2828187
BLAST score	40
E value	7.0e-13
Match length	48
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	191906
Contig ID	5110_2.R1039
5'-most EST	LIB3083-012-Q1-L1-G9

Seq. No.	191907
Contig ID	5112_1.R1039
5'-most EST	LIB3120-045-P1-K1-H2

Seq. No.	191908
Contig ID	5114_1.R1039
5'-most EST	LIB3147-010-Q1-K1-E2

Seq. No.	191909
Contig ID	5116_1.R1039
5'-most EST	uC-gsflnu33B091h10b1
Method	BLASTX
NCBI GI	g2661840
BLAST score	625
E value	7.0e-65
Match length	168

% identity	70
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	191910
Contig ID	5116_2.R1039
5'-most EST	g5045958
Method	BLASTX
NCBI GI	g2661840
BLAST score	1130
E value	1.0e-124
Match length	315
% identity	66
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	191911
Contig ID	5117_1.R1039
5'-most EST	LIB3145-038-Q1-K1-A8
Method	BLASTX
NCBI GI	g2497486
BLAST score	795
E value	9.0e-85
Match length	204
% identity	78
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi|2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	191912
Contig ID	5117_3.R1039
5'-most EST	LIB3145-038-Q1-K1-A9
Method	BLASTX
NCBI GI	g2497486
BLAST score	535
E value	2.0e-54
Match length	125
% identity	82
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi|2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	191913
Contig ID	5118_1.R1039
5'-most EST	LIB3197-026-Q1-M1-F7
Method	BLASTX
NCBI GI	g547683
BLAST score	2302
E value	0.0e+00
Match length	592
% identity	78
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi|170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi|445601|prf||1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	191914
Contig ID	5118_2.R1039
5'-most EST	LIB3149-007-Q1-K1-B12

Method	BLASTX
NCBI GI	g2495365
BLAST score	398
E value	1.0e-38
Match length	114
% identity	75
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi|445127|prf||1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	191915
Contig ID	5118_3.R1039
5'-most EST	LIB3148-057-Q1-K1-D2
Method	BLASTX
NCBI GI	g2495365
BLAST score	270
E value	2.0e-23
Match length	103
% identity	60
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi|445127|prf||1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	191916
Contig ID	5118_6.R1039
5'-most EST	LIB3148-055-Q1-K1-A1

Seq. No.	191917
Contig ID	5121_1.R1039
5'-most EST	LIB3083-013-Q1-L1-C2
Method	BLASTN
NCBI GI	g3985958
BLAST score	53
E value	6.0e-21
Match length	212
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	191918
Contig ID	5124_1.R1039
5'-most EST	LIB3083-037-Q1-G1-B6
Method	BLASTX
NCBI GI	g4371292
BLAST score	927
E value	1.0e-100
Match length	271
% identity	65
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	191919
Contig ID	5130_1.R1039
5'-most EST	LIB3083-014-Q1-L1-A1
Method	BLASTX
NCBI GI	g3522942
BLAST score	296
E value	9.0e-27
Match length	120
% identity	53

NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	191920
Contig ID	5137_1.R1039
5'-most EST	uC-gsflmaxxa093a11b1
Method	BLASTX
NCBI GI	g1354849
BLAST score	626
E value	3.0e-65
Match length	188
% identity	63
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	191921
Contig ID	5140_1.R1039
5'-most EST	LIB3083-014-Q1-L1-B2

Seq. No.	191922
Contig ID	5143_1.R1039
5'-most EST	LIB3166-057-P1-K1-B12
Method	BLASTN
NCBI GI	g2982302
BLAST score	46
E value	3.0e-16
Match length	443
% identity	80
NCBI Description	Picea mariana hypothetical protein (Sb50) mRNA, partial cds

Seq. No.	191923
Contig ID	5144_1.R1039
5'-most EST	LIB3083-014-Q1-L1-C1
Method	BLASTX
NCBI GI	g4115931
BLAST score	341
E value	5.0e-32
Match length	124
% identity	60
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	191924
Contig ID	5150_1.R1039
5'-most EST	LIB3197-026-Q1-M1-D12
Method	BLASTX
NCBI GI	g549060
BLAST score	986
E value	1.0e-107
Match length	272
% identity	68
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi|631656|pir||S43058 CCTeta protein eta chain - mouse >gi|468504|emb|CAA83274| (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	191925
Contig ID	5151_1.R1039
5'-most EST	LIB3272-042-P1-K1-A12

Method	BLASTX
NCBI GI	g1694976
BLAST score	372
E value	3.0e-35
Match length	82
% identity	83
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi|2832361|emb|CAA74402| (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	191926
Contig ID	5151_2.R1039
5'-most EST	LIB3146-011-Q1-K1-D1
Method	BLASTX
NCBI GI	g1694976
BLAST score	403
E value	7.0e-39
Match length	112
% identity	68
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi|2832361|emb|CAA74402| (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	191927
Contig ID	5151_3.R1039
5'-most EST	LIB3145-022-Q1-K1-A11
Method	BLASTX
NCBI GI	g1694976
BLAST score	366
E value	1.0e-34
Match length	82
% identity	82
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi|2832361|emb|CAA74402| (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	191928
Contig ID	5151_4.R1039
5'-most EST	uC-gsronu33B008g01b1
Method	BLASTX
NCBI GI	g1694976
BLAST score	370
E value	4.0e-35
Match length	82
% identity	83
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi|2832361|emb|CAA74402| (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	191929
Contig ID	5151_5.R1039
5'-most EST	uC-gsflmaxxa041c11b1
Method	BLASTX
NCBI GI	g1694976
BLAST score	217
E value	2.0e-17
Match length	71

% identity	59
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi|2832361|emb|CAA74402| (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	191930
Contig ID	5152_1.R1039
5'-most EST	LIB3166-024-P1-K1-C10

Seq. No.	191931
Contig ID	5152_2.R1039
5'-most EST	uC-gsronu33B137c09b1

Seq. No.	191932
Contig ID	5154_1.R1039
5'-most EST	LIB3145-016-Q1-K1-G6
Method	BLASTX
NCBI GI	g1362086
BLAST score	3430
E value	0.0e+00
Match length	765
% identity	87
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi|2129919|pir||S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi|886471|emb|CAA58474| (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	191933
Contig ID	5154_2.R1039
5'-most EST	LIB3147-035-Q1-K1-C12
Method	BLASTX
NCBI GI	g508304
BLAST score	236
E value	2.0e-19
Match length	82
% identity	56
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	191934
Contig ID	5154_3.R1039
5'-most EST	uC-gsflmaxxa041g10b1
Method	BLASTX
NCBI GI	g1362086
BLAST score	540
E value	7.0e-70
Match length	143
% identity	92
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi|2129919|pir||S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi|886471|emb|CAA58474| (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	191935
Contig ID	5154_4.R1039
5'-most EST	g3326245
Method	BLASTX
NCBI GI	g532530
BLAST score	946
E value	1.0e-102
Match length	251
% identity	71
NCBI Description	(U07953) 1-aminocyclopropane-1-carboxylate oxidase [Pelargonium hortorum] >gi|1093803|prf||2104412A aminocyclopropane carboxylate oxidase [Pelargonium hortorum]

Seq. No.	191936
Contig ID	5154_9.R1039
5'-most EST	LIB3147-039-Q1-K1-B7
Method	BLASTX
NCBI GI	g1814403
BLAST score	319
E value	1.0e-51
Match length	157
% identity	68
NCBI Description	(U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No.	191937
Contig ID	5154_10.R1039
5'-most EST	g3326473
Method	BLASTX
NCBI GI	g1527191
BLAST score	446
E value	4.0e-46
Match length	155
% identity	65
NCBI Description	(U67861) 1-aminocyclopropane-1-carboxylate oxidase [Pelargonium x hortorum]

Seq. No.	191938
Contig ID	5154_11.R1039
5'-most EST	uC-gsflmaxxa049f06b1
Method	BLASTX
NCBI GI	g974782
BLAST score	1120
E value	1.0e-123
Match length	228
% identity	95
NCBI Description	(Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No.	191939
Contig ID	5154_12.R1039
5'-most EST	LIB3135-035-Q1-K1-F4
Method	BLASTX
NCBI GI	g508304
BLAST score	241

E value 5.0e-20
Match length 82
% identity 57
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 191940
Contig ID 5154_13.R1039
5'-most EST LIB3147-028-Q1-K1-F8
Method BLASTX
NCBI GI g974782
BLAST score 265
E value 5.0e-23
Match length 57
% identity 93
NCBI Description (Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides]

Seq. No. 191941
Contig ID 5154_14.R1039
5'-most EST LIB3272-042-P1-K1-C3
Method BLASTX
NCBI GI g3037047
BLAST score 491
E value 1.0e-49
Match length 114
% identity 75
NCBI Description (AF053354) 1-aminocyclopropane-1-carboxylic acid oxidase [Phaseolus vulgaris]

Seq. No. 191942
Contig ID 5157_2.R1039
5'-most EST LIB3083-014-Q1-L1-D7

Seq. No. 191943
Contig ID 5163_1.R1039
5'-most EST LIB3083-014-Q1-L1-E5
Method BLASTX
NCBI GI g1245343
BLAST score 137
E value 3.0e-11
Match length 231
% identity 29
NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 191944
Contig ID 5170_1.R1039
5'-most EST LIB3197-059-Q1-M1-A9
Method BLASTX
NCBI GI g2435518
BLAST score 312
E value 3.0e-28
Match length 161
% identity 39
NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No. 191945

Contig ID 5171_1.R1039
5'-most EST LIB3083-046-Q1-G1-G1
Method BLASTX
NCBI GI g407992
BLAST score 176
E value 9.0e-13
Match length 84
% identity 46
NCBI Description (L25125) RNA helicase [Mus musculus]

Seq. No. 191946
Contig ID 5184_1.R1039
5'-most EST LIB3083-015-Q1-L1-A1
Method BLASTX
NCBI GI g3309583
BLAST score 1125
E value 1.0e-123
Match length 239
% identity 89
NCBI Description (AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No. 191947
Contig ID 5186_1.R1039
5'-most EST g5049692

Seq. No. 191948
Contig ID 5187_1.R1039
5'-most EST LIB3083-015-Q1-L2-A2

Seq. No. 191949
Contig ID 5188_1.R1039
5'-most EST LIB3083-015-Q1-L2-A3
Method BLASTX
NCBI GI g1362046
BLAST score 519
E value 9.0e-53
Match length 130
% identity 78
NCBI Description aspartate transaminase (EC 2.6.1.1) precursor - soybean >gi|710596 (L40579) mitochondrial aspartate aminotransferase [Glycine max]

Seq. No. 191950
Contig ID 5189_1.R1039
5'-most EST LIB3083-015-Q1-L2-A4
Method BLASTX
NCBI GI g4415936
BLAST score 223
E value 5.0e-18
Match length 154
% identity 41
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 191951
Contig ID 5192_1.R1039
5'-most EST g3325739

Seq. No.	191952
Contig ID	5192_2.R1039
5'-most EST	LIB3145-002-P1-K1-A12
Method	BLASTN
NCBI GI	g2865522
BLAST score	38
E value	1.0e-11
Match length	103
% identity	92
NCBI Description	Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA, complete cds

Seq. No.	191953
Contig ID	5192_3.R1039
5'-most EST	LIB3149-034-Q1-K1-C2
Method	BLASTN
NCBI GI	g2865522
BLAST score	33
E value	1.0e-08
Match length	144
% identity	92
NCBI Description	Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA, complete cds

Seq. No.	191954
Contig ID	5192_6.R1039
5'-most EST	uC-gsflnu33B070c12b1
Method	BLASTX
NCBI GI	g320585
BLAST score	193
E value	2.0e-14
Match length	42
% identity	83
NCBI Description	polygalacturonase (EC 3.2.1.15) 1 beta chain precursor - tomato >gi|170480 (M98466) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum] >gi|1762586 (U63374) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum]

Seq. No.	191955
Contig ID	5192_7.R1039
5'-most EST	LIB3149-001-P1-K1-D3
Method	BLASTN
NCBI GI	g2865522
BLAST score	34
E value	3.0e-09
Match length	105
% identity	71
NCBI Description	Lavatera thuringiaca cold regulated LTCOR18 (LtCor18) mRNA, complete cds

Seq. No.	191956
Contig ID	5193_1.R1039
5'-most EST	LIB3083-015-Q1-L2-A9

Seq. No. 191957

Contig ID	5194_1.R1039
5'-most EST	LIB3189-044-P1-K1-C12
Method	BLASTX
NCBI GI	g3650032
BLAST score	237
E value	1.0e-19
Match length	49
% identity	73
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	191958
Contig ID	5194_2.R1039
5'-most EST	LIB3189-035-P1-K1-C7
Method	BLASTX
NCBI GI	g3650032
BLAST score	241
E value	2.0e-20
Match length	55
% identity	67
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	191959
Contig ID	5195_1.R1039
5'-most EST	LIB3083-015-Q1-L1-B10

Seq. No.	191960
Contig ID	5200_1.R1039
5'-most EST	LIB3083-015-Q1-L2-B8
Method	BLASTX
NCBI GI	g4512667
BLAST score	858
E value	3.0e-92
Match length	180
% identity	87
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	191961
Contig ID	5201_1.R1039
5'-most EST	LIB3083-059-Q1-L1-E8
Method	BLASTX
NCBI GI	g135460
BLAST score	545
E value	9.0e-56
Match length	108
% identity	95
NCBI Description	TUBULIN BETA-2 CHAIN >gi|100933|pir||S14702 tubulin beta-2 chain - maize >gi|22184|emb|CAA37061| (X52879) beta 2 tubulin (AA 1-444) [Zea mays]

Seq. No.	191962
Contig ID	5201_2.R1039
5'-most EST	LIB3083-015-Q1-L1-B9
Method	BLASTX
NCBI GI	g135452
BLAST score	233

E value	2.0e-25
Match length	112
% identity	62
NCBI Description	TUBULIN BETA-1 CHAIN >gi|170060 (M21296) S-beta-1 tubulin [Glycine max]

Seq. No.	191963
Contig ID	5202_1.R1039
5'-most EST	LIB3083-015-Q1-L1-C1

Seq. No.	191964
Contig ID	5204_1.R1039
5'-most EST	g3326508
Method	BLASTX
NCBI GI	g3927825
BLAST score	570
E value	1.0e-58
Match length	146
% identity	78
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	191965
Contig ID	5204_2.R1039
5'-most EST	LIB3197-040-Q1-M1-G5
Method	BLASTX
NCBI GI	g3927825
BLAST score	1555
E value	1.0e-174
Match length	316
% identity	92
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	191966
Contig ID	5204_3.R1039
5'-most EST	uC-gsronu33B078h10b1
Method	BLASTX
NCBI GI	g3927825
BLAST score	281
E value	4.0e-25
Match length	61
% identity	85
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	191967
Contig ID	5205_1.R1039
5'-most EST	uC-gsflnu33B113f11b1
Method	BLASTX
NCBI GI	g2789660
BLAST score	743
E value	3.0e-89
Match length	307
% identity	59
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	191968
Contig ID	5206_1.R1039
5'-most EST	LIB3083-015-Q1-L2-C3
Method	BLASTX
NCBI GI	g4455158
BLAST score	1308
E value	1.0e-144
Match length	284
% identity	84
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	191969
Contig ID	5206_3.R1039
5'-most EST	LIB3197-010-P1-M1-A5
Method	BLASTX
NCBI GI	g4455158
BLAST score	430
E value	3.0e-51
Match length	117
% identity	83
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	191970
Contig ID	5209_1.R1039
5'-most EST	LIB3083-015-Q1-L1-C6

Seq. No.	191971
Contig ID	5211_1.R1039
5'-most EST	LIB3189-010-P1-K1-H8
Method	BLASTX
NCBI GI	g3618214
BLAST score	210
E value	2.0e-16
Match length	188
% identity	32
NCBI Description	(AL031579) dihydrofolate reductase [Schizosaccharomyces pombe]

Seq. No.	191972
Contig ID	5215_1.R1039
5'-most EST	uC-gsflnu33B092g10b1
Method	BLASTX
NCBI GI	g1076510
BLAST score	766
E value	1.0e-81
Match length	169
% identity	83
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi|829119|emb|CAA52414| (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No.	191973
Contig ID	5216_1.R1039
5'-most EST	LIB3083-015-Q1-L2-D12
Method	BLASTX
NCBI GI	g3287270
BLAST score	417

E value	6.0e-41
Match length	145
% identity	66
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	191974
Contig ID	5219_1.R1039
5'-most EST	g5048128
Method	BLASTX
NCBI GI	g3851001
BLAST score	1632
E value	0.0e+00
Match length	367
% identity	87
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No.	191975
Contig ID	5219_2.R1039
5'-most EST	LIB3189-025-P1-K1-G8
Method	BLASTX
NCBI GI	g3851001
BLAST score	552
E value	1.0e-56
Match length	136
% identity	81
NCBI Description	(AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]

Seq. No.	191976
Contig ID	5224_1.R1039
5'-most EST	LIB3083-015-Q1-L1-E11
Method	BLASTX
NCBI GI	g1706958
BLAST score	523
E value	4.0e-53
Match length	140
% identity	69
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	191977
Contig ID	5224_2.R1039
5'-most EST	LIB3083-104-Q1-L1-E2
Method	BLASTX
NCBI GI	g1706958
BLAST score	869
E value	1.0e-93
Match length	224
% identity	70
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	191978
Contig ID	5226_1.R1039
5'-most EST	LIB3083-015-Q1-L1-E2

Seq. No.	191979
Contig ID	5229_1.R1039

5'-most EST	LIB3272-019-P1-K1-B10
Seq. No.	191980
Contig ID	5231_1.R1039
5'-most EST	uC-gsflnu33B129d02b1
Method	BLASTX
NCBI GI	g2129825
BLAST score	501
E value	1.0e-50
Match length	115
% identity	86
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi|1217994 (U25547) SDL [Glycine max]
Seq. No.	191981
Contig ID	5233_1.R1039
5'-most EST	LIB3083-015-Q1-L1-F4
Seq. No.	191982
Contig ID	5234_1.R1039
5'-most EST	LIB3083-015-Q1-L2-F5
Method	BLASTX
NCBI GI	g2827141
BLAST score	972
E value	1.0e-105
Match length	369
% identity	57
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	191983
Contig ID	5235_1.R1039
5'-most EST	LIB3189-045-P1-K1-G4
Seq. No.	191984
Contig ID	5236_1.R1039
5'-most EST	g5044828
Method	BLASTX
NCBI GI	g3036816
BLAST score	299
E value	2.0e-26
Match length	432
% identity	28
NCBI Description	(AL022373) myosin-like protein [Arabidopsis thaliana]
Seq. No.	191985
Contig ID	5240_1.R1039
5'-most EST	LIB3083-015-Q1-L1-G10
Method	BLASTX
NCBI GI	g3023816
BLAST score	322
E value	8.0e-30
Match length	71
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi|968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No. 191986
Contig ID 5241_1.R1039
5'-most EST LIB3083-015-Q1-L2-G2

Seq. No. 191987
Contig ID 5242_1.R1039
5'-most EST g5049293
Method BLASTX
NCBI GI g1912286
BLAST score 506
E value 3.0e-51
Match length 101
% identity 90
NCBI Description (U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi|2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb|U39568). EST gb|T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No. 191988
Contig ID 5244_1.R1039
5'-most EST LIB3083-015-Q1-L2-G5

Seq. No. 191989
Contig ID 5247_1.R1039
5'-most EST LIB3145-026-Q1-K1-A4
Method BLASTX
NCBI GI g3334138
BLAST score 1050
E value 1.0e-127
Match length 330
% identity 69
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]

Seq. No. 191990
Contig ID 5247_2.R1039
5'-most EST g5046377
Method BLASTX
NCBI GI g3334138
BLAST score 543
E value 2.0e-55
Match length 160
% identity 68
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]

Seq. No. 191991
Contig ID 5248_1.R1039
5'-most EST uC-gsronu33B179c12b1
Method BLASTX
NCBI GI g1915974
BLAST score 734
E value 8.0e-78
Match length 177
% identity 79
NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi|2102693

(U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	191992
Contig ID	5251_1.R1039
5'-most EST	LIB3083-066-Q1-L1-E1

Seq. No.	191993
Contig ID	5255_1.R1039
5'-most EST	LIB3135-040-Q1-K1-E2
Method	BLASTX
NCBI GI	g2894598
BLAST score	774
E value	2.0e-82
Match length	291
% identity	59
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	191994
Contig ID	5257_1.R1039
5'-most EST	LIB3083-015-Q1-L1-H8

Seq. No.	191995
Contig ID	5261_1.R1039
5'-most EST	LIB3272-029-P1-K1-E12
Method	BLASTX
NCBI GI	g3096939
BLAST score	403
E value	5.0e-39
Match length	116
% identity	66
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	191996
Contig ID	5274_1.R1039
5'-most EST	LIB3083-015-Q1-L2-B12
Method	BLASTX
NCBI GI	g3914621
BLAST score	277
E value	6.0e-24
Match length	338
% identity	20
NCBI Description	RAN GTPASE ACTIVATING PROTEIN 1 >gi|2062660 (U88155) RanGTPase activating protein [Xenopus laevis]

Seq. No.	191997
Contig ID	5279_1.R1039
5'-most EST	LIB3083-015-Q1-L2-B7
Method	BLASTX
NCBI GI	g4115377
BLAST score	528
E value	9.0e-70
Match length	301
% identity	44
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	191998
Contig ID	5301_1.R1039

5'-most EST	LIB3149-037-Q1-K1-H9
Method	BLASTX
NCBI GI	g1173027
BLAST score	438
E value	3.0e-43
Match length	114
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi|915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	191999
Contig ID	5301_2.R1039
5'-most EST	LIB3147-046-Q1-K1-B3
Method	BLASTX
NCBI GI	g1173027
BLAST score	415
E value	2.0e-40
Match length	110
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi|915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	192000
Contig ID	5301_3.R1039
5'-most EST	LIB3196-035-P1-M1-C11
Method	BLASTX
NCBI GI	g1173027
BLAST score	414
E value	2.0e-40
Match length	112
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi|915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	192001
Contig ID	5308_1.R1039
5'-most EST	g5046421
Method	BLASTX
NCBI GI	g1174411
BLAST score	441
E value	4.0e-50
Match length	175
% identity	57
NCBI Description	MICROSOMAL SIGNAL PEPTIDASE 18 KD SUBUNIT (SPC18) >gi|206978 (L11319) signal peptidase [Rattus norvegicus]

Seq. No.	192002
Contig ID	5316_1.R1039
5'-most EST	uC-gsflnu33B012e02b1
Method	BLASTX
NCBI GI	g1173187
BLAST score	715
E value	1.0e-75
Match length	142
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden

strawberry >gi|643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	192003
Contig ID	5316_2.R1039
5'-most EST	uC-gsflnu33B135a03b1
Method	BLASTX
NCBI GI	g1173187
BLAST score	718
E value	5.0e-76
Match length	142
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi|643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	192004
Contig ID	5316_3.R1039
5'-most EST	uC-gsronu33B145c02b1
Method	BLASTX
NCBI GI	g1173187
BLAST score	715
E value	1.0e-75
Match length	142
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi|643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	192005
Contig ID	5349_1.R1039
5'-most EST	LIB3083-016-Q1-L1-A2

Seq. No.	192006
Contig ID	5350_1.R1039
5'-most EST	LIB3189-002-P1-K1-E11
Method	BLASTX
NCBI GI	g3831440
BLAST score	205
E value	3.0e-16
Match length	86
% identity	45
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi|4415946|gb|AAD20176| (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	192007
Contig ID	5351_1.R1039
5'-most EST	uC-gsflmaxxa067d03b1
Method	BLASTX
NCBI GI	g4454472
BLAST score	594
E value	2.0e-61
Match length	226
% identity	55

NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.	192008
Contig ID	5352_1.R1039
5'-most EST	LIB3147-056-Q1-K1-B5
Method	BLASTN
NCBI GI	g2924257
BLAST score	59
E value	3.0e-24
Match length	191
% identity	93
NCBI Description	Tobacco chloroplast genome DNA
Seq. No.	192009
Contig ID	5353_1.R1039
5'-most EST	g5045071
Method	BLASTX
NCBI GI	g3757514
BLAST score	1308
E value	1.0e-145
Match length	278
% identity	90
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]
Seq. No.	192010
Contig ID	5356_1.R1039
5'-most EST	g5045140
Method	BLASTX
NCBI GI	g3386621
BLAST score	1003
E value	1.0e-109
Match length	224
% identity	85
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	192011
Contig ID	5356_2.R1039
5'-most EST	g5049379
Method	BLASTX
NCBI GI	g3386621
BLAST score	652
E value	3.0e-68
Match length	136
% identity	92
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.	192012
Contig ID	5365_1.R1039
5'-most EST	LIB3083-056-Q1-L1-A7
Method	BLASTX
NCBI GI	g3193284
BLAST score	542
E value	2.0e-55
Match length	172
% identity	59
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 192013
Contig ID 5366_1.R1039
5'-most EST LIB3120-043-P1-K1-A9
Method BLASTX
NCBI GI g3068705
BLAST score 158
E value 1.0e-17
Match length 129
% identity 42
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 192014
Contig ID 5371_1.R1039
5'-most EST uC-gsflmaxxa039b05b1
Method BLASTX
NCBI GI g2500115
BLAST score 323
E value 4.0e-52
Match length 159
% identity 70
NCBI Description GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi|529375|dbj|BAA07108| (D37870) Glutathione Reductase precursor [Spinacia oleracea]

Seq. No. 192015
Contig ID 5372_1.R1039
5'-most EST LIB3146-039-Q1-K1-H7

Seq. No. 192016
Contig ID 5372_3.R1039
5'-most EST LIB3083-017-Q1-L1-C5

Seq. No. 192017
Contig ID 5373_1.R1039
5'-most EST LIB3083-018-Q1-L1-C1
Method BLASTX
NCBI GI g3128192
BLAST score 514
E value 2.0e-52
Match length 122
% identity 78
NCBI Description (AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No. 192018
Contig ID 5384_1.R1039
5'-most EST LIB3145-014-Q1-K1-C5
Method BLASTX
NCBI GI g3328804
BLAST score 485
E value 9.0e-49
Match length 188
% identity 53
NCBI Description (AE001311) GTP Binding Protein [Chlamydia trachomatis]

Seq. No. 192019
Contig ID 5385_1.R1039

5'-most EST	LIB3120-034-Q1-K1-E5
Method	BLASTN
NCBI GI	g3128143
BLAST score	42
E value	4.0e-14
Match length	348
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	192020
Contig ID	5389_1.R1039
5'-most EST	LIB3197-003-P1-M1-A7
Method	BLASTX
NCBI GI	g3128168
BLAST score	533
E value	1.0e-103
Match length	300
% identity	55
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	192021
Contig ID	5394_1.R1039
5'-most EST	g5045955
Method	BLASTX
NCBI GI	g2244799
BLAST score	548
E value	4.0e-56
Match length	180
% identity	57
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	192022
Contig ID	5395_1.R1039
5'-most EST	LIB3083-017-Q1-L1-G3

Seq. No.	192023
Contig ID	5399_1.R1039
5'-most EST	LIB3197-055-Q1-M1-C6
Method	BLASTX
NCBI GI	g4220476
BLAST score	1643
E value	0.0e+00
Match length	435
% identity	71
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	192024
Contig ID	5400_1.R1039
5'-most EST	g5044251
Method	BLASTX
NCBI GI	g1168191
BLAST score	1196
E value	1.0e-132
Match length	258
% identity	92

NCBI Description	14-3-3-LIKE PROTEIN 4 (PBLT4) >gi|1362089|pir||S57272 14-3-3 brain protein homolog (clone pBLT4) - tomato >gi|466336 (L29150) 14-3-3 protein homologue [Solanum lycopersicum] >gi|1090847|prf||2019487B 14-3-3 protein [Lycopersicon esculentum]

Seq. No.	192025
Contig ID	5400_2.R1039
5'-most EST	uC-gsronu33B051h09b1
Method	BLASTX
NCBI GI	g2921512
BLAST score	455
E value	4.0e-45
Match length	112
% identity	83
NCBI Description	(AF037460) GF14 protein [Fritillaria agrestis]

Seq. No.	192026
Contig ID	5400_3.R1039
5'-most EST	LIB3272-033-P1-K1-C4
Method	BLASTX
NCBI GI	g3912950
BLAST score	592
E value	3.0e-61
Match length	169
% identity	75
NCBI Description	14-3-3-LIKE PROTEIN E >gi|2689479 (U91726) 14-3-3 isoform e [Nicotiana tabacum]

Seq. No.	192027
Contig ID	5427_1.R1039
5'-most EST	g5049005
Method	BLASTX
NCBI GI	g3319921
BLAST score	579
E value	2.0e-59
Match length	223
% identity	56
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi|3319923|emb|CAA11304| (AJ223389) Hev b 3 [Hevea brasiliensis] >gi|3319925|emb|CAA11305| (AJ223390) Hev b 3 [Hevea brasiliensis] >gi|3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]

Seq. No.	192028
Contig ID	5430_1.R1039
5'-most EST	uC-gsronu33B157f10b1
Method	BLASTX
NCBI GI	g115484
BLAST score	762
E value	5.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN 1 >gi|71684|pir||MCPZDC calmodulin - carrot >gi|478632|pir||S22971 calmodulin - trumpet lily >gi|541839|pir||S40301 calmodulin - Red bryony >gi|2129970|pir||S70768 calmodulin CAM81 - garden petunia

>gi|18326|emb|CAA42423| (X59751) calmodulin [Daucus carota] >gi|19447|emb|CAA78301| (Z12839) calmodulin [Lilium longiflorum] >gi|169207 (M80836) calmodulin [Petunia hybrida] >gi|308900 (L18912) calmodulin [Lilium longiflorum] >gi|505154|emb|CAA43143| (X60738) Calmodulin [Malus domestica] >gi|535444 (U13882) calmodulin [Pisum sativum] >gi|445602|prf||1909349A calmodulin [Daucus carota]

Seq. No.	192029
Contig ID	5430_2.R1039
5'-most EST	LIB3189-052-P1-K1-G3
Method	BLASTX
NCBI GI	g115484
BLAST score	762
E value	4.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN 1 >gi|71684|pir||MCPZDC calmodulin - carrot >gi|478632|pir||S22971 calmodulin - trumpet lily >gi|541839|pir||S40301 calmodulin - Red bryony >gi|2129970|pir||S70768 calmodulin CAM81 - garden petunia >gi|18326|emb|CAA42423| (X59751) calmodulin [Daucus carota] >gi|19447|emb|CAA78301| (Z12839) calmodulin [Lilium longiflorum] >gi|169207 (M80836) calmodulin [Petunia hybrida] >gi|308900 (L18912) calmodulin [Lilium longiflorum] >gi|505154|emb|CAA43143| (X60738) Calmodulin [Malus domestica] >gi|535444 (U13882) calmodulin [Pisum sativum] >gi|445602|prf||1909349A calmodulin [Daucus carota]

Seq. No.	192030
Contig ID	5430_3.R1039
5'-most EST	LIB3166-046-P1-K1-D10
Method	BLASTX
NCBI GI	g115484
BLAST score	730
E value	3.0e-77
Match length	142
% identity	65
NCBI Description	CALMODULIN 1 >gi|71684|pir||MCPZDC calmodulin - carrot >gi|478632|pir||S22971 calmodulin - trumpet lily >gi|541839|pir||S40301 calmodulin - Red bryony >gi|2129970|pir||S70768 calmodulin CAM81 - garden petunia >gi|18326|emb|CAA42423| (X59751) calmodulin [Daucus carota] >gi|19447|emb|CAA78301| (Z12839) calmodulin [Lilium longiflorum] >gi|169207 (M80836) calmodulin [Petunia hybrida] >gi|308900 (L18912) calmodulin [Lilium longiflorum] >gi|505154|emb|CAA43143| (X60738) Calmodulin [Malus domestica] >gi|535444 (U13882) calmodulin [Pisum sativum] >gi|445602|prf||1909349A calmodulin [Daucus carota]

Seq. No.	192031
Contig ID	5430_4.R1039
5'-most EST	LIB3145-046-Q1-K1-F8
Method	BLASTX

NCBI GI g3121848
BLAST score 763
E value 4.0e-81
Match length 149
% identity 100
NCBI Description CALMODULIN >gi|1835521 (U83402) calmodulin [Capsicum annuum]

Seq. No. 192032
Contig ID 5430_6.R1039
5'-most EST LIB3135-051-Q1-K1-B2
Method BLASTX
NCBI GI g2119360
BLAST score 486
E value 6.0e-49
Match length 95
% identity 65
NCBI Description calmodulin (clone PCM2) - potato (fragment) >gi|687698 (U20291) calmodulin [Solanum tuberosum] >gi|687702 (U20293) calmodulin [Solanum tuberosum]

Seq. No. 192033
Contig ID 5430_7.R1039
5'-most EST uC-gsflmaxxa028h03b1
Method BLASTX
NCBI GI g115515
BLAST score 590
E value 3.0e-61
Match length 119
% identity 48
NCBI Description CALMODULIN >gi|71683|pir||MCAA calmodulin - alfalfa >gi|19579|emb|CAA36644| (X52398) calmodulin (AA 1-149) [Medicago sativa] >gi|170070 (L01430) calmodulin [Glycine max] >gi|170074 (L01432) calmodulin [Glycine max] >gi|506852 (L20507) calmodulin [Vigna radiata] >gi|4103957 (AF030032) calmodulin [Phaseolus vulgaris] >gi|1583767|prf||2121384A calmodulin [Glycine max] >gi|1583769|prf||2121384C calmodulin [Glycine max]

Seq. No. 192034
Contig ID 5431_1.R1039
5'-most EST uC-gsflmaxxa061e07b1
Method BLASTX
NCBI GI g4510400
BLAST score 515
E value 5.0e-56
Match length 139
% identity 76
NCBI Description (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No. 192035
Contig ID 5433_1.R1039
5'-most EST LIB3196-028-P1-M1-H6
Method BLASTX
NCBI GI g3913420
BLAST score 1069

E value	1.0e-117
Match length	324
% identity	63
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi|1421752 (U60592) S-adenosylmethionine decarboxylase [Pisum sativum]

Seq. No.	192036
Contig ID	5437_1.R1039
5'-most EST	LIB3083-020-Q1-L1-B6

Seq. No.	192037
Contig ID	5439_1.R1039
5'-most EST	LIB3083-064-Q1-L1-G2
Method	BLASTX
NCBI GI	g2129473
BLAST score	398
E value	4.0e-38
Match length	149
% identity	51
NCBI Description	arabinogalactan-like protein - loblolly pine >gi|607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	192038
Contig ID	5441_1.R1039
5'-most EST	LIB3197-050-Q1-M1-B7
Method	BLASTX
NCBI GI	g484656
BLAST score	650
E value	7.0e-68
Match length	194
% identity	64
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi|452165|dbj|BAA05408| (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	192039
Contig ID	5442_1.R1039
5'-most EST	uC-gsflnu33B005b09b1
Method	BLASTN
NCBI GI	g2760164
BLAST score	61
E value	1.0e-25
Match length	125
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	192040
Contig ID	5442_2.R1039
5'-most EST	uC-gsronu33B170b06b1

Seq. No.	192041
Contig ID	5443_1.R1039
5'-most EST	uC-gsflnu33B026c02b1
Method	BLASTX
NCBI GI	g542020

BLAST score	513
E value	7.0e-52
Match length	198
% identity	53
NCBI Description	sucrose transport protein - castor bean >gi|468562|emb|CAA83436| (Z31561) sucrose carrier [Ricinus communis]

Seq. No.	192042
Contig ID	5446_1.R1039
5'-most EST	LIB3166-036-P1-K1-F12
Method	BLASTX
NCBI GI	g3024434
BLAST score	1230
E value	1.0e-163
Match length	423
% identity	84
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi|2564337|dbj|BAA22951| (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	192043
Contig ID	5447_1.R1039
5'-most EST	uC-gsflnu33B058e12b1
Method	BLASTX
NCBI GI	g3738284
BLAST score	420
E value	8.0e-41
Match length	143
% identity	61
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	192044
Contig ID	5448_1.R1039
5'-most EST	LIB3083-020-Q1-L1-D1
Method	BLASTX
NCBI GI	g1076274
BLAST score	99
E value	4.0e-09
Match length	122
% identity	38
NCBI Description	cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No.	192045
Contig ID	5449_1.R1039
5'-most EST	LIB3145-040-Q1-K1-B5

Seq. No.	192046
Contig ID	5457_1.R1039
5'-most EST	g5044744
Method	BLASTX
NCBI GI	g461530
BLAST score	451
E value	1.0e-44
Match length	173
% identity	54
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG

>gi|159365 (L11348) ARD1 protein homologue [Leishmania donovani]

Seq. No.	192047
Contig ID	5457_2.R1039
5'-most EST	uC-gsronu33B144d07b1
Method	BLASTX
NCBI GI	g461530
BLAST score	459
E value	2.0e-45
Match length	173
% identity	56
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi|159365 (L11348) ARD1 protein homologue [Leishmania donovani]

Seq. No.	192048
Contig ID	5460_1.R1039
5'-most EST	LIB3083-020-Q1-L1-E12
Method	BLASTX
NCBI GI	g3377850
BLAST score	222
E value	4.0e-18
Match length	50
% identity	86
NCBI Description	(AF076274) contains simlarity to Canis familiaris signal peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis thaliana]

Seq. No.	192049
Contig ID	5461_1.R1039
5'-most EST	LIB3083-020-Q1-L1-E3

Seq. No.	192050
Contig ID	5462_1.R1039
5'-most EST	LIB3148-022-Q1-K1-B1
Method	BLASTX
NCBI GI	g2924520
BLAST score	1321
E value	1.0e-146
Match length	278
% identity	90
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	192051
Contig ID	5463_1.R1039
5'-most EST	LIB3083-020-Q1-L1-E5
Method	BLASTX
NCBI GI	g4185143
BLAST score	419
E value	4.0e-41
Match length	124
% identity	67
NCBI Description	(AC005724) putative signal recognition particle receptor beta subunit [Arabidopsis thaliana]

Seq. No.	192052
Contig ID	5467_1.R1039
5'-most EST	LIB3083-020-Q1-L1-F10
Method	BLASTX
NCBI GI	g4220482
BLAST score	362
E value	2.0e-34
Match length	119
% identity	36
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192053
Contig ID	5469_1.R1039
5'-most EST	LIB3083-020-Q1-L1-F12
Method	BLASTX
NCBI GI	g4467111
BLAST score	305
E value	1.0e-27
Match length	101
% identity	56
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	192054
Contig ID	5470_1.R1039
5'-most EST	LIB3166-015-P1-K1-F6
Method	BLASTX
NCBI GI	g1881585
BLAST score	206
E value	3.0e-31
Match length	143
% identity	54
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	192055
Contig ID	5470_2.R1039
5'-most EST	LIB3147-050-Q1-K1-G1
Method	BLASTX
NCBI GI	g320558
BLAST score	281
E value	6.0e-25
Match length	85
% identity	72
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi|601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	192056
Contig ID	5472_1.R1039
5'-most EST	LIB3083-101-Q1-L1-A9
Method	BLASTX
NCBI GI	g3297823
BLAST score	262
E value	7.0e-23
Match length	76
% identity	72
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 192057

Contig ID	5473_1.R1039
5'-most EST	LIB3083-020-Q1-L1-F5

Seq. No.	192058
Contig ID	5474_1.R1039
5'-most EST	LIB3165-027-P1-K1-A7
Method	BLASTX
NCBI GI	g4468812
BLAST score	669
E value	3.0e-70
Match length	170
% identity	29
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	192059
Contig ID	5479_1.R1039
5'-most EST	LIB3083-020-Q1-L1-G7

Seq. No.	192060
Contig ID	5480_1.R1039
5'-most EST	LIB3135-023-Q1-K1-H8
Method	BLASTX
NCBI GI	g2130073
BLAST score	1541
E value	1.0e-172
Match length	358
% identity	83
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi|786178|dbj|BAA08845| (D50307) aldolase C-1 [Oryza sativa] >gi|790970|dbj|BAA08830| (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	192061
Contig ID	5480_2.R1039
5'-most EST	g5046282
Method	BLASTX
NCBI GI	g113621
BLAST score	531
E value	3.0e-86
Match length	235
% identity	73
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi|68196|pir||ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi|168420 (M16220) aldolase [Zea mays] >gi|295850|emb|CAA31366| (X12872) fructose bisphosphate aldolase [Zea mays] >gi|225624|prf||1307278A cytoplasmic aldolase [Zea mays]

Seq. No.	192062
Contig ID	5480_3.R1039
5'-most EST	g5050659
Method	BLASTX
NCBI GI	g2130073
BLAST score	619
E value	2.0e-64
Match length	144
% identity	83

NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi|786178|dbj|BAA08845| (D50307) aldolase C-1 [Oryza sativa] >gi|790970|dbj|BAA08830| (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	192063
Contig ID	5480_4.R1039
5'-most EST	uC-gsronu33B021b07b1
Method	BLASTX
NCBI GI	g218157
BLAST score	561
E value	1.0e-57
Match length	128
% identity	88
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	192064
Contig ID	5480_5.R1039
5'-most EST	LIB3166-054-P1-K1-E2
Method	BLASTX
NCBI GI	g3901012
BLAST score	1144
E value	1.0e-125
Match length	279
% identity	72
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	192065
Contig ID	5480_6.R1039
5'-most EST	LIB3166-036-P1-K1-F3
Method	BLASTX
NCBI GI	g2129771
BLAST score	477
E value	5.0e-48
Match length	114
% identity	77
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi|1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi|4539299|emb|CAB39602.1| (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	192066
Contig ID	5480_8.R1039
5'-most EST	uC-gsronu33B012g12b1
Method	BLASTX
NCBI GI	g218157
BLAST score	535
E value	1.0e-54
Match length	122
% identity	88
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	192067
Contig ID	5480_9.R1039
5'-most EST	LIB3148-042-Q1-K1-C3

Method	BLASTX
NCBI GI	g218157
BLAST score	459
E value	1.0e-45
Match length	113
% identity	81
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	192068
Contig ID	5482_1.R1039
5'-most EST	uC-gsflmaxxa004h07b1
Method	BLASTX
NCBI GI	g4559358
BLAST score	268
E value	6.0e-23
Match length	97
% identity	51
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	192069
Contig ID	5482_4.R1039
5'-most EST	uC-gsronu33B139e11b1
Method	BLASTX
NCBI GI	g3127857
BLAST score	153
E value	5.0e-10
Match length	100
% identity	36
NCBI Description	(AJ005837) putative progesterone binding protein [Rattus norvegicus]

Seq. No.	192070
Contig ID	5483_1.R1039
5'-most EST	LIB3083-020-Q1-L1-H11
Method	BLASTX
NCBI GI	g2288887
BLAST score	832
E value	3.0e-89
Match length	229
% identity	71
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi|3250736|emb|CAA76803| (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi|3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	192071
Contig ID	5484_1.R1039
5'-most EST	LIB3083-020-Q1-L1-H3
Method	BLASTX
NCBI GI	g1497987
BLAST score	181
E value	5.0e-13
Match length	76
% identity	49
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	192072
Contig ID	5486_1.R1039
5'-most EST	uC-gsronu33B116h03b1

Seq. No.	192073
Contig ID	5487_1.R1039
5'-most EST	LIB3083-020-Q1-L1-H8
Method	BLASTX
NCBI GI	g2118017
BLAST score	591
E value	2.0e-61
Match length	133
% identity	74
NCBI Description	non-S-RNase (EC 3.1.-.-) - Japanese pear >gi|1526417|dbj|BAA08475| (D49529) ribonuclease [Pyrus pyrifolia]

Seq. No.	192074
Contig ID	5489_1.R1039
5'-most EST	LIB3083-021-Q1-L1-A10
Method	BLASTN
NCBI GI	g3046854
BLAST score	68
E value	9.0e-30
Match length	347
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	192075
Contig ID	5490_1.R1039
5'-most EST	LIB3083-021-Q1-L1-A11

Seq. No.	192076
Contig ID	5491_1.R1039
5'-most EST	LIB3145-048-Q1-K1-E11
Method	BLASTN
NCBI GI	g167346
BLAST score	42
E value	2.0e-14
Match length	138
% identity	83
NCBI Description	Gossypium hirsutum Lea5-A late embryogenesis-abundant protein (Lea5-A) gene, complete cds

Seq. No.	192077
Contig ID	5498_1.R1039
5'-most EST	LIB3083-021-Q1-L1-A8
Method	BLASTN
NCBI GI	g4454587
BLAST score	42
E value	5.0e-14
Match length	344
% identity	83
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 192078
Contig ID 5504_1.R1039
5'-most EST LIB3272-043-P1-K1-A2

Seq. No. 192079
Contig ID 5507_1.R1039
5'-most EST LIB3083-063-Q1-L1-E1
Method BLASTX
NCBI GI g3123908
BLAST score 610
E value 2.0e-63
Match length 182
% identity 37
NCBI Description (AF038392) pre-mRNA splicing factor [Homo sapiens]

Seq. No. 192080
Contig ID 5510_1.R1039
5'-most EST LIB3135-007-Q1-K1-B9

Seq. No. 192081
Contig ID 5517_1.R1039
5'-most EST LIB3083-100-Q1-L1-E10

Seq. No. 192082
Contig ID 5519_1.R1039
5'-most EST uC-gsflmaxxa061d02b1
Method BLASTX
NCBI GI g4406814
BLAST score 481
E value 4.0e-48
Match length 114
% identity 80
NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No. 192083
Contig ID 5519_2.R1039
5'-most EST LIB3165-006-P1-K4-B9
Method BLASTX
NCBI GI g4406814
BLAST score 303
E value 1.0e-42
Match length 115
% identity 79
NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No. 192084
Contig ID 5521_1.R1039
5'-most EST LIB3145-030-Q1-K1-F3
Method BLASTX
NCBI GI g1351279
BLAST score 959
E value 1.0e-104
Match length 241
% identity 77

NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi|602590|emb|CAA58230| (X83227) triosephosphate isomerase [Petunia x hybrida]
Seq. No.	192085
Contig ID	5523_1.R1039
5'-most EST	LIB3166-019-P1-K1-G5
Method	BLASTX
NCBI GI	g2506931
BLAST score	873
E value	1.0e-100
Match length	361
% identity	53
NCBI Description	APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE) >gi|2129977|pir||JC4616 apyrase (EC 3.6.1.5) - potato >gi|1381633 (U58597) ATP-diphosphohydrolase [Solanum tuberosum]
Seq. No.	192086
Contig ID	5525_1.R1039
5'-most EST	LIB3083-021-Q1-L1-E10
Seq. No.	192087
Contig ID	5526_1.R1039
5'-most EST	LIB3145-017-Q1-K1-C3
Seq. No.	192088
Contig ID	5527_1.R1039
5'-most EST	g5048335
Method	BLASTX
NCBI GI	g2435518
BLAST score	511
E value	3.0e-72
Match length	193
% identity	76
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]
Seq. No.	192089
Contig ID	5528_1.R1039
5'-most EST	LIB3083-021-Q1-L1-E3
Method	BLASTX
NCBI GI	g1769895
BLAST score	731
E value	1.0e-78
Match length	224
% identity	68
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]
Seq. No.	192090
Contig ID	5531_1.R1039
5'-most EST	LIB3147-060-Q1-K1-F5
Method	BLASTX
NCBI GI	g4454468
BLAST score	824
E value	1.0e-126

Match length	315
% identity	70
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	192091
Contig ID	5532_1.R1039
5'-most EST	LIB3083-021-Q1-L1-E7
Method	BLASTX
NCBI GI	g1707998
BLAST score	220
E value	1.0e-17
Match length	56
% identity	75
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi|481944|pir||S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi|438247|emb|CAA81082| (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	192092
Contig ID	5539_1.R1039
5'-most EST	LIB3083-021-Q1-L1-F3
Method	BLASTX
NCBI GI	g2316024
BLAST score	564
E value	6.0e-58
Match length	136
% identity	83
NCBI Description	(U96400) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	192093
Contig ID	5540_1.R1039
5'-most EST	uC-gsflmaxxa026d04b1
Method	BLASTX
NCBI GI	g2564237
BLAST score	1849
E value	0.0e+00
Match length	384
% identity	85
NCBI Description	(Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No.	192094
Contig ID	5541_1.R1039
5'-most EST	LIB3083-021-Q1-L1-F5

Seq. No.	192095
Contig ID	5547_1.R1039
5'-most EST	LIB3083-021-Q1-L1-G10
Method	BLASTX
NCBI GI	g3281870
BLAST score	229
E value	1.0e-18
Match length	99
% identity	62
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	192096
Contig ID	5548_1.R1039
5'-most EST	LIB3083-021-Q1-L1-G11
Method	BLASTX
NCBI GI	g2129840
BLAST score	438
E value	5.0e-43
Match length	200
% identity	49
NCBI Description	nucleosome assembly protein 1 - soybean >gi|1161252 (L38856) nucleosome assembly protein 1 [Glycine max]

Seq. No.	192097
Contig ID	5549_1.R1039
5'-most EST	LIB3083-021-Q1-L1-G12
Method	BLASTX
NCBI GI	g461498
BLAST score	670
E value	2.0e-70
Match length	195
% identity	67
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi|320619|pir||S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi|296204|emb|CAA49199| (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	192098
Contig ID	5552_1.R1039
5'-most EST	LIB3147-002-Q1-K1-D12
Method	BLASTX
NCBI GI	g1495768
BLAST score	275
E value	8.0e-44
Match length	141
% identity	66
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No.	192099
Contig ID	5558_1.R1039
5'-most EST	uC-gsflnu33B072h11b1
Method	BLASTX
NCBI GI	g4455206
BLAST score	1226
E value	1.0e-135
Match length	309
% identity	76
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	192100
Contig ID	5560_1.R1039
5'-most EST	uC-gsflnu33B098a09b1
Method	BLASTX
NCBI GI	g1854386

BLAST score	1105
E value	1.0e-121
Match length	269
% identity	76
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	192101
Contig ID	5562_1.R1039
5'-most EST	g5044844
Method	BLASTX
NCBI GI	g3176669
BLAST score	459
E value	1.0e-45
Match length	172
% identity	56
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	192102
Contig ID	5564_1.R1039
5'-most EST	uC-gsflnu33B089d11b1
Method	BLASTX
NCBI GI	g4105772
BLAST score	450
E value	1.0e-44
Match length	107
% identity	43
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	192103
Contig ID	5565_1.R1039
5'-most EST	LIB3083-021-Q1-L1-H6
Method	BLASTX
NCBI GI	g2833311
BLAST score	262
E value	2.0e-22
Match length	87
% identity	59
NCBI Description	HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi|630728|pir||S43605 R07E5.13 protein (clone R07E5) - Caenorhabditis elegans >gi|3878946|emb|CAA83622| (Z32683) R07E5.13 [Caenorhabditis elegans]

Seq. No.	192104
Contig ID	5567_1.R1039
5'-most EST	uC-gsflnu33B061e06b1
Method	BLASTX
NCBI GI	g1362051
BLAST score	1304
E value	1.0e-144
Match length	271
% identity	90
NCBI Description	protein kinase 3 - soybean >gi|310582 (L19361) protein kinase 3 [Glycine max]

Seq. No.	192105
Contig ID	5569_1.R1039

5'-most EST	LIB3148-017-Q1-K1-C8
Seq. No.	192106
Contig ID	5570_1.R1039
5'-most EST	LIB3083-050-Q1-L1-E3
Method	BLASTX
NCBI GI	g267073
BLAST score	178
E value	3.0e-15
Match length	58
% identity	79
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi|320184|pir||JQ1587 tubulin beta chain - Arabidopsis thaliana >gi|166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi|166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]
Seq. No.	192107
Contig ID	5574_1.R1039
5'-most EST	LIB3197-035-Q1-M1-F2
Method	BLASTX
NCBI GI	g1710551
BLAST score	281
E value	5.0e-25
Match length	51
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi|1177369|emb|CAA64728| (X95458) ribosomal protein L39 [Zea mays]
Seq. No.	192108
Contig ID	5574_2.R1039
5'-most EST	LIB3083-022-Q1-L1-A5
Method	BLASTX
NCBI GI	g1710551
BLAST score	260
E value	2.0e-22
Match length	49
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi|1177369|emb|CAA64728| (X95458) ribosomal protein L39 [Zea mays]
Seq. No.	192109
Contig ID	5574_3.R1039
5'-most EST	uC-gsflnu33B097f05b1
Method	BLASTX
NCBI GI	g1710551
BLAST score	268
E value	1.0e-23
Match length	51
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi|1177369|emb|CAA64728| (X95458) ribosomal protein L39 [Zea mays]
Seq. No.	192110
Contig ID	5575_1.R1039
5'-most EST	uC-gsronu33B107c09b1
Method	BLASTX
NCBI GI	g2275196

BLAST score 500
E value 1.0e-50
Match length 100
% identity 95
NCBI Description (AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No. 192111
Contig ID 5580_1.R1039
5'-most EST LIB3146-043-Q1-K1-A5
Method BLASTX
NCBI GI g3860308
BLAST score 174
E value 3.0e-12
Match length 80
% identity 51
NCBI Description (AJ012681) hypothetical protein [Cicer arietinum]

Seq. No. 192112
Contig ID 5586_1.R1039
5'-most EST uC-gsflmaxxa076d02b1
Method BLASTX
NCBI GI g3122703
BLAST score 477
E value 1.0e-47
Match length 113
% identity 81
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi|2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No. 192113
Contig ID 5586_2.R1039
5'-most EST LIB3148-004-Q1-K1-F10
Method BLASTX
NCBI GI g585876
BLAST score 485
E value 1.0e-48
Match length 154
% identity 65
NCBI Description 60S RIBOSOMAL PROTEIN L23A (L25) >gi|1084424|pir||S48026 ribosomal protein L25 - common tobacco >gi|310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No. 192114
Contig ID 5586_3.R1039
5'-most EST LIB3147-022-Q1-K1-E6
Method BLASTX
NCBI GI g3122703
BLAST score 416
E value 9.0e-41
Match length 106
% identity 78
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi|2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No. 192115
Contig ID 5590_1.R1039

5'-most EST	LIB3083-022-Q1-L1-C12
Method	BLASTX
NCBI GI	g3426039
BLAST score	146
E value	1.0e-18
Match length	76
% identity	58
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	192116
Contig ID	5593_1.R1039
5'-most EST	LIB3146-023-Q1-K1-D2
Method	BLASTX
NCBI GI	g2500354
BLAST score	1071
E value	1.0e-117
Match length	211
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi|1902894|dbj|BAA19462| (AB001891) QM family protein [Solanum melongena]

Seq. No.	192117
Contig ID	5596_1.R1039
5'-most EST	LIB3197-029-Q1-M1-B12
Method	BLASTX
NCBI GI	g3386619
BLAST score	520
E value	2.0e-52
Match length	443
% identity	32
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192118
Contig ID	5598_1.R1039
5'-most EST	LIB3149-018-Q1-K1-G6
Method	BLASTX
NCBI GI	g3860277
BLAST score	881
E value	6.0e-95
Match length	215
% identity	81
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi|4314394|gb|AAD15604| (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	192119
Contig ID	5598_2.R1039
5'-most EST	LIB3145-008-Q1-K1-A6
Method	BLASTX
NCBI GI	g3860277
BLAST score	525
E value	2.0e-53
Match length	111
% identity	92
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi|4314394|gb|AAD15604| (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 192120
Contig ID 5601_1.R1039
5'-most EST LIB3197-031-Q1-M1-F7

Seq. No. 192121
Contig ID 5607_1.R1039
5'-most EST LIB3189-035-P1-K1-E3
Method BLASTX
NCBI GI g3334138
BLAST score 526
E value 1.0e-53
Match length 114
% identity 81
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi|669003 (U20502) calnexin [Glycine max]

Seq. No. 192122
Contig ID 5608_1.R1039
5'-most EST LIB3083-022-Q1-L1-D7

Seq. No. 192123
Contig ID 5611_1.R1039
5'-most EST uC-gsflnu33B009g02b1
Method BLASTX
NCBI GI g457517
BLAST score 240
E value 5.0e-20
Match length 177
% identity 31
NCBI Description (L12579) alternatively spliced [Homo sapiens] >gi|4503169|ref|NP_001904.1|pCUTL1| cut (Drosophila)-like 1 (CCAAT displacement protein)

Seq. No. 192124
Contig ID 5612_1.R1039
5'-most EST LIB3083-022-Q1-L1-E10
Method BLASTX
NCBI GI g1170508
BLAST score 830
E value 4.0e-89
Match length 173
% identity 91
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi|2119931|pir||S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi|475219|emb|CAA55639| (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi|475221|emb|CAA55640| (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No. 192125
Contig ID 5614_1.R1039
5'-most EST g5049121
Method BLASTX
NCBI GI g4539383
BLAST score 694

E value	5.0e-73
Match length	187
% identity	68
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	192126
Contig ID	5615_1.R1039
5'-most EST	uC-gsflnu33B051f12b1
Method	BLASTX
NCBI GI	g3935181
BLAST score	1044
E value	1.0e-114
Match length	215
% identity	87
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	192127
Contig ID	5618_1.R1039
5'-most EST	LIB3197-035-Q1-M1-E6
Method	BLASTX
NCBI GI	g2570047
BLAST score	183
E value	2.0e-13
Match length	118
% identity	29
NCBI Description	(Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No.	192128
Contig ID	5625_1.R1039
5'-most EST	LIB3166-040-P1-K1-F4

Seq. No.	192129
Contig ID	5626_1.R1039
5'-most EST	LIB3083-022-Q1-L1-F3
Method	BLASTX
NCBI GI	g1839188
BLAST score	622
E value	1.0e-64
Match length	188
% identity	65
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	192130
Contig ID	5628_1.R1039
5'-most EST	LIB3147-020-Q1-K1-G12
Method	BLASTX
NCBI GI	g71498
BLAST score	366
E value	5.0e-35
Match length	112
% identity	65
NCBI Description	heat shock protein 17.7 - garden pea

Seq. No.	192131
Contig ID	5630_1.R1039
5'-most EST	uC-gsronu33B016c12b1

Method	BLASTX
NCBI GI	g2239089
BLAST score	650
E value	9.0e-68
Match length	311
% identity	44
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi|3288180|emb|CAB11466| (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	192132
Contig ID	5631_1.R1039
5'-most EST	uC-gsflnu33B146f08b1
Method	BLASTX
NCBI GI	g1825645
BLAST score	292
E value	2.0e-26
Match length	72
% identity	72
NCBI Description	(U88173) weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [Caenorhabditis elegans]

Seq. No.	192133
Contig ID	5632_1.R1039
5'-most EST	LIB3189-028-P1-K1-H3
Method	BLASTX
NCBI GI	g3935145
BLAST score	299
E value	4.0e-27
Match length	85
% identity	65
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	192134
Contig ID	5639_1.R1039
5'-most EST	LIB3272-014-P1-K1-G10
Method	BLASTX
NCBI GI	g3980406
BLAST score	446
E value	2.0e-44
Match length	135
% identity	67
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	192135
Contig ID	5642_1.R1039
5'-most EST	g5049866
Method	BLASTX
NCBI GI	g2623297
BLAST score	247
E value	8.0e-21
Match length	109
% identity	46
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi|3790583 (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

Seq. No. 192136
Contig ID 5645_1.R1039
5'-most EST LIB3083-022-Q1-L1-H1
Method BLASTX
NCBI GI g3135264
BLAST score 581
E value 8.0e-60
Match length 151
% identity 73
NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 192137
Contig ID 5650_1.R1039
5'-most EST LIB3135-047-Q1-K1-E3

Seq. No. 192138
Contig ID 5650_2.R1039
5'-most EST LIB3146-033-Q1-K1-B7

Seq. No. 192139
Contig ID 5655_1.R1039
5'-most EST LIB3145-031-Q1-K1-B3
Method BLASTX
NCBI GI g1905785
BLAST score 373
E value 2.0e-35
Match length 251
% identity 41
NCBI Description (Y10685) G/HBF-1 [Glycine max]

Seq. No. 192140
Contig ID 5664_1.R1039
5'-most EST LIB3083-023-Q1-L1-B3
Method BLASTX
NCBI GI g2146732
BLAST score 771
E value 1.0e-102
Match length 264
% identity 35
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi|1373396 (U57838) rof1 [Arabidopsis thaliana]

Seq. No. 192141
Contig ID 5670_1.R1039
5'-most EST uC-gsflmaxxa067d08b1
Method BLASTX
NCBI GI g4406780
BLAST score 609
E value 4.0e-63
Match length 176
% identity 66
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 192142

Contig ID 5670_2.R1039
5'-most EST g5047964
Method BLASTX
NCBI GI g4406780
BLAST score 1416
E value 1.0e-157
Match length 343
% identity 79
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 192143
Contig ID 5670_3.R1039
5'-most EST LIB3083-028-Q1-L1-E8
Method BLASTX
NCBI GI g4406780
BLAST score 808
E value 1.0e-136
Match length 286
% identity 83
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 192144
Contig ID 5670_4.R1039
5'-most EST LIB3149-032-Q1-K1-H2
Method BLASTX
NCBI GI g4406780
BLAST score 420
E value 4.0e-41
Match length 93
% identity 84
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 192145
Contig ID 5670_5.R1039
5'-most EST LIB3272-016-P1-K1-B5
Method BLASTX
NCBI GI g4406780
BLAST score 395
E value 2.0e-38
Match length 133
% identity 91
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 192146
Contig ID 5675_1.R1039
5'-most EST LIB3083-023-Q1-L1-C4
Method BLASTX
NCBI GI g3953478
BLAST score 410
E value 5.0e-52
Match length 148
% identity 77
NCBI Description (AC002328) F22O2.23 [Arabidopsis thaliana]

Seq. No.	192147
Contig ID	5678_1.R1039
5'-most EST	uC-gsronu33B160h09b1
Method	BLASTX
NCBI GI	g4103635
BLAST score	218
E value	1.0e-17
Match length	137
% identity	42
NCBI Description	(AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. No.	192148
Contig ID	5682_1.R1039
5'-most EST	uC-gsflnu33B109g01b1

Seq. No.	192149
Contig ID	5685_1.R1039
5'-most EST	LIB3166-024-P1-K1-B1
Method	BLASTX
NCBI GI	g3600032
BLAST score	178
E value	9.0e-13
Match length	99
% identity	41
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	192150
Contig ID	5688_1.R1039
5'-most EST	LIB3165-004-P1-K1-G5
Method	BLASTX
NCBI GI	g1129145
BLAST score	667
E value	5.0e-70
Match length	192
% identity	72
NCBI Description	(X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No.	192151
Contig ID	5689_1.R1039
5'-most EST	LIB3149-051-Q1-K1-D10
Method	BLASTX
NCBI GI	g3236242
BLAST score	438
E value	3.0e-43
Match length	111
% identity	79
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	192152
Contig ID	5689_2.R1039
5'-most EST	LIB3148-033-Q1-K1-D8
Method	BLASTX
NCBI GI	g3236242

BLAST score	450
E value	2.0e-44
Match length	111
% identity	81
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	192153
Contig ID	5689_4.R1039
5'-most EST	uC-gsflmaxxa041g12b1
Method	BLASTX
NCBI GI	g3236242
BLAST score	435
E value	6.0e-43
Match length	112
% identity	79
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	192154
Contig ID	5690_1.R1039
5'-most EST	LIB3145-042-Q1-K1-F12
Method	BLASTX
NCBI GI	g4115377
BLAST score	524
E value	2.0e-53
Match length	145
% identity	63
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	192155
Contig ID	5692_1.R1039
5'-most EST	LIB3196-019-P1-M1-B4
Method	BLASTX
NCBI GI	g3738302
BLAST score	635
E value	2.0e-66
Match length	144
% identity	83
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi|4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	192156
Contig ID	5693_1.R1039
5'-most EST	uC-gsflmaxxa098c09b1
Method	BLASTX
NCBI GI	g2129559
BLAST score	710
E value	4.0e-75
Match length	166
% identity	83
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi|1022807 (U37702) cellulase [Arabidopsis thaliana] >gi|3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi|3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi|3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

[Arabidopsis thaliana]

Seq. No.	192157
Contig ID	5694_1.R1039
5'-most EST	g5050220
Method	BLASTX
NCBI GI	g4103342
BLAST score	948
E value	1.0e-103
Match length	213
% identity	89
NCBI Description	(AF022377) agamous-like putative transcription factor [Cucumis sativus]

Seq. No.	192158
Contig ID	5694_3.R1039
5'-most EST	LIB3189-013-P1-K1-G5
Method	BLASTX
NCBI GI	g4103342
BLAST score	726
E value	5.0e-77
Match length	157
% identity	91
NCBI Description	(AF022377) agamous-like putative transcription factor [Cucumis sativus]

Seq. No.	192159
Contig ID	5698_1.R1039
5'-most EST	uC-gsflnu33B003c07b1
Method	BLASTX
NCBI GI	g4538929
BLAST score	222
E value	8.0e-18
Match length	167
% identity	35
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	192160
Contig ID	5699_1.R1039
5'-most EST	LIB3083-057-Q1-L1-H10
Method	BLASTX
NCBI GI	g3892055
BLAST score	642
E value	5.0e-76
Match length	159
% identity	85
NCBI Description	(AC002330) putative transport protein [Arabidopsis thaliana]

Seq. No.	192161
Contig ID	5708_1.R1039
5'-most EST	LIB3083-023-Q1-L1-F4

Seq. No.	192162
Contig ID	5712_1.R1039
5'-most EST	g5047188

Seq. No.	192163
Contig ID	5723_1.R1039
5'-most EST	g3325822

Seq. No.	192164
Contig ID	5728_1.R1039
5'-most EST	LIB3149-054-Q1-K1-B3
Method	BLASTX
NCBI GI	g3334323
BLAST score	708
E value	7.0e-75
Match length	177
% identity	78
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi|1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi|2104532|gb|AAC78700.1| (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi|2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	192165
Contig ID	5729_1.R1039
5'-most EST	g5050484
Method	BLASTX
NCBI GI	g3193298
BLAST score	188
E value	1.0e-13
Match length	125
% identity	38
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	192166
Contig ID	5732_1.R1039
5'-most EST	uC-gsronu33B103a01b1

Seq. No.	192167
Contig ID	5735_1.R1039
5'-most EST	LIB3197-051-Q1-M1-A11
Method	BLASTX
NCBI GI	g4406819
BLAST score	182
E value	3.0e-13
Match length	86
% identity	49
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	192168
Contig ID	5735_2.R1039
5'-most EST	LIB3145-006-Q1-K1-G5
Method	BLASTX
NCBI GI	g4406819
BLAST score	188
E value	4.0e-14
Match length	92
% identity	49
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	192169
Contig ID	5737_1.R1039
5'-most EST	g5045861
Method	BLASTX
NCBI GI	g398849
BLAST score	2188
E value	0.0e+00
Match length	430
% identity	95
NCBI Description	(X74656) beta-5 tubulin [Zea mays]

Seq. No.	192170
Contig ID	5737_2.R1039
5'-most EST	uC-gsronu33B109g12b1
Method	BLASTX
NCBI GI	g398849
BLAST score	676
E value	3.0e-71
Match length	133
% identity	93
NCBI Description	(X74656) beta-5 tubulin [Zea mays]

Seq. No.	192171
Contig ID	5739_1.R1039
5'-most EST	LIB3146-030-Q1-K1-E3
Method	BLASTX
NCBI GI	g2065531
BLAST score	979
E value	1.0e-106
Match length	225
% identity	78
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	192172
Contig ID	5739_2.R1039
5'-most EST	uC-gsflnu33B082d07b1
Method	BLASTX
NCBI GI	g2065531
BLAST score	1200
E value	1.0e-132
Match length	272
% identity	80
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	192173
Contig ID	5739_3.R1039
5'-most EST	LIB3145-051-Q1-K1-G9
Method	BLASTX
NCBI GI	g2065531
BLAST score	506
E value	3.0e-51
Match length	115
% identity	77
NCBI Description	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No.	192174
Contig ID	5745_1.R1039

5'-most EST	uC-gsronu33B132a02b1
Method	BLASTX
NCBI GI	g4580461
BLAST score	744
E value	5.0e-79
Match length	166
% identity	86
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	192175
Contig ID	5751_1.R1039
5'-most EST	LIB3083-088-Q1-L1-A4
Method	BLASTX
NCBI GI	g4510421
BLAST score	336
E value	7.0e-31
Match length	254
% identity	34
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	192176
Contig ID	5758_1.R1039
5'-most EST	LIB3083-024-Q1-L1-C10
Method	BLASTX
NCBI GI	g4336436
BLAST score	889
E value	7.0e-96
Match length	247
% identity	70
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	192177
Contig ID	5761_1.R1039
5'-most EST	LIB3083-024-Q1-L1-C2

Seq. No.	192178
Contig ID	5763_1.R1039
5'-most EST	LIB3083-024-Q1-L1-C4
Method	BLASTN
NCBI GI	g2736285
BLAST score	237
E value	1.0e-130
Match length	672
% identity	84
NCBI Description	Camptotheca acuminata isopentenyl diphosphate isomerase I (IPI1) mRNA, complete cds

Seq. No.	192179
Contig ID	5763_2.R1039
5'-most EST	LIB3148-026-Q1-K1-H4
Method	BLASTX
NCBI GI	g1213450
BLAST score	1128
E value	1.0e-124
Match length	272
% identity	78
NCBI Description	(U48963) isopentenyl pyrophosphate isomerase [Clarkia

breweri]

Seq. No.	192180
Contig ID	5763_4.R1039
5'-most EST	LIB3146-003-P1-K1-H10
Method	BLASTN
NCBI GI	g2736287
BLAST score	33
E value	8.0e-09
Match length	41
% identity	95
NCBI Description	Camptotheca acuminata isopentenyl diphosphate isomerase II (IPI2) mRNA, complete cds

Seq. No.	192181
Contig ID	5769_1.R1039
5'-most EST	LIB3083-024-Q1-L1-D1
Method	BLASTX
NCBI GI	g2271477
BLAST score	1204
E value	1.0e-132
Match length	323
% identity	88
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	192182
Contig ID	5771_1.R1039
5'-most EST	LIB3083-024-Q1-L1-D12
Method	BLASTX
NCBI GI	g1737222
BLAST score	595
E value	7.0e-62
Match length	130
% identity	78
NCBI Description	(U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No.	192183
Contig ID	5773_1.R1039
5'-most EST	LIB3083-056-Q1-L1-H2
Method	BLASTX
NCBI GI	g3327868
BLAST score	376
E value	2.0e-35
Match length	341
% identity	35
NCBI Description	(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	192184
Contig ID	5776_1.R1039
5'-most EST	LIB3165-013-P1-K1-F12

Seq. No.	192185
Contig ID	5779_1.R1039
5'-most EST	LIB3083-100-Q1-L1-H5
Method	BLASTN
NCBI GI	g1493835

BLAST score 37
E value 7.0e-11
Match length 53
% identity 92
NCBI Description Hevea brasiliensis latex pI 3.5 protein Hev b 5 mRNA, complete cds

Seq. No. 192186
Contig ID 5779_3.R1039
5'-most EST uC-gsflnu33B093b10b1
Method BLASTN
NCBI GI g2062705
BLAST score 34
E value 2.0e-09
Match length 35
% identity 59
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 192187
Contig ID 5781_1.R1039
5'-most EST LIB3145-019-Q1-K1-H10
Method BLASTX
NCBI GI g3763932
BLAST score 951
E value 1.0e-128
Match length 294
% identity 83
NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 192188
Contig ID 5788_1.R1039
5'-most EST g5047940
Method BLASTX
NCBI GI g4580395
BLAST score 816
E value 3.0e-87
Match length 326
% identity 53
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No. 192189
Contig ID 5788_2.R1039
5'-most EST LIB3189-040-P1-K1-H4
Method BLASTX
NCBI GI g4580395
BLAST score 242
E value 3.0e-20
Match length 121
% identity 48
NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No. 192190
Contig ID 5793_1.R1039
5'-most EST LIB3083-024-Q1-L1-F11
Method BLASTX

NCBI GI g2760320
BLAST score 513
E value 1.0e-53
Match length 215
% identity 56
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No. 192191
Contig ID 5798_1.R1039
5'-most EST uC-gsflmaxxa098g05b1
Method BLASTX
NCBI GI g2497543
BLAST score 2241
E value 0.0e+00
Match length 500
% identity 87
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|542061|pir||S41379 pyruvate kinase - common tobacco >gi|444023|emb|CAA82628| (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 192192
Contig ID 5798_2.R1039
5'-most EST LIB3189-013-P1-K1-E12
Method BLASTX
NCBI GI g2497543
BLAST score 498
E value 2.0e-50
Match length 122
% identity 82
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|542061|pir||S41379 pyruvate kinase - common tobacco >gi|444023|emb|CAA82628| (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 192193
Contig ID 5799_1.R1039
5'-most EST g5045859
Method BLASTX
NCBI GI g2739381
BLAST score 784
E value 9.0e-84
Match length 194
% identity 76
NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 192194
Contig ID 5802_1.R1039
5'-most EST LIB3166-058-P1-K1-D12
Method BLASTX
NCBI GI g294845
BLAST score 378
E value 8.0e-36
Match length 120
% identity 58
NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No. 192195

Contig ID	5803_1.R1039
5'-most EST	g5044451
Method	BLASTN
NCBI GI	g1732510
BLAST score	64
E value	5.0e-27
Match length	236
% identity	82
NCBI Description	Arabidopsis thaliana Ran binding protein 1 homolog (RanBP1) mRNA, complete cds

Seq. No.	192196
Contig ID	5803_2.R1039
5'-most EST	LIB3083-024-Q1-L1-G1
Method	BLASTX
NCBI GI	g2058282
BLAST score	652
E value	5.0e-68
Match length	169
% identity	73
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	192197
Contig ID	5804_1.R1039
5'-most EST	uC-gsflnu33B057e05b1
Method	BLASTX
NCBI GI	g1699024
BLAST score	797
E value	4.0e-85
Match length	231
% identity	64
NCBI Description	(U78866) gene1000 [Arabidopsis thaliana] >gi|1699057 (U78870) unknown [Arabidopsis thaliana]

Seq. No.	192198
Contig ID	5805_1.R1039
5'-most EST	LIB3147-022-Q1-K1-D8
Method	BLASTX
NCBI GI	g2388564
BLAST score	210
E value	2.0e-26
Match length	208
% identity	43
NCBI Description	(AC000098) ESTs gb|AA042402,gb|ATTS1380 come from this gene. [Arabidopsis thaliana]

Seq. No.	192199
Contig ID	5805_2.R1039
5'-most EST	LIB3145-013-Q1-K1-F2

Seq. No.	192200
Contig ID	5807_1.R1039
5'-most EST	LIB3083-024-Q1-L1-G2
Method	BLASTX
NCBI GI	g1330401
BLAST score	264
E value	7.0e-23

Match length 150
% identity 37
NCBI Description (U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No. 192201
Contig ID 5812_1.R1039
5'-most EST uC-gsronu33B038c06b1
Method BLASTX
NCBI GI g3063702
BLAST score 180
E value 6.0e-13
Match length 205
% identity 33
NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No. 192202
Contig ID 5815_1.R1039
5'-most EST LIB3083-024-Q1-L1-H1

Seq. No. 192203
Contig ID 5817_1.R1039
5'-most EST LIB3083-024-Q1-L1-H12
Method BLASTX
NCBI GI g2252828
BLAST score 193
E value 1.0e-22
Match length 111
% identity 54
NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 192204
Contig ID 5822_1.R1039
5'-most EST LIB3083-024-Q1-L1-H6

Seq. No. 192205
Contig ID 5825_1.R1039
5'-most EST LIB3083-024-Q1-L1-H9
Method BLASTX
NCBI GI g3894191
BLAST score 469
E value 1.0e-46
Match length 156
% identity 59
NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]

Seq. No. 192206
Contig ID 5828_1.R1039
5'-most EST LIB3083-027-Q1-L1-A11

Seq. No. 192207
Contig ID 5832_1.R1039
5'-most EST LIB3146-041-Q1-K1-H6
Method BLASTX
NCBI GI g133867
BLAST score 580
E value 4.0e-60
Match length 129

% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi|82722|pir||S16577 ribosomal protein S11 - maize >gi|22470|emb|CAA39438| (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	192208
Contig ID	5832_2.R1039
5'-most EST	LIB3149-042-Q1-K1-C8
Method	BLASTX
NCBI GI	g133867
BLAST score	227
E value	8.0e-19
Match length	56
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi|82722|pir||S16577 ribosomal protein S11 - maize >gi|22470|emb|CAA39438| (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	192209
Contig ID	5833_1.R1039
5'-most EST	LIB3083-027-Q1-L1-A5
Method	BLASTX
NCBI GI	g4455192
BLAST score	278
E value	3.0e-24
Match length	158
% identity	39
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	192210
Contig ID	5834_1.R1039
5'-most EST	g5045621
Method	BLASTX
NCBI GI	g4191774
BLAST score	297
E value	1.0e-26
Match length	71
% identity	83
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	192211
Contig ID	5836_1.R1039
5'-most EST	LIB3083-027-Q1-L1-A8
Method	BLASTX
NCBI GI	g498038
BLAST score	416
E value	7.0e-54
Match length	179
% identity	58
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	192212
Contig ID	5841_1.R1039
5'-most EST	LIB3083-027-Q1-L1-B12

Seq. No. 192213

Contig ID 5843_1.R1039
5'-most EST LIB3149-021-Q1-K1-G3
Method BLASTX
NCBI GI g2160191
BLAST score 1309
E value 1.0e-145
Match length 257
% identity 92
NCBI Description (AC000132) Identical to A. thaliana AtK-1 (gb|X79279). [Arabidopsis thaliana]

Seq. No. 192214
Contig ID 5844_1.R1039
5'-most EST LIB3165-020-P1-K1-E11

Seq. No. 192215
Contig ID 5847_1.R1039
5'-most EST LIB3146-051-Q1-K1-E3
Method BLASTX
NCBI GI g2995990
BLAST score 394
E value 4.0e-38
Match length 117
% identity 65
NCBI Description (AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi|2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No. 192216
Contig ID 5848_1.R1039
5'-most EST LIB3148-024-Q1-K1-E5
Method BLASTX
NCBI GI g2765837
BLAST score 219
E value 2.0e-17
Match length 76
% identity 67
NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 192217
Contig ID 5855_1.R1039
5'-most EST LIB3148-025-Q1-K1-F9

Seq. No. 192218
Contig ID 5856_1.R1039
5'-most EST LIB3083-114-Q1-L1-D7
Method BLASTX
NCBI GI g3694872
BLAST score 554
E value 1.0e-56
Match length 131
% identity 80
NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 192219
Contig ID 5856_2.R1039
5'-most EST uC-gsronu33B126g02b1

Method	BLASTX
NCBI GI	g3694872
BLAST score	566
E value	4.0e-58
Match length	130
% identity	82
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	192220
Contig ID	5856_3.R1039
5'-most EST	g5048708
Method	BLASTX
NCBI GI	g3694872
BLAST score	568
E value	3.0e-58
Match length	130
% identity	83
NCBI Description	(AF092547) profilin [Ricinus communis]

Seq. No.	192221
Contig ID	5856_5.R1039
5'-most EST	LIB3189-045-P1-K1-E11
Method	BLASTN
NCBI GI	g3694871
BLAST score	160
E value	1.0e-84
Match length	360
% identity	86
NCBI Description	Ricinus communis profilin (pro1) mRNA, complete cds

Seq. No.	192222
Contig ID	5857_1.R1039
5'-most EST	g5044723
Method	BLASTX
NCBI GI	g172945
BLAST score	506
E value	4.0e-51
Match length	219
% identity	44
NCBI Description	(J03964) Phe-RNA synthetase [Saccharomyces cerevisiae]

Seq. No.	192223
Contig ID	5860_1.R1039
5'-most EST	LIB3083-027-Q1-L1-C8
Method	BLASTX
NCBI GI	g4325282
BLAST score	827
E value	1.0e-88
Match length	202
% identity	79
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi|4325286|gb|AAD17314| (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	192224
Contig ID	5869_1.R1039
5'-most EST	g5048688

Method	BLASTX
NCBI GI	g629839
BLAST score	1729
E value	0.0e+00
Match length	344
% identity	94
NCBI Description	beta-6 tubulin - maize >gi|416147 (L10633) beta-6 tubulin [Zea mays]

Seq. No.	192225
Contig ID	5877_1.R1039
5'-most EST	LIB3147-040-Q1-K1-E4

Seq. No.	192226
Contig ID	5889_1.R1039
5'-most EST	uC-gsflnu33B006c02b1
Method	BLASTX
NCBI GI	g3367536
BLAST score	253
E value	9.0e-22
Match length	65
% identity	78
NCBI Description	(AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi|2961343 from A. thaliana BAC gb|AL022140. EST gb|T04695 comes from this gene. [Arabidopsis thaliana]

Seq. No.	192227
Contig ID	5890_1.R1039
5'-most EST	LIB3083-027-Q1-L1-F4

Seq. No.	192228
Contig ID	5891_1.R1039
5'-most EST	LIB3146-024-Q1-K1-B4
Method	BLASTX
NCBI GI	g2924792
BLAST score	654
E value	2.0e-68
Match length	169
% identity	74
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	192229
Contig ID	5891_2.R1039
5'-most EST	uC-gsronu33B157b01b1
Method	BLASTX
NCBI GI	g2924792
BLAST score	581
E value	6.0e-60
Match length	136
% identity	78
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	192230
Contig ID	5896_1.R1039
5'-most EST	LIB3272-047-P1-K1-D10

Seq. No.	192231
Contig ID	5901_2.R1039
5'-most EST	LIB3146-053-Q1-K1-A12
Method	BLASTX
NCBI GI	g169363
BLAST score	240
E value	3.0e-20
Match length	63
% identity	62
NCBI Description	(M75856) PVPR3 [Phaseolus vulgaris]

Seq. No.	192232
Contig ID	5902_1.R1039
5'-most EST	LIB3083-027-Q1-L1-G4
Method	BLASTX
NCBI GI	g2146746
BLAST score	298
E value	7.0e-27
Match length	72
% identity	81
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi|166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	192233
Contig ID	5913_1.R1039
5'-most EST	LIB3165-012-P1-K1-E12
Method	BLASTX
NCBI GI	g3377812
BLAST score	482
E value	2.0e-48
Match length	134
% identity	71
NCBI Description	(AF076275) contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA.hm, score: 12.02) [Arabidopsis thaliana]

Seq. No.	192234
Contig ID	5915_1.R1039
5'-most EST	LIB3083-027-Q1-L1-H5
Method	BLASTX
NCBI GI	g3929364
BLAST score	785
E value	2.0e-90
Match length	217
% identity	78
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi|1076356|pir||S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi|666977|emb|CAA59061| (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi|3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb|X84318 from A.thaliana. ESTs gb|Z27005, gb|T04711, gb|T45078 and gb|Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	192235
Contig ID	5919_2.R1039
5'-most EST	LIB3083-028-Q1-L1-A1

Method	BLASTX
NCBI GI	g2920839
BLAST score	344
E value	2.0e-32
Match length	127
% identity	52
NCBI Description	(U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No.	192236
Contig ID	5923_1.R1039
5'-most EST	g5045839
Method	BLASTX
NCBI GI	g1669573
BLAST score	498
E value	3.0e-50
Match length	157
% identity	66
NCBI Description	(D88399) endosperm kinase [Oryza sativa]

Seq. No.	192237
Contig ID	5923_2.R1039
5'-most EST	LIB3083-028-Q1-L1-A2
Method	BLASTX
NCBI GI	g1669573
BLAST score	810
E value	6.0e-87
Match length	162
% identity	93
NCBI Description	(D88399) endosperm kinase [Oryza sativa]

Seq. No.	192238
Contig ID	5925_1.R1039
5'-most EST	LIB3083-082-Q1-L1-G1
Method	BLASTX
NCBI GI	g2944446
BLAST score	393
E value	7.0e-38
Match length	92
% identity	76
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No.	192239
Contig ID	5927_1.R1039
5'-most EST	LIB3148-040-Q1-K1-D11

Seq. No.	192240
Contig ID	5936_1.R1039
5'-most EST	g5046023
Method	BLASTX
NCBI GI	g2864622
BLAST score	262
E value	2.0e-22
Match length	121
% identity	47
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	192241
Contig ID	5938_1.R1039
5'-most EST	uC-gsflnu33B001g12b1
Method	BLASTX
NCBI GI	g4097547
BLAST score	217
E value	3.0e-17
Match length	113
% identity	23
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	192242
Contig ID	5947_1.R1039
5'-most EST	uC-gsflmaxxa009f12b1
Method	BLASTX
NCBI GI	g3702332
BLAST score	668
E value	8.0e-70
Match length	238
% identity	54
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	192243
Contig ID	5947_2.R1039
5'-most EST	LIB3083-100-Q1-L1-G10
Method	BLASTX
NCBI GI	g3702332
BLAST score	661
E value	5.0e-69
Match length	249
% identity	53
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	192244
Contig ID	5947_3.R1039
5'-most EST	LIB3149-025-Q1-K1-D10
Method	BLASTX
NCBI GI	g4454032
BLAST score	332
E value	7.0e-31
Match length	102
% identity	70
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	192245
Contig ID	5948_1.R1039
5'-most EST	LIB3135-011-Q1-K1-G11
Method	BLASTX
NCBI GI	g557472
BLAST score	216
E value	5.0e-17
Match length	179
% identity	30
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	192246
Contig ID	5950_1.R1039

5'-most EST	LIB3165-004-P1-K1-C8
Method	BLASTX
NCBI GI	g4008159
BLAST score	1802
E value	0.0e+00
Match length	418
% identity	83
NCBI Description	(AB015601) DnaJ homolog [Salix gilgiana]

Seq. No.	192247
Contig ID	5950_2.R1039
5'-most EST	LIB3166-018-P1-K1-C3
Method	BLASTN
NCBI GI	g4210947
BLAST score	126
E value	2.0e-64
Match length	330
% identity	85
NCBI Description	Hevea brasiliensis DnaJ protein mRNA, complete cds

Seq. No.	192248
Contig ID	5951_1.R1039
5'-most EST	g5046807
Method	BLASTX
NCBI GI	g3831451
BLAST score	495
E value	2.0e-94
Match length	194
% identity	67
NCBI Description	(AC005700) putative O-GlcNAc transferase [Arabidopsis thaliana]

Seq. No.	192249
Contig ID	5960_1.R1039
5'-most EST	LIB3272-016-P1-K1-B11

Seq. No.	192250
Contig ID	5962_1.R1039
5'-most EST	LIB3083-028-Q1-L1-D8
Method	BLASTX
NCBI GI	g3834321
BLAST score	937
E value	1.0e-101
Match length	209
% identity	88
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi|3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb|AC004481. [Arabidopsis thaliana]

Seq. No.	192251
Contig ID	5962_2.R1039
5'-most EST	LIB3135-051-Q1-K1-G4
Method	BLASTX
NCBI GI	g3834321
BLAST score	291
E value	7.0e-26

Match length	61
% identity	93
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi|3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb|AC004481. [Arabidopsis thaliana]

Seq. No.	192252
Contig ID	5964_1.R1039
5'-most EST	LIB3083-028-Q1-L1-E1
Method	BLASTX
NCBI GI	g3046695
BLAST score	206
E value	3.0e-16
Match length	62
% identity	63
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	192253
Contig ID	5970_1.R1039
5'-most EST	LIB3166-038-P1-K1-H6
Method	BLASTX
NCBI GI	g2275196
BLAST score	824
E value	4.0e-88
Match length	252
% identity	72
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana]

Seq. No.	192254
Contig ID	5971_1.R1039
5'-most EST	LIB3135-055-Q1-K1-G11

Seq. No.	192255
Contig ID	5982_1.R1039
5'-most EST	LIB3166-014-P1-K1-E1
Method	BLASTX
NCBI GI	g3153154
BLAST score	845
E value	1.0e-90
Match length	201
% identity	84
NCBI Description	(AJ006225) small GTP-binding protein [Mesembryanthemum crystallinum]

Seq. No.	192256
Contig ID	5991_1.R1039
5'-most EST	LIB3083-028-Q1-L1-G3
Method	BLASTX
NCBI GI	g3128176
BLAST score	383
E value	1.0e-36
Match length	173
% identity	50
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	192257
Contig ID	5992_1.R1039
5'-most EST	LIB3083-028-Q1-L1-G4
Method	BLASTX
NCBI GI	g2980767
BLAST score	422
E value	3.0e-41
Match length	137
% identity	66
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	192258
Contig ID	5993_1.R1039
5'-most EST	LIB3149-062-Q1-K1-H11
Method	BLASTN
NCBI GI	g2980757
BLAST score	42
E value	4.0e-14
Match length	271
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	192259
Contig ID	6008_1.R1039
5'-most EST	g5047205
Method	BLASTX
NCBI GI	g2102696
BLAST score	996
E value	1.0e-108
Match length	530
% identity	39
NCBI Description	(U72761) karyopherin beta 3 [Homo sapiens] >gi|4504909|ref|NP_002262.1|pKPNB3| karyopherin (importin) beta

Seq. No.	192260
Contig ID	6016_2.R1039
5'-most EST	uC-gsflnu33B005e06b1
Method	BLASTX
NCBI GI	g4406780
BLAST score	619
E value	3.0e-64
Match length	143
% identity	80
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	192261
Contig ID	6018_1.R1039
5'-most EST	uC-gsronu33B148d06b1
Method	BLASTX
NCBI GI	g2119938
BLAST score	2037
E value	0.0e+00
Match length	413
% identity	95

NCBI Description	translation initiation factor eIF-4A.14 - common tobacco

Seq. No.	192262
Contig ID	6018_2.R1039
5'-most EST	uC-gsflmaxxa041d02b1
Method	BLASTX
NCBI GI	g1170508
BLAST score	582
E value	4.0e-60
Match length	124
% identity	90
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi|2119931|pir||S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi|475219|emb|CAA55639| (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi|475221|emb|CAA55640| (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]

Seq. No.	192263
Contig ID	6018_4.R1039
5'-most EST	uC-gsflmaxxa057g09b1
Method	BLASTX
NCBI GI	g2119937
BLAST score	437
E value	3.0e-43
Match length	90
% identity	93
NCBI Description	translation initiation factor eIF-4A.13 - common tobacco (fragment)

Seq. No.	192264
Contig ID	6022_1.R1039
5'-most EST	LIB3083-029-Q1-L1-G10
Method	BLASTX
NCBI GI	g3643594
BLAST score	978
E value	1.0e-106
Match length	245
% identity	78
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	192265
Contig ID	6023_1.R1039
5'-most EST	LIB3083-029-Q1-L1-G11
Method	BLASTX
NCBI GI	g3721540
BLAST score	1696
E value	0.0e+00
Match length	374
% identity	82
NCBI Description	(D83583) Sulfite Reductase [Nicotiana tabacum] >gi|3738234|dbj|BAA33796| (AB010717) sulfite reductase [Nicotiana tabacum]

Seq. No.	192266
Contig ID	6027_1.R1039

5'-most EST	LIB3149-008-Q1-K1-F11
Seq. No.	192267
Contig ID	6032_1.R1039
5'-most EST	g5049393
Method	BLASTX
NCBI GI	g2104681
BLAST score	537
E value	3.0e-54
Match length	357
% identity	41
NCBI Description	(X97907) transcription factor [Vicia faba]
Seq. No.	192268
Contig ID	6032_3.R1039
5'-most EST	LIB3148-035-Q1-K1-H6
Method	BLASTN
NCBI GI	g2104680
BLAST score	35
E value	5.0e-10
Match length	94
% identity	85
NCBI Description	V.faba mRNA for putative transciption factor (1556bp)
Seq. No.	192269
Contig ID	6034_1.R1039
5'-most EST	LIB3083-030-Q1-L1-A2
Method	BLASTN
NCBI GI	g3108252
BLAST score	203
E value	1.0e-110
Match length	329
% identity	91
NCBI Description	Gossypium barbadense clone pXP039 repetitive DNA sequence
Seq. No.	192270
Contig ID	6037_1.R1039
5'-most EST	LIB3083-030-Q1-L1-A6
Method	BLASTX
NCBI GI	g421941
BLAST score	931
E value	1.0e-100
Match length	200
% identity	90
NCBI Description	GTP-binding protein, ras-related - common tobacco >gi|296878|emb|CAA50609| (X71609) ras-related GTP-binding protein [Nicotiana tabacum]
Seq. No.	192271
Contig ID	6037_3.R1039
5'-most EST	LIB3145-006-Q1-K1-B12
Method	BLASTX
NCBI GI	g421941
BLAST score	361
E value	2.0e-34
Match length	74
% identity	95

NCBI Description	GTP-binding protein, ras-related - common tobacco >gi|296878|emb|CAA50609| (X71609) ras-related GTP-binding protein [Nicotiana tabacum]
Seq. No.	192272
Contig ID	6037_4.R1039
5'-most EST	LIB3166-013-P1-K1-F7
Method	BLASTX
NCBI GI	g400976
BLAST score	420
E value	5.0e-48
Match length	108
% identity	95
NCBI Description	RAS-RELATED PROTEIN RHA1 >gi|478671|pir||S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi|16484|emb|CAA41863| (X59152) RHA1 [Arabidopsis thaliana] >gi|397594|emb|CAA80534| (Z22958) GTP-binding protein [Arabidopsis thaliana]
Seq. No.	192273
Contig ID	6038_1.R1039
5'-most EST	LIB3083-030-Q1-L1-A7
Method	BLASTX
NCBI GI	g1125691
BLAST score	170
E value	6.0e-12
Match length	54
% identity	63
NCBI Description	(X94301) DnaJ protein [Solanum tuberosum]
Seq. No.	192274
Contig ID	6042_1.R1039
5'-most EST	LIB3145-023-Q1-K1-E11
Method	BLASTX
NCBI GI	g2914703
BLAST score	258
E value	5.0e-22
Match length	78
% identity	62
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.	192275
Contig ID	6052_1.R1039
5'-most EST	LIB3083-030-Q1-L1-C5
Method	BLASTX
NCBI GI	g3928089
BLAST score	145
E value	7.0e-09
Match length	36
% identity	61
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]
Seq. No.	192276
Contig ID	6052_2.R1039
5'-most EST	LIB3083-060-Q1-L1-F6
Seq. No.	192277

Contig ID	6053_1.R1039
5'-most EST	LIB3083-030-Q1-L1-C6
Method	BLASTX
NCBI GI	g3927826
BLAST score	196
E value	1.0e-14
Match length	133
% identity	37
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192278
Contig ID	6055_1.R1039
5'-most EST	g3326673

Seq. No.	192279
Contig ID	6055_2.R1039
5'-most EST	LIB3083-030-Q1-L1-C8
Method	BLASTX
NCBI GI	g2275219
BLAST score	387
E value	4.0e-37
Match length	87
% identity	82
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	192280
Contig ID	6056_1.R1039
5'-most EST	LIB3196-037-P1-M1-A9

Seq. No.	192281
Contig ID	6058_1.R1039
5'-most EST	LIB3147-001-Q1-K2-G4
Method	BLASTX
NCBI GI	g3983665
BLAST score	434
E value	2.0e-42
Match length	111
% identity	77
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	192282
Contig ID	6065_1.R1039
5'-most EST	uC-gsflnu33B009h01b1
Method	BLASTX
NCBI GI	g22490
BLAST score	263
E value	2.0e-22
Match length	202
% identity	33
NCBI Description	(X01380) ORF1 [Zea mays]

Seq. No.	192283
Contig ID	6066_1.R1039
5'-most EST	LIB3083-030-Q1-L1-E4
Method	BLASTX
NCBI GI	g1354849
BLAST score	512

E value	7.0e-52
Match length	149
% identity	63
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	192284
Contig ID	6078_1.R1039
5'-most EST	LIB3083-030-Q1-L1-G3
Method	BLASTX
NCBI GI	g2499489
BLAST score	914
E value	7.0e-99
Match length	212
% identity	83
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi|483536|emb|CAA83683| (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]

Seq. No.	192285
Contig ID	6080_1.R1039
5'-most EST	LIB3083-030-Q1-L1-G8

Seq. No.	192286
Contig ID	6080_2.R1039
5'-most EST	LIB3197-025-Q1-M1-A1

Seq. No.	192287
Contig ID	6081_1.R1039
5'-most EST	LIB3147-051-Q1-K1-A5
Method	BLASTX
NCBI GI	g2500378
BLAST score	437
E value	3.0e-43
Match length	95
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	192288
Contig ID	6081_2.R1039
5'-most EST	LIB3083-030-Q1-L1-G6
Method	BLASTX
NCBI GI	g2500378
BLAST score	428
E value	4.0e-42
Match length	89
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	192289
Contig ID	6081_3.R1039
5'-most EST	uC-gsronu33B158f12b2
Method	BLASTX
NCBI GI	g2500378
BLAST score	395

E value 2.0e-38
Match length 83
% identity 86
NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 192290
Contig ID 6084_1.R1039
5'-most EST LIB3083-030-Q1-L1-H1
Method BLASTX
NCBI GI g2146732
BLAST score 516
E value 3.0e-64
Match length 188
% identity 70
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi|1373396 (U57838) rof1 [Arabidopsis thaliana]

Seq. No. 192291
Contig ID 6089_1.R1039
5'-most EST LIB3083-030-Q1-L1-H6

Seq. No. 192292
Contig ID 6090_1.R1039
5'-most EST LIB3148-020-Q1-K1-B3
Method BLASTX
NCBI GI g1518540
BLAST score 2340
E value 0.0e+00
Match length 479
% identity 92
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 192293
Contig ID 6095_1.R1039
5'-most EST LIB3083-031-Q1-L1-A4

Seq. No. 192294
Contig ID 6096_1.R1039
5'-most EST LIB3083-031-Q1-L1-A5
Method BLASTX
NCBI GI g2511598
BLAST score 294
E value 2.0e-26
Match length 63
% identity 86
NCBI Description (Y13696) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana]

Seq. No. 192295
Contig ID 6098_1.R1039
5'-most EST LIB3083-031-Q1-L1-A7
Method BLASTX
NCBI GI g2765837
BLAST score 156
E value 3.0e-10
Match length 41
% identity 71

NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	192296
Contig ID	6100_1.R1039
5'-most EST	LIB3148-027-Q1-K1-A11
Method	BLASTX
NCBI GI	g3212879
BLAST score	330
E value	1.0e-30
Match length	70
% identity	83
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	192297
Contig ID	6101_1.R1039
5'-most EST	LIB3083-031-Q1-L1-B1

Seq. No.	192298
Contig ID	6104_1.R1039
5'-most EST	LIB3148-039-Q1-K1-B2
Method	BLASTX
NCBI GI	g4544403
BLAST score	280
E value	8.0e-25
Match length	75
% identity	64
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	192299
Contig ID	6104_2.R1039
5'-most EST	LIB3083-081-Q1-L1-F8
Method	BLASTX
NCBI GI	g4544403
BLAST score	331
E value	6.0e-31
Match length	91
% identity	66
NCBI Description	(AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No.	192300
Contig ID	6106_1.R1039
5'-most EST	uC-gsronu33B076c10b1

Seq. No.	192301
Contig ID	6119_1.R1039
5'-most EST	uC-gsflmaxxa058f11b1

Seq. No.	192302
Contig ID	6126_1.R1039
5'-most EST	LIB3083-031-Q1-L1-D2
Method	BLASTX
NCBI GI	g549010
BLAST score	1019
E value	1.0e-111

Match length	217
% identity	89
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi|322554|pir||S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi|16514|emb|CAA49172| (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi|1402882|emb|CAA66813| (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi|1495249|emb|CAA66118| (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	192303
Contig ID	6129_1.R1039
5'-most EST	LIB3083-031-Q1-L1-D7
Method	BLASTX
NCBI GI	g3881976
BLAST score	280
E value	1.0e-24
Match length	60
% identity	85
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	192304
Contig ID	6131_1.R1039
5'-most EST	LIB3083-031-Q1-L1-D9

Seq. No.	192305
Contig ID	6131_2.R1039
5'-most EST	LIB3148-052-Q1-K1-C7

Seq. No.	192306
Contig ID	6133_1.R1039
5'-most EST	uC-gsflnu33B074b09b1

Seq. No.	192307
Contig ID	6137_1.R1039
5'-most EST	LIB3083-077-Q1-L1-F1
Method	BLASTX
NCBI GI	g4100433
BLAST score	312
E value	3.0e-28
Match length	84
% identity	63
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	192308
Contig ID	6138_1.R1039
5'-most EST	LIB3083-031-Q1-L1-E4
Method	BLASTX
NCBI GI	g4455198
BLAST score	277
E value	2.0e-24
Match length	109
% identity	59
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	192309
Contig ID	6141_1.R1039
5'-most EST	LIB3189-010-P1-K1-F12
Method	BLASTN
NCBI GI	g3434970
BLAST score	34
E value	2.0e-09
Match length	62
% identity	97
NCBI Description	Arabidopsis thaliana AtERF-3 mRNA for ethylene responsive element binding factor 3, complete cds

Seq. No.	192310
Contig ID	6142_1.R1039
5'-most EST	LIB3083-031-Q1-L1-E9
Method	BLASTX
NCBI GI	g4455349
BLAST score	238
E value	4.0e-20
Match length	100
% identity	56
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	192311
Contig ID	6144_1.R1039
5'-most EST	uC-gsflmaxxa070g10b1
Method	BLASTX
NCBI GI	g3822036
BLAST score	364
E value	2.0e-34
Match length	185
% identity	43
NCBI Description	(AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No.	192312
Contig ID	6145_1.R1039
5'-most EST	LIB3083-031-Q1-L1-F2
Method	BLASTX
NCBI GI	g4115925
BLAST score	337
E value	3.0e-31
Match length	174
% identity	33
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi|4539439|emb|CAB40027.1| (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	192313
Contig ID	6151_1.R1039
5'-most EST	LIB3148-014-Q1-K1-C7
Method	BLASTX
NCBI GI	g2344781
BLAST score	219
E value	1.0e-17
Match length	47

% identity	89
NCBI Description	(D83041) 2-oxogulutarate 3-dioxygenase [Ipomoea nil]

Seq. No.	192314
Contig ID	6151_2.R1039
5'-most EST	LIB3083-068-Q1-L1-A10
Method	BLASTX
NCBI GI	g729508
BLAST score	290
E value	4.0e-26
Match length	90
% identity	67
NCBI Description	NARINGENIN,2-OXOGLUTARATE 3-DIOXYGENASE (FLAVONONE-3-HYDROXYLASE) (FHT) >gi|499020|emb|CAA53579| (X75965) flavanone 3-hydroxylase [Vitis vinifera]

Seq. No.	192315
Contig ID	6153_1.R1039
5'-most EST	LIB3148-015-Q1-K1-F11
Method	BLASTX
NCBI GI	g2654208
BLAST score	389
E value	1.0e-37
Match length	118
% identity	74
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi|2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	192316
Contig ID	6159_1.R1039
5'-most EST	LIB3135-056-Q1-K1-C3
Method	BLASTX
NCBI GI	g1717949
BLAST score	1021
E value	1.0e-111
Match length	216
% identity	86
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) >gi|100375|pir||B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) >gi|170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]

Seq. No.	192317
Contig ID	6160_1.R1039
5'-most EST	LIB3083-031-Q1-L1-G9

Seq. No.	192318
Contig ID	6169_1.R1039
5'-most EST	LIB3083-031-Q1-L1-H7
Method	BLASTX
NCBI GI	g1346172
BLAST score	143
E value	7.0e-09
Match length	37

% identity	81
NCBI Description	78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >gi|170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum]
Seq. No.	192319
Contig ID	6172_1.R1039
5'-most EST	LIB3272-058-P1-K1-D7
Seq. No.	192320
Contig ID	6175_1.R1039
5'-most EST	LIB3083-037-Q1-G1-A2
Method	BLASTN
NCBI GI	g343239
BLAST score	138
E value	2.0e-71
Match length	456
% identity	90
NCBI Description	Mustard (S.alba) chloroplast 16S rRNA, 5' end, and Val-tRNA
Seq. No.	192321
Contig ID	6180_1.R1039
5'-most EST	LIB3083-119-Q1-L1-F4
Method	BLASTX
NCBI GI	g1402888
BLAST score	1034
E value	1.0e-113
Match length	321
% identity	65
NCBI Description	(X98130) unknown [Arabidopsis thaliana]
Seq. No.	192322
Contig ID	6185_1.R1039
5'-most EST	uC-gsronu33B153b07b2
Seq. No.	192323
Contig ID	6187_1.R1039
5'-most EST	LIB3146-053-Q1-K1-B3
Method	BLASTX
NCBI GI	g4049349
BLAST score	423
E value	2.0e-41
Match length	122
% identity	67
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]
Seq. No.	192324
Contig ID	6187_2.R1039
5'-most EST	LIB3147-032-Q1-K1-D10
Method	BLASTX
NCBI GI	g4049349
BLAST score	212
E value	2.0e-17
Match length	97
% identity	54

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No. 192325
Contig ID 6190_1.R1039
5'-most EST LIB3083-114-Q1-L1-E3
Method BLASTX
NCBI GI g1619602
BLAST score 829
E value 1.0e-88
Match length 265
% identity 63
NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 192326
Contig ID 6195_1.R1039
5'-most EST LIB3147-038-Q1-K2-H7
Method BLASTX
NCBI GI g4510383
BLAST score 507
E value 3.0e-51
Match length 124
% identity 81
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 192327
Contig ID 6198_1.R1039
5'-most EST LIB3083-083-Q1-L1-F1
Method BLASTX
NCBI GI g4218121
BLAST score 163
E value 1.0e-10
Match length 102
% identity 29
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 192328
Contig ID 6203_1.R1039
5'-most EST LIB3148-003-P1-K1-G12
Method BLASTX
NCBI GI g3309269
BLAST score 1110
E value 1.0e-122
Match length 240
% identity 90
NCBI Description (AF074940) ferric leghemoglobin reductase-2 precursor [Glycine max]

Seq. No. 192329
Contig ID 6207_1.R1039
5'-most EST LIB3083-052-Q1-L1-H5

Seq. No. 192330
Contig ID 6212_1.R1039
5'-most EST LIB3083-037-Q1-G1-E7

Seq. No. 192331

Contig ID	6213_1.R1039
5'-most EST	LIB3083-037-Q1-G1-E8
Method	BLASTX
NCBI GI	g2459446
BLAST score	529
E value	6.0e-54
Match length	169
% identity	59
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	192332
Contig ID	6215_1.R1039
5'-most EST	g5046874
Method	BLASTX
NCBI GI	g3201969
BLAST score	668
E value	1.0e-69
Match length	177
% identity	64
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	192333
Contig ID	6218_1.R1039
5'-most EST	LIB3083-094-Q1-L1-A9
Method	BLASTX
NCBI GI	g3236252
BLAST score	653
E value	3.0e-68
Match length	203
% identity	60
NCBI Description	(AC004684) CER1-like protein [Arabidopsis thaliana]

Seq. No.	192334
Contig ID	6219_1.R1039
5'-most EST	LIB3083-037-Q1-G1-F6
Method	BLASTX
NCBI GI	g3914449
BLAST score	583
E value	2.0e-60
Match length	123
% identity	93
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi|3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	192335
Contig ID	6222_1.R1039
5'-most EST	g5044571
Method	BLASTX
NCBI GI	g100226
BLAST score	566
E value	5.0e-58
Match length	277
% identity	42
NCBI Description	hypothetical protein - tomato >gi|19275|emb|CAA78112| (Z12127) protein of unknown function [Lycopersicon

esculentum] >gi|445619|prf||1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	192336
Contig ID	6226_1.R1039
5'-most EST	LIB3083-040-Q1-G1-A6
Method	BLASTX
NCBI GI	g1705678
BLAST score	242
E value	1.0e-20
Match length	57
% identity	86
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi|862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	192337
Contig ID	6228_1.R1039
5'-most EST	uC-gsronu33B027f02b1
Method	BLASTX
NCBI GI	g2827699
BLAST score	330
E value	1.0e-30
Match length	172
% identity	49
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	192338
Contig ID	6229_1.R1039
5'-most EST	uC-gsflmaxxa045f11b1
Method	BLASTX
NCBI GI	g2129533
BLAST score	545
E value	6.0e-56
Match length	148
% identity	72
NCBI Description	adenine nucleotide translocase - Arabidopsis thaliana >gi|1051109|emb|CAA89201| (Z49227) adenine nucleotide translocase [Arabidopsis thaliana]

Seq. No.	192339
Contig ID	6233_1.R1039
5'-most EST	uC-gsronu33B127c02b1
Method	BLASTX
NCBI GI	g2765240
BLAST score	212
E value	6.0e-17
Match length	119
% identity	40
NCBI Description	(Y12805) invertase inhibitor [Nicotiana tabacum]

Seq. No.	192340
Contig ID	6236_1.R1039
5'-most EST	uC-gsflnu33B051d11b1
Method	BLASTX
NCBI GI	g3212879
BLAST score	414

E value	3.0e-40
Match length	196
% identity	45
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	192341
Contig ID	6240_1.R1039
5'-most EST	LIB3083-040-Q1-G1-E3
Method	BLASTX
NCBI GI	g2911075
BLAST score	206
E value	3.0e-16
Match length	71
% identity	58
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	192342
Contig ID	6242_1.R1039
5'-most EST	LIB3146-008-Q1-K1-C7
Method	BLASTX
NCBI GI	g4102861
BLAST score	753
E value	5.0e-80
Match length	152
% identity	91
NCBI Description	(AF016893) copper/zinc-superoxide dismutase [Populus tremuloides]

Seq. No.	192343
Contig ID	6243_1.R1039
5'-most EST	LIB3083-040-Q1-G1-F2

Seq. No.	192344
Contig ID	6244_1.R1039
5'-most EST	g5044720
Method	BLASTX
NCBI GI	g3024501
BLAST score	1008
E value	1.0e-110
Match length	216
% identity	90
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi|1370146|emb|CAA98179| (Z73951) RAB11C [Lotus japonicus]

Seq. No.	192345
Contig ID	6244_2.R1039
5'-most EST	LIB3272-021-P1-K1-E3
Method	BLASTX
NCBI GI	g3024501
BLAST score	967
E value	1.0e-105
Match length	216
% identity	87
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi|1370146|emb|CAA98179| (Z73951) RAB11C [Lotus japonicus]

Seq. No. 192346
Contig ID 6246_1.R1039
5'-most EST LIB3166-052-P1-K1-D6
Method BLASTX
NCBI GI g2764574
BLAST score 670
E value 2.0e-70
Match length 198
% identity 67
NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No. 192347
Contig ID 6247_1.R1039
5'-most EST uC-gsronu33B044f05b1
Method BLASTX
NCBI GI g1170504
BLAST score 562
E value 7.0e-83
Match length 187
% identity 83
NCBI Description EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi|452440 (M95747) initiation factor (iso)4f p82 subunit [Triticum aestivum]

Seq. No. 192348
Contig ID 6253_1.R1039
5'-most EST LIB3083-040-Q1-G1-G5

Seq. No. 192349
Contig ID 6255_1.R1039
5'-most EST LIB3083-040-Q1-G1-G7

Seq. No. 192350
Contig ID 6258_1.R1039
5'-most EST LIB3083-040-Q1-G1-H4
Method BLASTX
NCBI GI g4263786
BLAST score 926
E value 1.0e-100
Match length 224
% identity 79
NCBI Description (AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]

Seq. No. 192351
Contig ID 6259_1.R1039
5'-most EST LIB3165-041-Q1-K1-A9
Method BLASTX
NCBI GI g4127456
BLAST score 422
E value 2.0e-41
Match length 139
% identity 40
NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 192352
Contig ID 6261_1.R1039

5'-most EST	LIB3083-072-Q1-L1-D1
Method	BLASTX
NCBI GI	g3036816
BLAST score	277
E value	5.0e-24
Match length	154
% identity	38
NCBI Description	(AL022373) myosin-like protein [Arabidopsis thaliana]

Seq. No.	192353
Contig ID	6262_1.R1039
5'-most EST	LIB3083-063-Q1-L1-E7
Method	BLASTX
NCBI GI	g3695388
BLAST score	281
E value	7.0e-25
Match length	91
% identity	55
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	192354
Contig ID	6265_1.R1039
5'-most EST	LIB3272-021-P1-K1-A5
Method	BLASTX
NCBI GI	g3402758
BLAST score	308
E value	1.0e-27
Match length	167
% identity	44
NCBI Description	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	192355
Contig ID	6268_1.R1039
5'-most EST	LIB3083-041-Q1-G1-E10
Method	BLASTX
NCBI GI	g3128176
BLAST score	372
E value	2.0e-35
Match length	138
% identity	54
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	192356
Contig ID	6273_1.R1039
5'-most EST	LIB3083-041-Q1-G1-H12

Seq. No.	192357
Contig ID	6284_1.R1039
5'-most EST	LIB3197-040-Q1-M1-D2
Method	BLASTX
NCBI GI	g3068705
BLAST score	269
E value	4.0e-23
Match length	150
% identity	41
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	192358
Contig ID	6284_2.R1039
5'-most EST	uC-gsronu33B125b06b1
Seq. No.	192359
Contig ID	6287_1.R1039
5'-most EST	uC-gsflnu33B019a10b1
Seq. No.	192360
Contig ID	6291_1.R1039
5'-most EST	LIB3197-053-Q1-M1-H6
Seq. No.	192361
Contig ID	6294_1.R1039
5'-most EST	uC-gsronu33B168a11b1
Seq. No.	192362
Contig ID	6295_1.R1039
5'-most EST	LIB3197-049-Q1-M1-G3
Method	BLASTX
NCBI GI	g2586127
BLAST score	904
E value	1.0e-97
Match length	263
% identity	67
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]
Seq. No.	192363
Contig ID	6296_1.R1039
5'-most EST	LIB3145-044-Q1-K1-H4
Method	BLASTX
NCBI GI	g3201969
BLAST score	881
E value	7.0e-95
Match length	192
% identity	80
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]
Seq. No.	192364
Contig ID	6297_1.R1039
5'-most EST	LIB3083-042-Q1-G1-H11
Seq. No.	192365
Contig ID	6301_1.R1039
5'-most EST	LIB3148-037-Q1-K1-B6
Method	BLASTX
NCBI GI	g4454051
BLAST score	348
E value	1.0e-32
Match length	117
% identity	60
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]
Seq. No.	192366
Contig ID	6305_1.R1039

5'-most EST	LIB3083-046-Q1-G1-A12
Seq. No.	192367
Contig ID	6328_1.R1039
5'-most EST	LIB3083-046-Q1-G1-C7
Method	BLASTX
NCBI GI	g2213884
BLAST score	887
E value	1.0e-99
Match length	250
% identity	74
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]
Seq. No.	192368
Contig ID	6329_1.R1039
5'-most EST	uC-gsronu33B037f11b1
Seq. No.	192369
Contig ID	6332_1.R1039
5'-most EST	uC-gsflmaxxa054h12b1
Method	BLASTX
NCBI GI	g2317910
BLAST score	740
E value	2.0e-78
Match length	224
% identity	59
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]
Seq. No.	192370
Contig ID	6333_1.R1039
5'-most EST	LIB3272-050-P1-K1-F2
Method	BLASTX
NCBI GI	g3660467
BLAST score	1297
E value	1.0e-143
Match length	306
% identity	81
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]
Seq. No.	192371
Contig ID	6333_2.R1039
5'-most EST	LIB3147-004-Q1-K1-D12
Method	BLASTX
NCBI GI	g3660467
BLAST score	319
E value	2.0e-29
Match length	75
% identity	83
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]
Seq. No.	192372
Contig ID	6334_1.R1039
5'-most EST	uC-gsflnu33B136c03b1
Method	BLASTX

NCBI GI	g2435517
BLAST score	329
E value	1.0e-30
Match length	133
% identity	54
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	192373
Contig ID	6339_1.R1039
5'-most EST	g5047657
Method	BLASTX
NCBI GI	g3153205
BLAST score	1386
E value	1.0e-154
Match length	292
% identity	87
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	192374
Contig ID	6342_1.R1039
5'-most EST	LIB3272-028-P1-K1-B4

Seq. No.	192375
Contig ID	6349_1.R1039
5'-most EST	g5046016

Seq. No.	192376
Contig ID	6349_2.R1039
5'-most EST	LIB3197-059-Q1-M1-D8

Seq. No.	192377
Contig ID	6351_1.R1039
5'-most EST	LIB3083-046-Q1-G1-F7
Method	BLASTX
NCBI GI	g3367534
BLAST score	1499
E value	1.0e-167
Match length	330
% identity	84
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb|U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	192378
Contig ID	6357_1.R1039
5'-most EST	LIB3166-015-P1-K1-H11
Method	BLASTX
NCBI GI	g832876
BLAST score	589
E value	8.0e-61
Match length	192
% identity	70
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi|1097368|prf||2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	192379
Contig ID	6357_2.R1039
5'-most EST	LIB3197-047-Q1-M1-C5
Method	BLASTX
NCBI GI	g832876
BLAST score	1206
E value	1.0e-133
Match length	265
% identity	87
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi|1097368|prf||2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	192380
Contig ID	6359_1.R1039
5'-most EST	LIB3197-045-Q1-M1-D3
Method	BLASTN
NCBI GI	g2351373
BLAST score	71
E value	2.0e-31
Match length	443
% identity	84
NCBI Description	Arabidopsis thaliana putative 26S proteasome subunit athMOV34 mRNA, complete cds

Seq. No.	192381
Contig ID	6360_1.R1039
5'-most EST	LIB3083-087-Q1-L1-G2

Seq. No.	192382
Contig ID	6367_1.R1039
5'-most EST	LIB3135-039-Q1-K1-B7
Method	BLASTX
NCBI GI	g2129915
BLAST score	529
E value	1.0e-53
Match length	149
% identity	67
NCBI Description	ferredoxin precursor - sweet orange >gi|1360725|emb|CAA87068| (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	192383
Contig ID	6368_1.R1039
5'-most EST	LIB3083-046-Q1-G1-H7

Seq. No.	192384
Contig ID	6369_1.R1039
5'-most EST	LIB3083-046-Q1-G1-H8
Method	BLASTX
NCBI GI	g3687237
BLAST score	773
E value	3.0e-82
Match length	334
% identity	50
NCBI Description	(AC005169) putative Cys3His zinc-finger protein

[Arabidopsis thaliana]

Seq. No.	192385
Contig ID	6376_1.R1039
5'-most EST	LIB3272-011-P1-K1-D11
Method	BLASTX
NCBI GI	g3643609
BLAST score	650
E value	4.0e-68
Match length	175
% identity	69
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	192386
Contig ID	6380_1.R1039
5'-most EST	uC-gsronu33B031c12b1
Method	BLASTX
NCBI GI	g3885338
BLAST score	146
E value	1.0e-08
Match length	178
% identity	26
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	192387
Contig ID	6386_1.R1039
5'-most EST	LIB3083-047-Q1-G1-G2
Method	BLASTX
NCBI GI	g4510377
BLAST score	179
E value	4.0e-13
Match length	47
% identity	72
NCBI Description	(AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	192388
Contig ID	6392_1.R1039
5'-most EST	LIB3083-060-Q1-L1-G2
Method	BLASTX
NCBI GI	g2829899
BLAST score	263
E value	9.0e-23
Match length	132
% identity	42
NCBI Description	(AC002311) similar to ripening-induced protein, gp|AJ001449|2465015 and major#latex protein, gp|X91961|1107495 [Arabidopsis thaliana]

Seq. No.	192389
Contig ID	6393_1.R1039
5'-most EST	LIB3083-047-Q1-G1-H2
Method	BLASTX
NCBI GI	g2129753
BLAST score	899
E value	3.0e-97
Match length	198

% identity	85
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi|1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	192390
Contig ID	6396_1.R1039
5'-most EST	uC-gsronu33B008c09b1
Method	BLASTX
NCBI GI	g4039152
BLAST score	178
E value	7.0e-13
Match length	38
% identity	87
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi|4325219|gb|AAD17303| (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	192391
Contig ID	6397_1.R1039
5'-most EST	LIB3083-047-Q1-G1-H7
Method	BLASTX
NCBI GI	g3421096
BLAST score	1163
E value	1.0e-128
Match length	249
% identity	88
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi|3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	192392
Contig ID	6402_1.R1039
5'-most EST	LIB3083-048-Q1-G1-D1
Method	BLASTX
NCBI GI	g1651828
BLAST score	252
E value	2.0e-21
Match length	102
% identity	46
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	192393
Contig ID	6405_1.R1039
5'-most EST	LIB3197-033-Q1-M1-E12

Seq. No.	192394
Contig ID	6405_2.R1039
5'-most EST	LIB3148-043-Q1-K1-A11

Seq. No.	192395
Contig ID	6406_1.R1039
5'-most EST	LIB3189-046-P1-K1-C1
Method	BLASTX
NCBI GI	g1665817
BLAST score	193
E value	2.0e-14

Match length	94
% identity	36
NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	192396
Contig ID	6412_1.R1039
5'-most EST	LIB3149-035-Q1-K1-D9
Method	BLASTX
NCBI GI	g445613
BLAST score	875
E value	3.0e-94
Match length	236
% identity	71
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	192397
Contig ID	6412_2.R1039
5'-most EST	LIB3166-023-P1-K1-C5
Method	BLASTX
NCBI GI	g445613
BLAST score	839
E value	2.0e-97
Match length	239
% identity	75
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	192398
Contig ID	6412_3.R1039
5'-most EST	LIB3196-035-P1-M1-E4
Method	BLASTX
NCBI GI	g445613
BLAST score	305
E value	7.0e-28
Match length	95
% identity	65
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	192399
Contig ID	6417_1.R1039
5'-most EST	LIB3189-002-P1-K1-C5

Seq. No.	192400
Contig ID	6420_1.R1039
5'-most EST	uC-gsflmaxxa012b02b1
Method	BLASTX
NCBI GI	g2154715
BLAST score	335
E value	4.0e-31
Match length	178
% identity	48
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	192401
Contig ID	6421_1.R1039
5'-most EST	LIB3083-049-Q1-L1-H12
Method	BLASTX

NCBI GI g549010
BLAST score 1022
E value 1.0e-111
Match length 218
% identity 90
NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi|322554|pir||S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi|16514|emb|CAA49172| (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi|1402882|emb|CAA66813| (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi|1495249|emb|CAA66118| (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No. 192402
Contig ID 6421_2.R1039
5'-most EST g3325772
Method BLASTX
NCBI GI g549010
BLAST score 749
E value 1.0e-79
Match length 175
% identity 83
NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi|322554|pir||S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi|16514|emb|CAA49172| (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi|1402882|emb|CAA66813| (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi|1495249|emb|CAA66118| (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No. 192403
Contig ID 6422_1.R1039
5'-most EST LIB3135-053-Q1-K1-A5
Method BLASTX
NCBI GI g3719211
BLAST score 630
E value 1.0e-65
Match length 154
% identity 81
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 192404
Contig ID 6423_1.R1039
5'-most EST LIB3149-063-Q1-K1-A4
Method BLASTX
NCBI GI g466160
BLAST score 373
E value 1.0e-35
Match length 84
% identity 85
NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III

>gi|630771|pir||S44903 ZK652.3 protein - Caenorhabditis elegans >gi|289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	192405
Contig ID	6424_1.R1039
5'-most EST	g5049445
Method	BLASTX
NCBI GI	g2129630
BLAST score	415
E value	2.0e-40
Match length	106
% identity	67
NCBI Description	lamin - Arabidopsis thaliana >gi|1262754|emb|CAA65750| (X97023) lamin [Arabidopsis thaliana] >gi|3395760 (U77721) unknown [Arabidopsis thaliana]

Seq. No.	192406
Contig ID	6431_1.R1039
5'-most EST	LIB3083-048-Q1-G1-H4
Method	BLASTX
NCBI GI	g4538897
BLAST score	895
E value	1.0e-131
Match length	355
% identity	64
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	192407
Contig ID	6433_1.R1039
5'-most EST	LIB3148-012-Q1-K1-G9
Method	BLASTX
NCBI GI	g2947062
BLAST score	268
E value	7.0e-23
Match length	246
% identity	36
NCBI Description	(AC002521) unknown protein [Arabidopsis thaliana]

Seq. No.	192408
Contig ID	6438_1.R1039
5'-most EST	LIB3135-044-Q1-K1-A9

Seq. No.	192409
Contig ID	6439_1.R1039
5'-most EST	LIB3083-049-Q1-L1-G12
Method	BLASTX
NCBI GI	g3834322
BLAST score	167
E value	2.0e-11
Match length	162
% identity	38
NCBI Description	(AC005679) EST gb|R30300 comes from this gene. [Arabidopsis thaliana]

Seq. No.	192410
Contig ID	6449_1.R1039

5'-most EST	LIB3165-052-Q1-K1-B8
Method	BLASTX
NCBI GI	g2677828
BLAST score	1387
E value	1.0e-154
Match length	338
% identity	77
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	192411
Contig ID	6449_2.R1039
5'-most EST	LIB3197-020-Q1-M1-C12
Method	BLASTX
NCBI GI	g2677828
BLAST score	416
E value	8.0e-41
Match length	119
% identity	68
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	192412
Contig ID	6449_4.R1039
5'-most EST	LIB3166-026-P1-K1-G12
Method	BLASTX
NCBI GI	g2677828
BLAST score	357
E value	6.0e-34
Match length	111
% identity	59
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	192413
Contig ID	6450_1.R1039
5'-most EST	g5047298
Method	BLASTX
NCBI GI	g3668092
BLAST score	515
E value	3.0e-52
Match length	194
% identity	61
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	192414
Contig ID	6451_1.R1039
5'-most EST	LIB3083-050-Q1-L1-A4
Method	BLASTX
NCBI GI	g2281115
BLAST score	173
E value	5.0e-23
Match length	70
% identity	83
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	192415
Contig ID	6452_1.R1039
5'-most EST	uC-gsronu33B087b04b1

Seq. No.	192416
Contig ID	6453_1.R1039
5'-most EST	LIB3083-050-Q1-L1-A6
Method	BLASTX
NCBI GI	g3202042
BLAST score	333
E value	8.0e-31
Match length	151
% identity	52
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	192417
Contig ID	6455_1.R1039
5'-most EST	LIB3083-119-Q1-L1-A12

Seq. No.	192418
Contig ID	6456_1.R1039
5'-most EST	LIB3083-053-Q1-L1-E6

Seq. No.	192419
Contig ID	6457_1.R1039
5'-most EST	LIB3083-050-Q1-L1-B10

Seq. No.	192420
Contig ID	6459_1.R1039
5'-most EST	LIB3083-050-Q1-L1-B2
Method	BLASTX
NCBI GI	g3426039
BLAST score	865
E value	4.0e-93
Match length	263
% identity	63
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	192421
Contig ID	6460_1.R1039
5'-most EST	uC-gsronu33B166a12b2
Method	BLASTX
NCBI GI	g4432844
BLAST score	341
E value	6.0e-32
Match length	166
% identity	42
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	192422
Contig ID	6465_1.R1039
5'-most EST	LIB3083-050-Q1-L1-B8
Method	BLASTX
NCBI GI	g1170603
BLAST score	185
E value	1.0e-13
Match length	97
% identity	41
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN C2F7.03C

>gi|2130372|pir||S58147 hypothetical protein SPAC2F7.03c - fission yeast (Schizosaccharomyces pombe) >gi|1052786|emb|CAA90490| (Z50142) protein kinase [Schizosaccharomyces pombe]

Seq. No.	192423
Contig ID	6471_1.R1039
5'-most EST	LIB3149-031-Q1-K1-A7
Method	BLASTX
NCBI GI	g2500376
BLAST score	463
E value	5.0e-46
Match length	95
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi|4262177|gb|AAD14494| (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	192424
Contig ID	6471_2.R1039
5'-most EST	LIB3166-031-P1-K1-F12
Method	BLASTX
NCBI GI	g3024632
BLAST score	242
E value	4.0e-20
Match length	214
% identity	27
NCBI Description	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA) >gi|1685288 (U78107) gamma SNAP [Homo sapiens] >gi|4505331|ref|NP_003817.1|pNAPG| UNKNOWN

Seq. No.	192425
Contig ID	6471_3.R1039
5'-most EST	LIB3145-001-P1-K1-G10
Method	BLASTX
NCBI GI	g2500376
BLAST score	361
E value	5.0e-34
Match length	82
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi|4262177|gb|AAD14494| (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	192426
Contig ID	6471_4.R1039
5'-most EST	uC-gsflmaxxa028c09b1
Method	BLASTX
NCBI GI	g730558
BLAST score	494
E value	4.0e-50
Match length	100
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi|1076636|pir||S48027 ribosomal protein L34 - common tobacco >gi|2129964|pir||S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi|436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi|436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No.	192427
Contig ID	6480_1.R1039
5'-most EST	uC-gsronu33B005g11b1
Method	BLASTX
NCBI GI	g4204300
BLAST score	547
E value	1.0e-55
Match length	217
% identity	53
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	192428
Contig ID	6482_1.R1039
5'-most EST	LIB3135-040-Q1-K1-D3
Method	BLASTX
NCBI GI	g2982432
BLAST score	334
E value	3.0e-31
Match length	76
% identity	80
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	192429
Contig ID	6484_1.R1039
5'-most EST	g5050877
Method	BLASTX
NCBI GI	g4455207
BLAST score	440
E value	2.0e-43
Match length	95
% identity	91
NCBI Description	(AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	192430
Contig ID	6484_2.R1039
5'-most EST	uC-gsflnu33B127b02b1
Method	BLASTX
NCBI GI	g2501449
BLAST score	337
E value	2.0e-31
Match length	68
% identity	94
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3 >gi|1668773|emb|CAA67922| (X99608) ubiquitin-like protein [Oryza sativa]

Seq. No.	192431
Contig ID	6487_1.R1039
5'-most EST	LIB3120-043-P1-K1-B11
Method	BLASTX
NCBI GI	g629541
BLAST score	291
E value	6.0e-26
Match length	81
% identity	74
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi|472875|emb|CAA53476| (X75882) plasma membrane intrinsic

protein 1c [Arabidopsis thaliana]

Seq. No.	192432
Contig ID	6487_2.R1039
5'-most EST	LIB3166-011-P1-K1-F7
Method	BLASTX
NCBI GI	g1175012
BLAST score	1299
E value	1.0e-144
Match length	286
% identity	86
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi|396218|emb|CAA49155| (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	192433
Contig ID	6487_4.R1039
5'-most EST	uC-gsronu33B149f12b1
Method	BLASTX
NCBI GI	g2440044
BLAST score	342
E value	3.0e-57
Match length	127
% identity	89
NCBI Description	(AJ001293) major intrinsic protein PIPB [Craterostigma plantagineum]

Seq. No.	192434
Contig ID	6487_7.R1039
5'-most EST	uC-gsflnu33B142f03b1
Method	BLASTX
NCBI GI	g1175012
BLAST score	237
E value	5.0e-20
Match length	45
% identity	89
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi|396218|emb|CAA49155| (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	192435
Contig ID	6491_1.R1039
5'-most EST	LIB3083-050-Q1-L1-E4
Method	BLASTX
NCBI GI	g2960216
BLAST score	1029
E value	1.0e-112
Match length	238
% identity	84
NCBI Description	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]

Seq. No.	192436
Contig ID	6492_1.R1039
5'-most EST	uC-gsflmaxxa069d01b1
Method	BLASTX
NCBI GI	g3549669

BLAST score	743
E value	7.0e-79
Match length	167
% identity	86
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	192437
Contig ID	6495_1.R1039
5'-most EST	LIB3083-050-Q1-L1-E8
Method	BLASTX
NCBI GI	g541979
BLAST score	977
E value	1.0e-106
Match length	218
% identity	87
NCBI Description	guanine nucleotide regulatory protein - fava bean >gi|303744|dbj|BAA02113| (D12545) GTP-binding protein [Pisum sativum] >gi|452361|emb|CAA82709| (Z29592) guanine nucleotide regulatory protein [Vicia faba] >gi|738937|prf||2001457E GTP-binding protein [Pisum sativum] >gi|1098295|prf||2115367C small GTP-binding protein [Vicia faba]

Seq. No.	192438
Contig ID	6495_2.R1039
5'-most EST	LIB3145-024-Q1-K1-H12
Method	BLASTX
NCBI GI	g4539399
BLAST score	525
E value	1.0e-53
Match length	120
% identity	88
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	192439
Contig ID	6497_1.R1039
5'-most EST	g5050747
Method	BLASTX
NCBI GI	g3702333
BLAST score	403
E value	6.0e-39
Match length	182
% identity	48
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192440
Contig ID	6500_1.R1039
5'-most EST	g5050780
Method	BLASTX
NCBI GI	g4455800
BLAST score	406
E value	4.0e-39
Match length	145
% identity	55
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	192441
Contig ID	6500_2.R1039
5'-most EST	LIB3147-008-Q1-K1-H3
Method	BLASTX
NCBI GI	g1729891
BLAST score	190
E value	3.0e-14
Match length	113
% identity	36
NCBI Description	TEGT PROTEIN (TESTIS ENHANCED GENE TRANSCRIPT) >gi|2136254|pir||I38334 TEGT (testis enhanced gene transcript) - human >gi|458545|emb|CAA53472| (X75861) TEGT [Homo sapiens] >gi|4507433|ref|NP_003208.1|pTEGT| testis enhanced gene transcript

Seq. No.	192442
Contig ID	6500_3.R1039
5'-most EST	LIB3146-055-Q1-K1-B7
Method	BLASTX
NCBI GI	g4455800
BLAST score	270
E value	1.0e-23
Match length	114
% identity	48
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	192443
Contig ID	6512_1.R1039
5'-most EST	LIB3083-101-Q1-L1-D2
Method	BLASTX
NCBI GI	g1076274
BLAST score	309
E value	2.0e-28
Match length	111
% identity	57
NCBI Description	cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No.	192444
Contig ID	6522_1.R1039
5'-most EST	LIB3197-035-Q1-M1-B3
Method	BLASTX
NCBI GI	g3420055
BLAST score	711
E value	3.0e-75
Match length	173
% identity	83
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No.	192445
Contig ID	6525_1.R1039
5'-most EST	uC-gsronu33B160g07b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	726
E value	2.0e-80
Match length	179
% identity	85

NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	192446
Contig ID	6525_2.R1039
5'-most EST	uC-gsflnu33B018e01b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	564
E value	1.0e-73
Match length	151
% identity	98
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi|466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	192447
Contig ID	6526_1.R1039
5'-most EST	LIB3083-050-Q1-L1-H9
Method	BLASTX
NCBI GI	g2213590
BLAST score	200
E value	2.0e-15
Match length	86
% identity	44
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	192448
Contig ID	6530_1.R1039
5'-most EST	g5044633
Method	BLASTX
NCBI GI	g3548804
BLAST score	576
E value	3.0e-59
Match length	233
% identity	49
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	192449
Contig ID	6538_1.R1039
5'-most EST	LIB3135-055-Q1-K1-D6
Method	BLASTX
NCBI GI	g4559358
BLAST score	401
E value	8.0e-39
Match length	100
% identity	75
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	192450
Contig ID	6539_1.R1039
5'-most EST	uC-gsflnu33B001h03b1
Method	BLASTX
NCBI GI	g71498
BLAST score	389
E value	1.0e-37
Match length	117

% identity	65
NCBI Description	heat shock protein 17.7 - garden pea

Seq. No.	192451
Contig ID	6540_1.R1039
5'-most EST	LIB3196-023-P1-M1-C12
Method	BLASTX
NCBI GI	g1170851
BLAST score	399
E value	1.0e-38
Match length	174
% identity	48
NCBI Description	MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A) >gi|1083410|pir||A54408 mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - mouse >gi|474280 (U04299) mannosyl-oligosaccharide alpha-1,2-mannosidase [Mus musculus]

Seq. No.	192452
Contig ID	6542_1.R1039
5'-most EST	LIB3197-016-P1-M1-B5

Seq. No.	192453
Contig ID	6544_1.R1039
5'-most EST	LIB3148-013-Q1-K1-F9
Method	BLASTX
NCBI GI	g2789466
BLAST score	149
E value	2.0e-09
Match length	105
% identity	31
NCBI Description	(AB008798) nuclear pore complex glycoprotein p62 [Oncorhynchus mykiss]

Seq. No.	192454
Contig ID	6545_1.R1039
5'-most EST	uC-gsronu33B029b02b1
Method	BLASTX
NCBI GI	g3080414
BLAST score	742
E value	1.0e-78
Match length	185
% identity	83
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	192455
Contig ID	6546_1.R1039
5'-most EST	LIB3083-099-Q1-L1-H4

Seq. No.	192456
Contig ID	6555_1.R1039
5'-most EST	LIB3189-048-P1-K1-F3
Method	BLASTX
NCBI GI	g541951
BLAST score	554
E value	7.0e-57

Match length	167
% identity	68
NCBI Description	SPCP2 protein - soybean >gi|310578 (L12258) nodulin-26 [Glycine max]

Seq. No.	192457
Contig ID	6556_1.R1039
5'-most EST	g5049193
Method	BLASTX
NCBI GI	g3080420
BLAST score	1038
E value	1.0e-113
Match length	325
% identity	62
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	192458
Contig ID	6557_1.R1039
5'-most EST	LIB3147-007-Q1-K1-D9
Method	BLASTX
NCBI GI	g4539292
BLAST score	443
E value	1.0e-43
Match length	93
% identity	87
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	192459
Contig ID	6557_2.R1039
5'-most EST	uC-gsflnu33B137g11b1
Method	BLASTX
NCBI GI	g4539292
BLAST score	452
E value	8.0e-45
Match length	96
% identity	86
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	192460
Contig ID	6557_3.R1039
5'-most EST	LIB3197-049-Q1-M1-G6
Method	BLASTX
NCBI GI	g4539292
BLAST score	452
E value	1.0e-44
Match length	96
% identity	86
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	192461
Contig ID	6558_1.R1039
5'-most EST	LIB3145-028-Q1-K1-D9

Seq. No.	192462
Contig ID	6558_2.R1039
5'-most EST	LIB3083-091-Q1-L1-G5
Method	BLASTX
NCBI GI	g586797
BLAST score	278
E value	3.0e-24
Match length	194
% identity	33
NCBI Description	HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III

Seq. No.	192463
Contig ID	6565_1.R1039
5'-most EST	LIB3083-051-Q1-L1-D11
Method	BLASTX
NCBI GI	g2541876
BLAST score	369
E value	3.0e-35
Match length	142
% identity	54
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	192464
Contig ID	6566_1.R1039
5'-most EST	uC-gsf1nu33B049g12b1
Method	BLASTX
NCBI GI	g2190992
BLAST score	391
E value	6.0e-38
Match length	121
% identity	64
NCBI Description	(AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No.	192465
Contig ID	6568_1.R1039
5'-most EST	LIB3083-051-Q1-L1-D3

Seq. No.	192466
Contig ID	6570_1.R1039
5'-most EST	uC-gsronu33B017a07b1

Seq. No.	192467
Contig ID	6572_1.R1039
5'-most EST	LIB3083-051-Q1-L1-D7

Seq. No.	192468
Contig ID	6573_1.R1039
5'-most EST	g5049036
Method	BLASTX
NCBI GI	g3395432
BLAST score	1337
E value	1.0e-148
Match length	315
% identity	80
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 192469
Contig ID 6574_1.R1039
5'-most EST LIB3189-002-P1-K1-A11
Method BLASTX
NCBI GI g2431769
BLAST score 254
E value 1.0e-21
Match length 111
% identity 51
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 192470
Contig ID 6574_2.R1039
5'-most EST LIB3147-007-Q1-K1-F2

Seq. No. 192471
Contig ID 6574_3.R1039
5'-most EST LIB3166-001-Q1-K1-B5

Seq. No. 192472
Contig ID 6574_4.R1039
5'-most EST LIB3197-047-Q1-M1-F9
Method BLASTX
NCBI GI g2431769
BLAST score 233
E value 2.0e-23
Match length 77
% identity 79
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 192473
Contig ID 6574_5.R1039
5'-most EST uC-gsronu33B150a07b1
Method BLASTX
NCBI GI g2431769
BLAST score 201
E value 1.0e-15
Match length 56
% identity 70
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 192474
Contig ID 6574_6.R1039
5'-most EST LIB3166-035-P1-K1-B1
Method BLASTX
NCBI GI g2431769
BLAST score 228
E value 6.0e-19
Match length 56
% identity 79
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 192475
Contig ID 6574_7.R1039
5'-most EST uC-gsflnu33B071a09b1

Seq. No.	192476
Contig ID	6576_1.R1039
5'-most EST	g5045297
Method	BLASTX
NCBI GI	g541800
BLAST score	806
E value	1.0e-157
Match length	294
% identity	94
NCBI Description	protein kinase (EC 2.7.1.37) cdc2-Pa - Norway spruce >gi|454980|emb|CAA54746| (X77680) cdc2Pa [Picea abies]

Seq. No.	192477
Contig ID	6576_2.R1039
5'-most EST	LIB3083-051-Q1-L1-E10
Method	BLASTX
NCBI GI	g1377890
BLAST score	249
E value	3.0e-21
Match length	52
% identity	96
NCBI Description	(L77083) cdc2 gene product [Nicotiana tabacum]

Seq. No.	192478
Contig ID	6580_1.R1039
5'-most EST	uC-gsflnu33B093b07b1
Method	BLASTX
NCBI GI	g3935167
BLAST score	466
E value	2.0e-46
Match length	98
% identity	93
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No.	192479
Contig ID	6580_2.R1039
5'-most EST	uC-gsronu33B156g12b1
Method	BLASTX
NCBI GI	g3935167
BLAST score	555
E value	8.0e-57
Match length	122
% identity	89
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No.	192480
Contig ID	6583_1.R1039
5'-most EST	uC-gsflmaxxa057c06b1

Seq. No.	192481
Contig ID	6585_1.R1039
5'-most EST	LIB3083-051-Q1-L1-E9

Seq. No.	192482
Contig ID	6590_1.R1039
5'-most EST	uC-gsflmaxxa042d08b1
Method	BLASTX

NCBI GI	g456568
BLAST score	787
E value	6.0e-84
Match length	148
% identity	98
NCBI Description	(L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No.	192483
Contig ID	6590_2.R1039
5'-most EST	g5045420
Method	BLASTX
NCBI GI	g456568
BLAST score	787
E value	7.0e-84
Match length	148
% identity	98
NCBI Description	(L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No.	192484
Contig ID	6590_3.R1039
5'-most EST	LIB3146-025-Q1-K1-C7
Method	BLASTX
NCBI GI	g2130088
BLAST score	166
E value	1.0e-11
Match length	34
% identity	91
NCBI Description	ubiquitin conjugating enzyme - rice >gi|1373001 (U15971) ubiquitin conjugating enzyme [Oryza sativa]

Seq. No.	192485
Contig ID	6591_1.R1039
5'-most EST	LIB3189-011-P1-K1-D9

Seq. No.	192486
Contig ID	6595_1.R1039
5'-most EST	LIB3083-113-Q1-L1-B5
Method	BLASTX
NCBI GI	g132825
BLAST score	162
E value	5.0e-11
Match length	67
% identity	54
NCBI Description	50S RIBOSOMAL PROTEIN CL25, CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein PsCL25 precursor, chloroplast - garden pea >gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein (AA -30 to 74) [Pisum sativum]

Seq. No.	192487
Contig ID	6610_1.R1039
5'-most EST	LIB3083-065-Q1-L1-H2
Method	BLASTX
NCBI GI	g3927825
BLAST score	1180
E value	1.0e-130
Match length	256
% identity	88

NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	192488
Contig ID	6614_1.R1039
5'-most EST	LIB3083-051-Q1-L1-H5
Method	BLASTX
NCBI GI	g4426565
BLAST score	341
E value	1.0e-31
Match length	215
% identity	33
NCBI Description	(AF031483) unknown [Rattus norvegicus]

Seq. No.	192489
Contig ID	6615_1.R1039
5'-most EST	LIB3165-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2493895
BLAST score	1177
E value	1.0e-129
Match length	271
% identity	85
NCBI Description	CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi|1071911|pir||S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi|540497|dbj|BAA05965| (D28777) cysteine synthase [Citrullus lanatus]

Seq. No.	192490
Contig ID	6618_1.R1039
5'-most EST	LIB3083-086-Q1-L1-D11
Method	BLASTX
NCBI GI	g2827141
BLAST score	228
E value	1.0e-18
Match length	106
% identity	53
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	192491
Contig ID	6621_1.R1039
5'-most EST	LIB3083-052-Q1-L1-A11

Seq. No.	192492
Contig ID	6626_1.R1039
5'-most EST	LIB3166-022-P1-K1-G9
Method	BLASTN
NCBI GI	g1890316
BLAST score	44
E value	5.0e-15
Match length	162
% identity	86
NCBI Description	A.thaliana mRNA for peroxidase ATP26a, partial

Seq. No.	192493

Contig ID 6628_1.R1039
5'-most EST LIB3148-052-Q1-K1-B8
Method BLASTX
NCBI GI g1565225
BLAST score 743
E value 2.0e-78
Match length 236
% identity 64
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No. 192494
Contig ID 6631_1.R1039
5'-most EST LIB3083-052-Q1-L1-B10
Method BLASTX
NCBI GI g4204315
BLAST score 491
E value 2.0e-49
Match length 160
% identity 58
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 192495
Contig ID 6632_1.R1039
5'-most EST LIB3083-052-Q1-L1-B11
Method BLASTX
NCBI GI g4204265
BLAST score 746
E value 2.0e-79
Match length 177
% identity 77
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 192496
Contig ID 6635_1.R1039
5'-most EST LIB3120-036-Q1-K1-E8
Method BLASTX
NCBI GI g3650030
BLAST score 378
E value 4.0e-36
Match length 135
% identity 61
NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 192497
Contig ID 6638_1.R1039
5'-most EST LIB3083-052-Q1-L1-B6
Method BLASTX
NCBI GI g4469020
BLAST score 454
E value 3.0e-45
Match length 123
% identity 73
NCBI Description (AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 192498
Contig ID 6643_1.R1039

5'-most EST	uC-gsflnu33B128h12b1
Seq. No.	192499
Contig ID	6650_1.R1039
5'-most EST	LIB3146-022-Q1-K1-C10
Seq. No.	192500
Contig ID	6651_1.R1039
5'-most EST	LIB3083-052-Q1-L1-C8
Seq. No.	192501
Contig ID	6657_1.R1039
5'-most EST	LIB3272-016-P1-K1-A6
Method	BLASTX
NCBI GI	g3421094
BLAST score	1136
E value	1.0e-124
Match Length	279
% identity	78
NCBI Description	(AF043527) 20S proteasome subunit PAF2 [Arabidopsis thaliana]
Seq. No.	192502
Contig ID	6657_2.R1039
5'-most EST	uC-gsflnu33B024g12b1
Method	BLASTX
NCBI GI	g464444
BLAST score	538
E value	3.0e-55
Match length	118
% identity	89
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi|541889|pir||S39900 proteasome - Arabidopsis thaliana >gi|166830 (M98495) proteasome [Arabidopsis thaliana]
Seq. No.	192503
Contig ID	6658_1.R1039
5'-most EST	LIB3197-052-Q1-M1-D1
Method	BLASTX
NCBI GI	g2995953
BLAST score	311
E value	2.0e-28
Match length	99
% identity	63
NCBI Description	(AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
Seq. No.	192504
Contig ID	6659_1.R1039
5'-most EST	LIB3083-052-Q1-L1-D6
Seq. No.	192505
Contig ID	6660_1.R1039
5'-most EST	LIB3083-052-Q1-L1-D7
Method	BLASTX
NCBI GI	g1076580
BLAST score	331

E value	7.0e-31
Match length	117
% identity	54
NCBI Description	alcohol dehydrogenase homolog ADH3b - tomato >gi|913446|bbs|160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum]

Seq. No.	192506
Contig ID	6662_1.R1039
5'-most EST	g5044831
Method	BLASTX
NCBI GI	g2739046
BLAST score	697
E value	6.0e-84
Match length	228
% identity	63
NCBI Description	(AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]

Seq. No.	192507
Contig ID	6664_1.R1039
5'-most EST	LIB3083-052-Q1-L1-E10
Method	BLASTX
NCBI GI	g1730630
BLAST score	280
E value	9.0e-25
Match length	167
% identity	38
NCBI Description	HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III >gi|458956 (U00031) similar to cytoplasmic domain of synaptobrevin [Caenorhabditis elegans]

Seq. No.	192508
Contig ID	6665_1.R1039
5'-most EST	LIB3189-034-P1-K1-A2
Method	BLASTX
NCBI GI	g1914683
BLAST score	1133
E value	1.0e-124
Match length	383
% identity	62
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	192509
Contig ID	6666_1.R1039
5'-most EST	uC-gsflnu33B066e07b1
Method	BLASTX
NCBI GI	g464621
BLAST score	718
E value	9.0e-76
Match length	232
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi|280374|pir||S28586 ribosomal protein ML16 - common ice plant >gi|19539|emb|CAA49175| (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	192510
Contig ID	6666_2.R1039
5'-most EST	LIB3146-049-Q1-K1-B9
Method	BLASTX
NCBI GI	g4455129
BLAST score	385
E value	7.0e-37
Match length	126
% identity	56
NCBI Description	(AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

Seq. No.	192511
Contig ID	6666_3.R1039
5'-most EST	LIB3135-046-Q1-K1-B6
Method	BLASTX
NCBI GI	g2498706
BLAST score	171
E value	6.0e-12
Match length	59
% identity	47
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi|1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi|3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	192512
Contig ID	6666_7.R1039
5'-most EST	uC-gsflnu33B002e08b1

Seq. No.	192513
Contig ID	6667_1.R1039
5'-most EST	LIB3135-054-Q1-K1-C3
Method	BLASTN
NCBI GI	g3421122
BLAST score	106
E value	4.0e-52
Match length	569
% identity	80
NCBI Description	Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA, complete cds

Seq. No.	192514
Contig ID	6668_1.R1039
5'-most EST	LIB3272-047-P1-K1-F7
Method	BLASTX
NCBI GI	g3421123
BLAST score	952
E value	1.0e-103
Match length	215
% identity	83
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	192515
Contig ID	6669_1.R1039
5'-most EST	LIB3147-024-Q1-K1-A2

Method	BLASTX
NCBI GI	g398994
BLAST score	774
E value	2.0e-82
Match length	181
% identity	82
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi|166313 (M97961) tomato and apple ACC oxidase homologue [Actinidia deliciosa]

Seq. No.	192516
Contig ID	6669_2.R1039
5'-most EST	uC-gsronu33B155e04b2
Method	BLASTX
NCBI GI	g4090533
BLAST score	528
E value	6.0e-54
Match length	113
% identity	86
NCBI Description	(U68215) ACC oxidase [Carica papaya]

Seq. No.	192517
Contig ID	6669_3.R1039
5'-most EST	LIB3147-028-Q1-K1-G12
Method	BLASTX
NCBI GI	g129646
BLAST score	543
E value	3.0e-88
Match length	237
% identity	68
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) (RIPENING-RELATED PROTEIN PAVOE3) >gi|99498|pir||S11879 ethylene-forming enzyme - avocado >gi|166945 (M32692) ripening-related protein (pAVOe3) [Persea americana]

Seq. No.	192518
Contig ID	6669_4.R1039
5'-most EST	uC-gsflmaxxa096g09b1
Method	BLASTX
NCBI GI	g4090533
BLAST score	552
E value	1.0e-56
Match length	132
% identity	77
NCBI Description	(U68215) ACC oxidase [Carica papaya]

Seq. No.	192519
Contig ID	6672_1.R1039
5'-most EST	g5044433
Method	BLASTX
NCBI GI	g4006878
BLAST score	911
E value	1.0e-137
Match length	343
% identity	67
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	192520
Contig ID	6673_1.R1039
5'-most EST	g5044557

Seq. No.	192521
Contig ID	6674_1.R1039
5'-most EST	LIB3083-063-Q1-L1-B6
Method	BLASTX
NCBI GI	g3928089
BLAST score	372
E value	3.0e-35
Match length	137
% identity	55
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	192522
Contig ID	6674_2.R1039
5'-most EST	LIB3165-034-P1-K3-C11
Method	BLASTX
NCBI GI	g120658
BLAST score	1642
E value	0.0e+00
Match length	402
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi|66025|pir||DEPMNA glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - garden pea >gi|12159|emb|CAA36396| (X52148) GAPA [Pisum sativum]

Seq. No.	192523
Contig ID	6674_3.R1039
5'-most EST	LIB3165-047-Q1-K1-A4
Method	BLASTX
NCBI GI	g20729
BLAST score	596
E value	8.0e-62
Match length	148
% identity	79
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	192524
Contig ID	6674_4.R1039
5'-most EST	LIB3120-013-Q1-K1-A6
Method	BLASTX
NCBI GI	g120659
BLAST score	692
E value	6.0e-73
Match length	168
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST >gi|81721|pir||B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi|829288|emb|CAA27845| (X04302) chloroplast GAPDH (233aa)

[Sinapis alba]

Seq. No.	192525
Contig ID	6674_9.R1039
5'-most EST	LIB3166-036-P1-K1-G1
Method	BLASTX
NCBI GI	g20729
BLAST score	433
E value	9.0e-43
Match length	117
% identity	75
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	192526
Contig ID	6678_1.R1039
5'-most EST	g5045242
Method	BLASTX
NCBI GI	g3668082
BLAST score	725
E value	1.0e-76
Match length	180
% identity	78
NCBI Description	(AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No.	192527
Contig ID	6680_1.R1039
5'-most EST	uC-gsronu33B116a11b1

Seq. No.	192528
Contig ID	6680_2.R1039
5'-most EST	LIB3165-037-P1-K1-C5

Seq. No.	192529
Contig ID	6680_3.R1039
5'-most EST	uC-gsflnu33B146h12b1

Seq. No.	192530
Contig ID	6681_1.R1039
5'-most EST	LIB3083-052-Q1-L1-F4
Method	BLASTX
NCBI GI	g4539383
BLAST score	596
E value	1.0e-61
Match length	207
% identity	56
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	192531
Contig ID	6686_1.R1039
5'-most EST	LIB3146-043-Q1-K1-F12
Method	BLASTN
NCBI GI	g4567259
BLAST score	41
E value	1.0e-13
Match length	164
% identity	94

NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	192532
Contig ID	6692_1.R1039
5'-most EST	LIB3197-034-Q1-M1-C2
Method	BLASTX
NCBI GI	g4263507
BLAST score	736
E value	1.0e-77
Match length	514
% identity	31
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	192533
Contig ID	6693_1.R1039
5'-most EST	LIB3165-023-P1-K1-F11
Method	BLASTX
NCBI GI	g3121825
BLAST score	959
E value	1.0e-104
Match length	242
% identity	81
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi|1498247|emb|CAA63910| (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	192534
Contig ID	6694_1.R1039
5'-most EST	LIB3083-052-Q1-L1-G6
Method	BLASTX
NCBI GI	g4115377
BLAST score	229
E value	8.0e-19
Match length	58
% identity	74
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	192535
Contig ID	6695_1.R1039
5'-most EST	LIB3197-048-Q1-M1-D10
Method	BLASTX
NCBI GI	g3236237
BLAST score	801
E value	7.0e-88
Match length	248
% identity	65
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	192536
Contig ID	6700_1.R1039
5'-most EST	uC-gsronu33B041e05b1
Method	BLASTX
NCBI GI	g3549666
BLAST score	357
E value	1.0e-33